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UTILITY PATENT APPLICATION TRANSMITTAL <i>(Only for new nonprovisional applications under 37 CFR 1.53(h))</i>	Attorney Docket No.	04983.0207.US00/38-10(15498)A	
	First Named Inventor or Application Identifier		CAO
	Title	Emericella Nidulans Genome Sequence and Uses Thereof	
	Express Mail Label No.		

APPLICATION ELEMENTS <i>See MPEP chapter 600 concerning utility patent application contents</i>	ADDRESS TO: Assistant Commissioner for Patents Box Patent Application Washington, DC 20231
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1. <input checked="" type="checkbox"/> *Fee Transmittal Form (Form PTO-1082) <i>(Submit an original and a duplicate for fee processing)</i>	6. <input type="checkbox"/> Microfiche Computer Program <i>(Appendix)</i>
2. <input checked="" type="checkbox"/> Specification [Total Pages 1686] <i>(preferred arrangement set forth below)</i> <ul style="list-style-type: none">- Descriptive title of the Invention- Cross References to Related Applications- Statement Regarding Fed sponsored R&D- Reference to Microfiche Appendix- Background of the Invention- Brief Summary of the Invention- Brief Description of the Drawings (if filed)- Detailed Description- Claims- Abstract of the Disclosure	7. Nucleotide and/or Amino Acid Sequence Submission <i>(if applicable, all necessary)</i> <ul style="list-style-type: none">a. <input checked="" type="checkbox"/> Computer Readable Copyb. <input checked="" type="checkbox"/> Paper Copy (identical to computer copy)c. <input checked="" type="checkbox"/> Statement verifying identity of above copies
<input type="checkbox"/> Drawing(s) <i>(35 USC 113)</i> [Total Sheets]	ACCOMPANYING APPLICATION PARTS 8. <input type="checkbox"/> Assignment Papers (cover sheet & document(s)) 9. <input type="checkbox"/> 37 CFR 3.73(b) Statement <input type="checkbox"/> Power of Attorney <i>(when there is an assignee)</i> 10. <input type="checkbox"/> English Translation Document <i>(if applicable)</i> 11. <input type="checkbox"/> Information Disclosure Statement (IDS)/PTO-1449 <input type="checkbox"/> Copies of IDS Citations 12. <input type="checkbox"/> Preliminary Amendment 13. <input checked="" type="checkbox"/> Return Receipt Postcard (MPEP 503) (Two) <i>(should be specifically itemized)</i> 14. <input type="checkbox"/> *Small Entity Statement(s) <input type="checkbox"/> Statement filed in prior application, Status still proper and desired 15. <input type="checkbox"/> Certified Copy of Priority Document(s) <i>(if foreign priority is claimed)</i> 16. <input checked="" type="checkbox"/> Other: Statement Regarding Sequence Submission
3. <input type="checkbox"/> Oath or Declaration [Total Pages] <ul style="list-style-type: none">a. <input type="checkbox"/> Newly executed (original or copy)b. <input type="checkbox"/> Copy from a prior application (37 CFR 1.63(d)) <i>(for continuation/divisional with Box 17 completed)</i> <i>[Note Box 5 below]</i>i. <input type="checkbox"/> DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).	
4. <input type="checkbox"/> Incorporation By Reference <i>(useable if Box 4b is checked)</i> The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.	
5. <input type="checkbox"/> Drawing(s) <i>(35 USC 113)</i> [Total Sheets]	
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17. If a **CONTINUING APPLICATION**, check appropriate box and supply the requisite information:
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Prior Application Information: Examiner: Group/Art Unit:

18. CORRESPONDENCE ADDRESS					
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Signature	<i>David R. Marsh</i>			Date	September 23, 1999

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Attorney Docket No. 04983.0207.US00/38-10(15498)A

ASSISTANT COMMISSIONER FOR PATENTS
 Washington, DC 20231

Sir:

Transmitted herewith for filing is the patent application of

Inventors: Yongwei CAO *et al.*

For: *Emericella Nidulans* Genome Sequence and Uses Thereof

Enclosed are:

- ☒ U.S. Utility Patent Application (consisting of 1,677 pages of description prior to the claims; 8 pages of claims, 1 page abstract and 31,579 pages of a sequence listing)
- ☒ CD-ROM containing the sequence listing
- ☒ Statement regarding Sequence Submission

This application is being filed without an executed Declaration.

The filing fee has been calculated as shown below:

(Col. 1)		(Col. 2)		SMALL ENTITY		OR	OTHER THAN A SMALL ENTITY	
FOR	NO. FILED	NO. EXTRA		RATE	FEE		RATE	FEE
BASIC FEE					365.00	OR		760.00
TOTAL CLAIMS	46 - 20 =	* 26		x 9 =		OR	x 18 =	468.00
INDEP. CLAIMS	14 - 3 =	* 11		x 39 =		OR	x 78 =	858.00
<input type="checkbox"/> MULTIPLE DEPENDENT CLAIM PRESENTED				+ 130 =		OR	+ 260 =	
*If the difference in Col. 1 is less than zero, enter "0" in Col. 2				TOTAL	\$	OR	TOTAL	\$ 2086.00

- ☐ Please charge by Deposit Account No. 08-3038 in the amount of _____. A duplicate copy of this sheet is attached.
- ☒ Howrey & Simon Check No. 316494 in the amount of \$ 2,086.00 to cover the basic filing fee and extra claims fee is enclosed.
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- ☒ Any additional filing fees required under 37 C.F.R. § 1.16.
- ☒ Any patent application processing fees under 37 C.F.R. § 1.17.
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- ☐ Any patent application processing fees under 37 C.F.R. § 1.17.
- ☐ The issue fee set in 37 C.F.R. § 1.18 at or before mailing of the Notice of Allowance, pursuant to 37 C.F.R. § 1.311(b).
- ☐ Any filing fees under 37 C.F.R. § 1.16 for presentation of extra claims.

Date: September 23, 1999



David R. Marsh (Reg. No. 41,408)

September 23, 1999

Box Patent Application

Assistant Commissioner for Patents
Washington, D.C. 20231

Re: U.S. Non-Provisional Utility Patent Application
Application No.: To Be Assigned
Filed: Herewith
For: ***Emericella Nidulans* Genome Sequence
and Uses Thereof**
Inventors: Yongwei CAO *et al.*
Atty. Docket: 04983.0207.US00/38-10(15498)A

Sir:

The following documents are forwarded herewith for appropriate action by the U.S.
Patent and Trademark Office:

1. Utility Patent Application Transmittal (PTO/SB/05);
2. Form PTO-1082 (in duplicate);
3. U.S. Utility Patent Application entitled:

***Emericella Nidulans* Genome Sequence and Uses Thereof**

and naming as inventors:

**Yongwei CAO, Azita GHODSSI, Gregory J. HINKLE, James McININCH,
William E. TIMBERLAKE, and Jaehyuk YU**

the application consisting of:

- a. A specification containing:
 - (i) 1,677 pages of a description prior to the claims;
 - (ii) 8 pages of claims (46 claims);
 - (iii) a one (1) page abstract; and
 - (iv) 31,579 pages of a sequence listing;

4. A CD-ROM containing the sequence listing;
5. Statement Regarding Sequence Submission;
6. Howrey & Simon Check No. 316494 in the amount of \$2,086.00 to cover the basic filing fee; and
7. Two (2) return postcards.

It is respectfully requested that, of the two attached postcards, one be stamped with the filing date of these documents and returned to our courier, and the other, prepaid postcard, be stamped with the filing date and unofficial application number and returned as soon as possible.

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the sequence listing and the computer readable copy of the sequence listing submitted herewith in the above application are the same.

The U.S. Patent and Trademark Office is hereby authorized to charge any fee deficiency, or credit any overpayment, to our Deposit Account No. 08-3038. A duplicate copy of this letter is enclosed.

Respectfully submitted,



David R. Marsh (Reg. No. 41,408)

Enclosures

EMERICELLA NIDULANS GENOME SEQUENCE AND USES THEREOF

This application claims priority under 35 U.S.C §119(e) of U.S. Provisional Applications Nos. 60/ 101,665; 60/101,666; 60/102,358; 60/113,361; 60/126,265; 60/130,189; 60/130,190; 60/132,861; 60/138,103; and 60/149,882, the disclosures of which provisional applications are
5 incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

Included in the disclosure are nucleic acid molecules representing the genome of the filamentous fungus, *Emericella nidulans* (previously and still sometimes called *Aspergillus*
10 *nidulans*) and, in particular, to nucleic acid molecules having nucleic acid sequences corresponding to genes, promoters, other regulatory elements, and introns found in the *E. nidulans* genome, a specific set of genes of *E. nidulans* and a set of primers based on the *E. nidulans* genes. Also disclosed are homologous nucleic acid molecules, complementary nucleic acid molecules, polypeptides expressed by such genes, constructs comprising such promoters,
15 regulatory elements and/or genes, transformed cells and organisms comprising such genes and/or promoters and regulatory elements, primers useful for replicating parts of such genes and nucleic acid molecules, computer readable media comprising sets of such nucleic acid sequences, polypeptides and primers, collections of nucleic acid molecules and methods of using such molecules and sequences including the use of collections of nucleic acid molecules in genetic
20 research and clinical analysis, *e.g.* for gene expression.

BACKGROUND OF THE INVENTION

Filamentous fungi have a complex multicellular organization involving production of highly specialized cell types as part of their normal asexual and sexual lifecycles. Fungi as experimental systems are good models for plant and animal cell functions because of their evolutionary relatedness. *E. nidulans* is a model eukaryotic organism and has been used extensively to address fundamental questions of biology. *E. nidulans* is a more complex organism than yeast and has many genes which have a similar function to genes found in plants and animals. This filamentous fungus has been employed in investigations into a variety of genetic phenomena including the mechanisms regulating carbon and nitrogen metabolism, cell cycle, cytoskeletal functions, and development. A set of nucleic acid molecules representing substantially most of the genes in the *E. nidulans* genome is useful in transcription profiling work to find, identify and characterize counterpart genes in other species, particularly microbial and plant species. For instance, it is possible to identify unknown plant gene function by studying a similar (homologous) gene in a microbe in which genetic modification can more easily be done. That is, if unknown genes are disrupted or overexpressed, transcription profiling can be carried out to understand effects of the genetic modification.

Moreover, chemical/drug discovery can be practiced using such transcription profiling with nucleic acids molecules of the *E. nidulans* genome. And, because many human or plant pathogens are filamentous fungi and *E. nidulans* is a model organism for filamentous fungi, transcription profiling with genome-wide expression of the *E. nidulans* genome is an efficient way to understand the action of such pathogens and their secondary metabolites, e.g. mycotoxins which can be deleterious to food and feed supplies. In addition environmental stress studies of

the *E. nidulans* genome will provide insight into related mechanisms in plants, *e.g.* yield, stability, thermal resistance, water/drought tolerance, *etc.*

Nucleic acid molecules comprising the *E. nidulans* genome disclosed herein were identified and isolated from a sample of filamentous fungus identified as *Aspergillus nidulans*,
5 FGSC Number A4, obtained from the Fungal Genetics Stock Center (FGSC) at the University of Kansas Medical Center, Kansas City, Kansas. It has been determined that this fungus is more properly named *Emericella, nidulans*. As used herein the terms *Emericella nidulans*, *E. nidulans*, *Aspergillus nidulans* and *A. nidulans* refer to the filamentous fungus previously and still sometimes called *Aspergillus nidulans*.

10 Nucleic acid sequences of a species, *e.g.* the *E. nidulans*, can be generated by random shotgun sequencing of cloned genomic DNA and assembled into longer lengths of contiguous sequence (contigs). The final data set from an assembly process comprises a collection of sequences, which includes the contigs resulting from linking of two or more overlapping sequences as well as singleton nucleic acid sequences, *i.e.* trace sequences which are not
15 incorporated into contigs. Such sequences can be screened for genes, *e.g.* full length or substantially full length or partial length genes. Screening methods include homology searches against databases of known genes and predictive methods using algorithms which infer the presence and extent of a gene.

The nucleic acid sequences disclosed herein are believed to represent substantially all, or
20 at least a major part, of the genes in the *E. nidulans* genome. Genome sequence information from *E. nidulans* permits identification of genetic sequences from other organisms, including plants, mammals such as humans, bacteria, other filamentous fungi and non-filamentous fungi such as a yeast, *e.g.* by comparison of such sequences with *E. nidulans* sequences. The

availability of a substantially complete set genes or partial genes of the *E. nidulans* genome permits the definition of primers for fabricating representative nucleic acid molecules of the genome which can be used on microarrays facilitating transcription profile studies. In addition the identification of the *E. nidulans* genome permits the fabrication of a wide variety of DNA
5 constructs useful for imparting unique genetic properties into transgenic organisms. These and other advantages attendant with the various aspects of this invention will be apparent from the following description of the invention and its various embodiments.

SUMMARY OF THE INVENTION

10 The present invention contemplates and provides a substantial part of the genome of the filamentous fungus *Emmericella nidulans*. One aspect of the invention is a set of more than 16,000 contig and singleton sequences comprising coding sequence as well as promoters, other regulatory elements and introns represented by SEQ ID NO: 1 through SEQ ID NO: 16206. Contigs in SEQ ID NO: 1 through SEQ ID NO: 16206 are recognized as those sequences whose
15 designations begin with ANI61C or ANI50C. Singleton sequences are recognized as those having designations which begin with ANI61S or ANI50S. Thus, a subset of the nucleic acid molecules of this invention comprises promoters and/or other regulatory elements of the *E. nidulans* genome as present in SEQ ID NO: 1 through SEQ ID NO: 16206 or complements thereof.

20 Another aspect of this invention comprises a set of about 12,000 genes or partial genes of the *E. nidulans* genome including genes represented by SEQ ID NO: 16207 through SEQ ID NO: 27905 and a small set of previously reported genes represented by SEQ ID NO: 27906 through SEQ ID NO: 28165. As used herein, a substantially complete set of genes for an

organism is referred to as a unigene set. Thus, as used herein reference is made to specific genes comprising the unigene set of *E. nidulas* as "ENUxxxxx" where ENU is an acronym for *Emericella nidulans unigene* and xxxxx represents a number. Thus, ENU00001 to ENU27905 are used to designate the genes of *E. nidulas* identified herein; and, ENU27906 to ENU28165 are used to designate the previously reported genes of *E. nidulas*. Moreover, the term "ENU" by itself is also used herein to mean any of the nucleic acid molecules comprising genes or partial genes of the unigene set for *E. nidulas*. More particularly the term "ENU of this invention" as used herein means a nucleic acid molecule representing a gene or partial gene of *E. nidulas* disclosed herein selected from the group consisting of ENU00001 to ENU27905.

10 The present invention also contemplates and provides substantially purified nucleic acid molecules comprising the ENUs and other nucleic acid molecules of this invention as well as molecules which are complementary to, and capable of specifically hybridizing to, the ENU or its complement.

15 The present invention also contemplates and provides substantially purified nucleic acids molecules which are homologous to the nucleic acid molecules of this invention including, for example, those which are homologous to the ENUs of this invention, e.g. a plurality of related sets of homologous nucleic acid molecules in other species which are homologous to the ENUs.

20 The present invention also contemplates and provides substantially purified protein, or polypeptide fragments thereof, which are encoded by cDNA associated with the ENUs of the present invention.

The present invention also contemplates and provides constructs comprising promoters, regulatory elements and/or the ENUs which are useful in making transgenic cells or organisms. In particular this invention also provides transformed cell or organism having a nucleic acid

molecule which comprises: (a) a promoter region which functions in the cell to cause the production of a mRNA molecule; which is linked to (b) a structural nucleic acid molecule, which is linked to (c) a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule, where components (a) and/or (b) are selected from *E. nidulans* nucleic acid sequences provided herein and more preferably selected *E. nidulans* nucleic acid sequences from the group consisting of ENU00001 to ENU27905.

Still another aspect of this invention is a set (and subsets thereof) of about 24,000 primers for the ENUs of this invention, including a specific subset of about 16,000 primers represented by SEQ ID NO: 28166 through SEQ ID NO: 44345 which can be used to generate and isolate nucleic acid molecules representative ENUs of this invention and homologs thereof in other non-*E. Nidulans* species. The nucleic acids molecules of this invention including primers represent a useful tool in genetic research not only for the species *E. nidulans*, but also for other fungal species, other microorganisms and life forms with more differentiated cell structure such as plants and animals. The present invention also contemplates and provides primer pairs for replicating or identifying parts of the ENUs.

The present invention also contemplates and provides computer readable media having recorded thereon one or more of the nucleotide sequences provided by this invention and methods for using such media, *e.g.* in searching to identify genes associated with nucleic acid sequences.

The present invention also contemplates and provides collections of nucleic acid molecules, including oligonucleotides, representing the *E. nidulans* genome including collections on solid substrates, *e.g.* substrates having attached thereto in array form nucleic acid molecules

or oligonucleotides representing genes of the *E. nidulans* genome. The invention also contemplates and provides methods of using such collections and arrays, *e.g.* in transcription profiling analysis. The present invention also contemplates and provides methods for using the nucleic acid molecules of this invention, *e.g.* for identifying genetic material and/or determining gene expression by hybridizing expressed and labeled nucleic acid molecules or fragments thereof to arrayed collections of the nucleic acid molecules of this invention.

The present invention also contemplates and provides oligonucleotides which are identical or complementary to a sequence of similar length for an ENU. Such oligonucleotides are useful, for example, for hybridizing to and identifying nucleic acid molecules which are homologous and/or complementary to the ENUs of the present invention.

DETAILED DESCRIPTION OF THE INVENTION

As used herein, a nucleic acid molecule and/or polypeptide molecule, be it a naturally occurring molecule or otherwise, may be "substantially purified", if the molecule is separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

The ENUs of this invention and other nucleic acid molecules and/or polypeptide molecules of the present invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid

molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic, and thus involve the capacity of the agent to mediate a chemical reaction or response.

As used herein the term "polypeptide" means a protein or fragment thereof expressed by
5 a nucleic acid molecule in a cell.

The ENUs of this invention and other nucleic acid molecules of the present invention may also be recombinant. As used herein, the term recombinant means any molecule (*e.g.* DNA, peptide *etc.*), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

10 It is understood that the nucleic acid molecules of the present invention may be labeled with reagents that facilitate detection of the agent, *e.g.* fluorescent labels as disclosed in US Patent 4,653,417, chemical labels as disclosed in U.S. Patents 4,582,789 and 4,563,417 and modified bases as disclosed in US Patent 4,605,735, all of which are incorporated herein by reference in their entirety.

15 The term "oligonucleotide" as used herein refers to short nucleic acid molecules useful, *e.g.* for hybridizing probes, nucleotide array elements or amplification primers. Oligonucleotide molecules are comprised of two or more nucleotides, *i.e.* deoxyribonucleotides or ribonucleotides, preferably more than five and up to 30 or more. The exact size will depend on many factors, which in turn depend on the ultimate function or use of the oligonucleotide.

20 Oligonucleotides can comprise ligated natural nucleic molecules acids or synthesized nucleic acid molecules and comprise between 5 to 150 nucleotides or between about 15 and about 100 nucleotides, or preferably up to 100 nucleotides, and even more preferably between 15 to 30

nucleotides or most preferably between 18-25 nucleotides, identical or complementary to a sequence of similar length for an ENU.

This invention provides oligonucleotides specific for ENU sequences. Such oligonucleotides may be nucleic acid elements for use on solid arrays (*e.g.* synthesized or spotted) or primers for amplification of ENUs of this invention. Such primers for use in polymerase chain reaction (PCR) primers are preferably designed with the goal of amplifying nucleic acids from either the 3' or the 5' end of an ENU or a fragment of an ENU, *e.g.* about 500 to 800 bp of nucleic acids from the at the 3' end of such a nucleic acid molecule.

The term "primer" as used herein refers to a nucleic acid molecule, preferably an oligonucleotide whether derived from a naturally occurring molecule, such as one isolated from a restriction digest or one produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced, *i.e.*, in the presence of nucleotides and an agent for polymerization such as DNA polymerase and at a suitable temperature and pH. The primer is preferably single stranded for maximum efficiency in amplification, but may alternatively be double stranded. If double stranded, the primer is first treated to separate its strands before being used to prepare extension products. Preferably, the primer is an oligodeoxyribonucleotide. The primer must be sufficiently long to prime the synthesis of extension products in the presence of the agent for polymerization. The exact lengths of the primers will depend on many factors, including temperature and source of primer. For example, depending on the complexity of the target sequence, the oligonucleotide primer typically contains at least 15, more preferably 18 nucleotides, which are identical or complementary to the template and optionally a tail of variable length which need not match the template. The length

of the tail should not be so long that it interferes with the recognition of the template. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

The primers herein are selected to be "substantially" complementary to the different strands of each specific sequence to be amplified. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the strand to be amplified to hybridize therewith and thereby form a template for synthesis of the extension product of the other primer. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline ([www-STSPipeline](http://www-genome.wi.mit.edu/cgi-bin/www-STSPipeline)), or GeneUp (Pesole *et al.*, *BioTechniques* 25:112-123 (1998)), for example, can be used to identify potential PCR primers. Exemplary primers include primers that are 18 to 50 bases long, where at least between 18 to 25 bases are identical or complementary to at least 18 to 25 bases segment of the template sequence. Preferred template sequences for such primers are selected from a fragment of any one of SEQ ID NO: 16207 through SEQ ID NO: 28905 or complements thereof.

This invention also contemplates and provides primer pairs for amplification of nucleic acid molecules representing the ENUs. As used herein "primer pair" means a set of two oligonucleotide primers based on two separated sequence segments of a target nucleic acid

sequence. One primer of the pair is a "forward primer" or "5' primer" having a sequence which is identical to the more 5' of the separated sequence segments. The other primer of the pair is a "reverse primer" or "3' primer" having a sequence which is complementary to the more 3' of the separated sequence segments. A primer pair allows for amplification of the nucleic acid

5 sequence between and including the separated sequence segments. Optionally, each primer pair can comprise additional sequences, *e.g.* universal primer sequences or restriction endonuclease sites, at the 5' end of each primer, *e.g.* to facilitate cloning, DNA sequencing, or reamplification of the target nucleic acid sequence.

Nucleic acid molecules of the present invention include those having a nucleic acid
 10 sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 44,435 and complements thereof and fragments of either. Preferred nucleic acid molecules include those having a nucleic acid sequence selected from the following groups: SEQ ID NO: 16207 through SEQ ID NO: 27905 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 26804 or complements thereof; SEQ ID NO: 26000 through SEQ ID NO: 26804 or complements thereof;
 15 SEQ ID NO: 16207 through SEQ ID NO: 25999 or complements thereof; SEQ ID NO: 24035 through SEQ ID NO: 25999 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 24034 or complements thereof; SEQ ID NO: 22710 through SEQ ID NO: 24034 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 22709 or complements thereof; ; SEQ ID NO: 17681 through SEQ ID NO: 22709 or complements thereof; SEQ ID NO: 16207 through SEQ ID
 20 NO: 17680 or complements thereof; SEQ ID NO: 17618 through SEQ ID NO: 17680 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17617 or complements thereof; SEQ ID NO: 17295 through SEQ ID NO: 17617 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17294 or complements thereof. Other preferred nucleic acid molecules

include any of the above groups but where such groups also include fragments of such sequences.

Nucleic acid molecules or fragments thereof are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. As used herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure along a sufficient portion of the molecule to allow for stable binding under laboratory hybridizing conditions. A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are said to exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), and by Haymes *et al.*, *Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, DC (1985), the entirety of both of which are herein incorporated by reference. Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule to serve as a primer or probe it need only be

sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 X SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 X SSC at 50°C to a high stringency of about 0.2 X SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

Preferred embodiments of the nucleic acid of this invention will specifically hybridize to one or more of the ENUs of this invention or complements thereof under low stringency conditions, for example at about 2.0 X SSC and about 50°C. In a particularly preferred embodiment, a nucleic acid of the present invention will include those nucleic acid molecules that specifically hybridize to one or more of the ENUs of this invention or complements thereof under moderate stringency conditions. In an especially preferred embodiment, a nucleic acid of the present invention will include those nucleic acid molecules that specifically hybridize to one or more of the ENUs of this invention or complements thereof under high stringency conditions.

In another aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 90% sequence identity with one or more of the ENUs of this invention or complements thereof. In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 95%

sequence identity with one or more of the ENUs of this invention or complements thereof. In a more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 98% sequence identity with one or more of the ENUs of this invention or complements thereof. In an even more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 99% sequence identity with one or more of the ENUs of this invention or complements thereof.

The present invention also encompasses the use of nucleic acids of the present invention in recombinant constructs. Using methods known to those of ordinary skill in the art, an ENU sequence and/or a promoter sequence of the invention can be inserted into constructs which can be introduced into a host cell of choice for expression of the encoded protein if an ENU is used or for use of an *E. nidulans* promoter to direct expression of a heterologous protein. Potential host cells include both prokaryotic and eukaryotic cells. A host cell may be unicellular or found in a multicellular differentiated or undifferentiated organism depending upon the intended use. It is understood that useful exogenous genetic material may be introduced into any non-fungal cell or organism such as a plant cell, plant, mammalian cell, mammal, fish cell, fish, bird cell, bird or bacterial cell.

Depending upon the host, the regulatory regions for expression of ENU sequences will vary, including regions from viral, plasmid or chromosomal genes, or the like. For expression in prokaryotic or eukaryotic microorganisms, particularly unicellular hosts, a wide variety of constitutive or regulatable promoters may be employed. Among transcriptional initiation regions which have been described are regions from bacterial and yeast hosts, such as *E. coli*, *B. subtilis*, *Sacchormyces cerevisiae*, including genes such as beta-galactosidase, T7 polymerase and

tryptophan E.

Furthermore, for use in transformation of *E. nidulans*, constructs may include those in which an ENU sequence or portion thereof of the present invention is positioned with respect to a promoter sequence such that production of antisense mRNA complementary to native mRNA molecules is provided. In this manner, expression of the native gene may be decreased. Such methods may find use for modification of particular functions of the targeted host, and/or for discovering the function of a protein naturally expressed in *E. nidulans*.

Complements and homologs of ENUs

Another embodiment of the present invention comprises a nucleic acid molecule which is a homolog of an ENU of this invention which encodes a polypeptide also found in a plant, animal or bacterial organism. Yet another embodiment comprises a nucleic acid molecule which encodes a polypeptide which is homologous to a polypeptide encoded by an ENU of this invention where the percent identity between the polypeptides is between about 25% and about 40%, more preferably of between about 40 and about 70%, even more preferably of between about 70% and about 90%, and even more preferably between about 90% and 99% and most preferably 100%.

Genomic sequences can be screened for the presence of protein homologs utilizing one or a number of different search algorithms that have been developed, one example of which are the suite of programs referred to as BLAST programs. In addition, unidentified reading frames may be screened for by gene prediction software such as GenScan available for downloading from the Stanford University web site. The degeneracy of the genetic code allows different nucleic acid sequences to code for the same protein or peptide, *e.g. see* U.S. Patent No. 4,757,006, the entirety

of which is herein incorporated by reference. As used herein a nucleic acid molecule is degenerate of another nucleic acid molecule when the nucleic acid molecules encode for the same amino acid sequences but comprise different nucleotide sequences. An aspect of the present invention is that the nucleic acid molecules of the present invention include nucleic acid
5 molecules that are degenerate from the ENUs of this invention.

A further aspect of the present invention comprises one or more nucleic acid molecules which differ in nucleic acid sequence from those of an ENU of this invention due to the degeneracy in the genetic code in that they encode the same protein but differ in nucleic acid sequence or a protein having one or more conservative amino acid residue. Codons capable of
10 coding for such conservative substitutions are known in the art. For instance, serine is a conservative substitute of alanine and threonine is a conservative substitute for serine.

Regulatory Elements

One class of agents of the present invention includes nucleic acid molecules having
15 promoter regions or partial promoter regions or other regulatory elements, particularly those found in SEQ ID NO: 1 through SEQ ID NO: 16144 and located upstream of the trinucleotide ATG sequence at the start site of a protein coding region. As used herein, a promoter region is a region of a nucleic acid molecule that is capable, when located in *cis* to a nucleic acid sequence that encodes for a protein or peptide to function in a way that directs expression of one or more
20 mRNA molecules that encodes for the protein or peptide. Promoters of the present invention can comprise nucleic acids in the range from about 300 bp to at least 1000 bp or more, say about 2000 bp or even higher say about 5000 bp and up to about 10 kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. While in many circumstances a 300 bp

promoter may be sufficient for expression, additional sequences may act to further regulate expression, for example, in response to biochemical, developmental or environmental signals. In a preferred embodiment of the present invention, the promoter is upstream of a nucleic acid sequence that encodes an *E. nidulans* protein homolog or fragment thereof or preferably

5 upstream of an ENU of this invention. It is also preferred that the promoters of the present invention contain a CAAT and a TATA *cis* element. Moreover, the promoters of the present invention can include one or more *cis* elements in addition to a CAAT and a TATA box. For the most part, the promoters of the present invention will be located in contig sequences which generally represent longer nucleic acids than do singleton sequences of the present invention.

10 Contigs in SEQ ID NO:1 through SEQ ID NO:16144 are recognized as those sequences whose designations begin with ANI61C or ANI50C, as opposed to singletons whose designations begin with ANI61S or ANI50S. Where an ENU is specified as being located on two different contigs, the promoter region will be located on the contig representing the 5' region of the gene encoding sequence.

15 By "regulatory element" it is intended a series of nucleotides that determines if, when, and at what level a particular gene is expressed. The regulatory DNA sequences specifically interact with regulatory or other proteins. Many regulatory elements act in *cis* ("*cis* elements") and are believed to affect DNA topology, producing local conformations that selectively allow or restrict access of RNA polymerase to the DNA template or that facilitate selective opening of the
20 double helix at the site of transcriptional initiation. *Cis* elements occur within, but are not limited to promoters, and promoter modulating sequences (inducible elements). *Cis* elements can be identified using known *cis* elements as a target sequence or target motif in the BLAST programs of the present invention. Promoters of the present invention include homologs of *cis*

elements known to effect gene regulation that show homology with the nucleic acid molecules of the present invention.

Polypeptides

Other aspects of this invention comprises one or more of the polypeptides, including
5 proteins or peptide molecules, encoded by the coding region of an ENU of this invention or fragments thereof or homologs thereof. Protein and peptide molecules can be identified using known protein or peptide molecules as a target sequence or target motif in the BLAST programs of the present invention. In a preferred embodiment the protein or fragment molecules of the present invention are derived from *E. nidulans*.

10 As used herein, the term "protein molecule" or "peptide molecule" includes any molecule that comprises five or more amino acids. It is well known in the art that proteins or peptides may undergo modification, including post-translational modifications, such as, but not limited to, disulfide bond formation, glycosylation, phosphorylation, or oligomerization. Thus, as used herein, the term "protein molecule" or "peptide molecule" includes any protein molecule that is
15 modified by any biological or non-biological process. The terms "amino acid" and "amino acids" refer to all naturally occurring L-amino acids. This definition is meant to include norleucine, ornithine, homocysteine, and homoserine.

One or more of the protein or peptide molecules may be produced via chemical synthesis, or more preferably, by expression in a suitable bacterial or eukaryotic host. Suitable methods for
20 expression are described by Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual, 2nd Edition*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), or similar texts.

A "protein fragment" comprises a subset of the amino acid sequence of that protein. A protein fragment which comprises one or more additional peptide regions not derived from a

base protein is a "fusion" protein. Such molecules may be derivatized to contain carbohydrate or other groups (such as keyhole limpet hemocyanin, *etc.*). Fusion protein or peptide molecules of the present invention are preferably produced via recombinant means.

Another class of agents comprises protein or peptide molecules encoded by the coding region of an ENU of this invention or complements thereof or, fragments or fusions thereof in which conservative, non-essential, or not relevant, amino acid residues have been added, replaced, or deleted. An example of such a homolog is the homolog protein of a non-*E. nidulans* filamentous fungus. Such a homolog can be obtained by any of a variety of methods. For example, as indicated above, one or more of the disclosed sequences for primers of this invention can be used to define a pair of primers that may be used to isolate the homolog-encoding nucleic acid molecules from any desired species. Such molecules can be expressed to yield homologs by recombinant means.

Antibodies

One aspect of the present invention concerns antibodies, single-chain antigen binding molecules, or other proteins that specifically bind to one or more of the protein or peptide molecules of the present invention and their homologs, fusions or fragments. Such antibodies may be used to quantitatively or qualitatively detect the protein or peptide molecules of the present invention. As used herein, an antibody or peptide is said to "specifically bind" to a protein or peptide molecule of the present invention if such binding is not competitively inhibited by the presence of non-related molecules. In a preferred embodiment the antibodies of the present invention bind to proteins of the present invention, in a more preferred embodiment of the antibodies of the present invention bind to proteins derived from *E. nidulans*.

Nucleic acid molecules that encode all or part of the protein of the present invention can be expressed, via recombinant means, to yield protein or peptides that can in turn be used to elicit antibodies that are capable of binding the expressed protein or peptide. Such antibodies may be used in immunoassays for that protein. Such protein-encoding molecules, or their fragments may be a "fusion" molecule (*i.e.*, a part of a larger nucleic acid molecule) such that, upon expression, a fusion protein is produced. It is understood that any of the nucleic acid molecules of the present invention may be expressed, via recombinant means, to yield proteins or peptides encoded by these nucleic acid molecules.

The antibodies that specifically bind proteins and protein fragments of the present invention may be polyclonal or monoclonal. It is understood that practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of antibodies (see, for example, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1988), the entirety of which is herein incorporated by reference).

It is understood that any of the antibodies of the present invention can be substantially purified and/or be biologically active and/or recombinant.

Fungal Constructs and Fungal Transformants

The present invention also relates to a fungal recombinant vector, *e.g.* comprising exogenous genetic material. In a preferred embodiment the exogenous genetic material includes at least one nucleic acid molecule of the present invention which can preferably be (a) an ENU of this invention or fragment or homolog thereof or (b) a regulatory element, promoter or partial promoter of the present invention. In a further more preferred embodiment of the present invention exogenous genetic material includes a regulatory element, promoter or partial promoter

of the present invention and a nucleic acid molecule of the present invention having a sequence within a contig selected from the group identified by SEQ ID NO: 1 through SEQ ID NO: 16206 or complements thereof or fragments of either. In a further more preferred embodiment of the present invention exogenous genetic material includes a regulatory element, promoter or partial promoter of the present invention and a nucleic acid molecule encoding an *E. nidulans* protein homolog or fragments thereof. It is also understood that such exogenous genetic material may be introduced into any non-fungal cell or organism such as a plant cell, plant, mammalian cell, mammal, fish cell, fish, bird cell, bird or bacterial cell.

The recombinant vector may be any vector which can be conveniently subjected to recombinant DNA procedures. The choice of a vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host.

The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides, for example biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like. The selectable marker may be selected from the group including, but not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin acetyltransferase), *hygB* (hygromycin phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase), *sC* (sulfate adenylyltransferase), *trpC* (anthranilate synthase) and *gfp* (green fluorescent protein). Preferred for use in an *Emericella* cell are the *amdS* and *pyrG* markers of *Emericella nidulans* or *Aspergillus, oryzae* and the *bar* marker of

Streptomyces hygroscopicus. Furthermore, selection may be accomplished by co-transformation, e.g., as described in WO 91/17243, the entirety of which is herein incorporated by reference.

A nucleic acid sequence of the present invention may be operably linked to a suitable promoter sequence. A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be operably linked to a suitable leader sequence. A leader sequence is a nontranslated region of a mRNA which is important for translation by the fungal host. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the protein or fragment thereof. The leader sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. A polyadenylation sequence may also be operably linked to the 3' terminus of the nucleic acid sequence of the present invention.

To avoid the necessity of disrupting the cell to obtain the protein or fragment thereof, and to minimize the amount of possible degradation of the expressed protein or fragment thereof within the cell, it may be preferred that expression of the protein or fragment thereof gives rise to a product secreted outside the cell, especially in the case of expression in host cells of fungus or bacteria. To this end, the protein or fragment thereof of the present invention may be linked to a signal peptide linked to the amino terminus of the protein or fragment thereof. A signal peptide is an amino acid sequence which permits the secretion of the protein or fragment thereof from the host into the culture medium.

A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be linked to a propeptide coding region. A propeptide is an amino acid sequence found at the amino terminus of a protein or proenzyme. Cleavage of the propeptide from the proprotein yields a mature biochemically active protein. The resulting polypeptide is known as a

propolypeptide or proenzyme (or a zymogen in some cases). Propolypeptides are generally inactive and can be converted to mature active polypeptides by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide or proenzyme. The propeptide coding region may be native to the protein or fragment thereof or may be obtained from foreign sources.

5 The expressed protein or fragment thereof may be detected using methods known in the art that are specific for the particular protein or fragment. These detection methods may include the use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, if the protein or fragment thereof has enzymatic activity, an enzyme assay may be used. Alternatively, if polyclonal or monoclonal antibodies specific to the protein or fragment thereof are available, immunoassays may be employed using the antibodies to the
10 protein or fragment thereof. The techniques of enzyme assay and immunoassay are well known to those skilled in the art.

 The resulting protein or fragment thereof may be recovered by methods known in the arts. For example, the protein or fragment thereof may be recovered from the nutrient medium by
15 conventional procedures including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation. The recovered protein or fragment thereof may then be further purified by a variety of chromatographic procedures, *e.g.*, ion exchange chromatography, gel filtration chromatography, affinity chromatography, or the like.

Plant Constructs and Plant Transformants

20 ENUs or other nucleic acid molecules of this invention may be used in plant transformation or transfection. Exogenous genetic material may be transferred into a plant cell and the plant cell regenerated into a whole, fertile or sterile plant. Exogenous genetic material is any genetic material, whether naturally occurring or otherwise, from any source that is capable of

being inserted into any organism. Such genetic material may be transferred into either monocotyledons and dicotyledons including but not limited to the plants, alfalfa, *Arabidopsis thaliana*, barley, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, maize, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, soybean, strawberry, 5 sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *etc.*

Exogenous genetic material may be transferred into a plant cell by the use of a DNA vector or construct designed for such a purpose. Vectors have been engineered for transformation of large DNA inserts into plant genomes. Binary bacterial artificial chromosomes 10 have been designed to replicate in both *E. coli* and *Agrobacterium tumefaciens* and have all of the features required for transferring large inserts of DNA into plant chromosomes. BAC vectors, *e.g.* a pBACwich, have been developed to achieve site-directed integration of DNA into a genome.

A construct or vector may also include a plant promoter to express the protein or protein 15 fragment of choice. A number of promoters which are active in plant cells have been described in the literature. These include the nopaline synthase (NOS) promoter, the octopine synthase (OCS) promoter, a caulimovirus promoter such as the CaMV 19S promoter and the CaMV 35S promoter, the figwort mosaic virus 35S promoter, the light-inducible promoter from the small subunit of ribulose-1,5-bis-phosphate carboxylase (ssRUBISCO), the Adh promoter, the sucrose 20 synthase promoter, the R gene complex promoter, and the chlorophyll a/b binding protein gene promoter. For the purpose of expression in source tissues of the plant, such as the leaf, seed, root or stem, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. For this purpose, one may choose from a number of

promoters for genes with tissue- or cell-specific or -enhanced expression. Examples of such promoters reported in the literature include the chloroplast glutamine synthetase GS2 promoter from pea, the chloroplast fructose-1,6-bisphosphatase (FBPase) promoter from wheat, the nuclear photosynthetic ST-LS1 promoter from potato, the phenylalanine ammonia-lyase (PAL) promoter and the chalcone synthase (CHS) promoter from *Arabidopsis thaliana*. Also reported to be active in photosynthetically active tissues are the ribulose-1,5-bisphosphate carboxylase (RbcS) promoter from eastern larch (*Larix laricina*), the promoter for the *cab* gene, *cab6*, from pine, the promoter for the *Cab-1* gene from wheat, the promoter for the *CAB-1* gene from spinach, the promoter for the *cab1R* gene from rice, the pyruvate, orthophosphate dikinase (PPDK) promoter from *Zea mays*, the promoter for the tobacco *Lhcb1*2* gene, the *Arabidopsis thaliana* SUC2 sucrose-H⁺ symporter promoter, and the promoter for the thylacoid membrane proteins from spinach (*psaD*, *psaF*, *psaE*, *PC*, *FNR*, *atpC*, *atpD*, *cab*, *rbcS*). Other promoters for the chlorophyll a/b-binding proteins may also be utilized in the present invention, such as the promoters for *LhcB* gene and *PsbP* gene from white mustard (*Sinapis alba*). Additional promoters that may be utilized are described, for example, in U.S. Patent Nos. 5,378,619; 5,391,725; 5,428,147; 5,447,858; 5,608,144; 5,608,144; 5,614,399; 5,633,441; 5,633,435 and 4,633,436, all of which are herein incorporated in their entirety.

Constructs or vectors may also include, with the coding region of interest, a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. For example, such sequences have been isolated including the Tr7 3' sequence and the nos 3' sequence or the like. It is understood that one or more sequences of the present invention that act to terminate transcription may be used.

A vector or construct may also include other regulatory elements or selectable markers.

Selectable markers may also be used to select for plants or plant cells that contain the exogenous genetic material. Examples of such include, but are not limited to, a neo gene which codes for kanamycin resistance and can be selected for using kanamycin, G418, *etc.*; a bar gene which
 5 codes for bialaphos resistance; a mutant EPSP synthase gene which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil, a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance; and a methotrexate resistant DHFR gene.

A vector or construct may also include a screenable marker to monitor expression.

10 Exemplary screenable markers include a β -glucuronidase or uidA gene (GUS), an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues; a β -lactamase gene, a gene which encodes an enzyme for which various chromogenic substrates are known (*e.g.*, PADAC, a chromogenic cephalosporin); a luciferase
 15 gene, a xyle gene which encodes a catechol dioxygenase that can convert chromogenic catechols; an α -amylase gene, a tyrosinase gene which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to melanin; an α -galactosidase, which will turn a chromogenic α -galactose substrate. Included within the terms "selectable or screenable marker genes" are also genes which encode a secretable marker whose secretion can
 20 be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, *e.g.*, by ELISA, small active enzymes detectable in extracellular solution (*e.g.*, α -amylase, β -lactamase, phosphinothricin transferase),

or proteins which are inserted or trapped in the cell wall (such as proteins which include a leader sequence such as that found in the expression unit of extension or tobacco PR-S). Other possible selectable and/or screenable marker genes will be apparent to those of skill in the art.

Technology for introduction of DNA into cells is well known to those of skill in the art.

- 5 Four general methods for delivering a gene into cells have been described: (1) chemical methods, (2) physical methods such as microinjection and bombardment, (3) viral vectors and (4) receptor-mediated mechanisms.

It is also to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating added, exogenous genes.

- 10 The present invention also provides for parts of the plants of the present invention. Plant parts, without limitation, include seed, endosperm, ovule and pollen. In a particularly preferred embodiment of the present invention, the plant part is a seed.

- Transformation of plant protoplasts can be achieved using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation, and combinations of
15 these treatments.

- Any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters enhancers *etc.* Further any of the nucleic acid molecules encoding an *E. nidulans* protein or fragment thereof or homologs of the present invention may be introduced
20 into a plant cell in a manner that allows for over expression of the protein or fragment thereof encoded by the nucleic acid molecule.

Uses of the Agents of the Present Invention

Nucleic acid molecules of the present invention may be employed to obtain *other E. nidulans* nucleic acid molecules. Such molecules can be readily obtained by using the above-described nucleic acid molecules to screen *E. nidulans* libraries.

5 Nucleic acid molecules and fragments thereof of the present invention may also be employed to obtain nucleic acid molecule homologs of non-*E. nidulans* species including the nucleic acid molecules that encode, in whole or in part, protein homologs of other species or other organisms, sequences of genetic elements such as promoters and transcriptional regulatory elements. Such molecules can be readily obtained by using the above-described nucleic acid
10 molecules to screen cDNA or genomic libraries of non-*E. nidulans* species. Methods for forming such libraries are well known in the art. Such homolog molecules may differ in their nucleotide sequences from those found in one or more of the *E. nidulans* genes of this invention or complements thereof because complete complementarity is not needed for stable hybridization. The nucleic acid molecules of the present invention therefore also include molecules that,
15 although capable of specifically hybridizing with the nucleic acid molecules may lack "complete complementarity."

The disclosed nucleic acid molecules may be used to define one or more primer pairs that can be used with the polymerase chain reaction to amplify and obtain any desired nucleic acid molecule or fragment thereof. Such molecules will find particular use in generation of nucleic
20 acid arrays, including microarrays, containing portions of or the entire encoding region for the identified *E. nidulans* genes. It is noted that the molecules on such arrays may contain native intervening sequences (introns) of the genes and will still find use in microarray based methods

such as transcriptional profiling for functional analysis of *E. nidulans* genes and metabolic pathways. Particularly preferred primers are those set forth in table 3.

The nucleic acid molecules of the present invention may be used for physical mapping. Physical mapping, in conjunction with linkage analysis, can enable the isolation of genes.

- 5 Physical mapping has been reported to identify the markers closest in terms of genetic recombination to a gene target for cloning. Once a DNA marker is linked to a gene of interest, the chromosome walking technique can be used to find the genes via overlapping clones. For chromosome walking, random molecular markers or established molecular linkage maps are used to conduct a search to localize the gene adjacent to one or more markers. A chromosome walk is
- 10 then initiated from the closest linked marker. Starting from the selected clones, labeled probes specific for the ends of the insert DNA are synthesized and used as probes in hybridizations against a representative library. Clones hybridizing with one of the probes are picked and serve as templates for the synthesis of new probes; by subsequent analysis, contigs are produced.

- The degree of overlap of the hybridizing clones used to produce a contig can be
- 15 determined by comparative restriction analysis. Comparative restriction analysis can be carried out in different ways all of which exploit the same principle; two clones of a library are very likely to overlap if they contain a limited number of restriction sites for one or more restriction endonucleases located at the same distance from each other. The most frequently used procedures are, fingerprinting, restriction fragment mapping or the "landmarking" technique. It is
- 20 understood that the nucleic acid molecules of the present invention may in one embodiment be used in physical mapping. In a preferred embodiment, nucleic acid molecules of the present invention may in one embodiment be used in the physical mapping of *E. nidulans*.

Nucleic acid molecules of the present invention can be used in comparative mapping. Comparative mapping within families provides a method to assess the degree of sequence conservation, gene order, ploidy of species, ancestral relationships and the rates at which individual genomes are evolving. Comparative mapping has been carried out by cross-

5 hybridizing molecular markers across species within a given family. As in genetic mapping, molecular markers are needed but instead of direct hybridization to mapping filters, the markers are used to select large insert clones from a total genomic DNA library of a related species. The selected clones, each a representative of a single marker, can then be used to physically map the region in the target species. The advantage of this method for comparative mapping is that no

10 mapping population or linkage map of the target species is needed and the clones may also be used in other closely related species. By comparing the results obtained by genetic mapping in model organisms, with those from other species, similarities of genomic structure among species can be established. Cross-hybridization of RFLP markers has been reported and conserved gene order has been established in many studies. Such macroscopic synteny is utilized for the

15 estimation of correspondence of loci among these organisms. It is understood that nucleic acid molecules of the present invention may in another embodiment be used in comparative mapping. In a preferred embodiment the nucleic acid molecules of present invention may be used in the comparative mapping of filamentous fungi.

In an aspect of the present invention, one or more of the agents of the present invention

20 may be used to detecting the presence, absence or level of a organism, preferably a filamentous fungus and more preferably an *E. nidulans* in a sample. In another aspect of the present invention, one or more of the nucleic acid molecules of the present invention are used to determine the level (*i.e.*, the concentration of mRNA in a sample, *etc.*) or pattern (*i.e.*, the

kinetics of expression, rate of decomposition, stability profile, *etc.*) of the expression of a protein encoded in part or whole by one or more of the nucleic acid molecule of the present invention (collectively, the "Expression Response" of a cell or tissue). As used herein, the Expression Response manifested by a cell or tissue is said to be "altered" if it differs from the Expression Response of cells or tissues of organisms not exhibiting the phenotype. To determine whether a Expression Response is altered, the Expression Response manifested by the cell or tissue of the organism exhibiting the phenotype is compared with that of a similar cell or tissue sample of a organism not exhibiting the phenotype. As will be appreciated, it is not necessary to re-determine the Expression Response of the cell or tissue sample of organisms not exhibiting the phenotype each time such a comparison is made; rather, the Expression Response of a particular organism may be compared with previously obtained values of normal organism. As used herein, the phenotype of the organism is any of one or more characteristics of an organism.

Nucleic acid molecules of the present invention can be used to monitor expression. A microarray-based method for high-throughput monitoring of gene expression may be utilized to measure gene-specific hybridization targets. This 'chip'-based approach involves using microarrays of nucleic acid molecules as gene-specific hybridization targets to quantitatively measure expression of the corresponding genes. Every nucleotide in a large sequence can be queried at the same time. Hybridization can be used to efficiently analyze nucleotide sequences.

Several methods have been described for fabricating microarrays of nucleic acid molecules and using such microarrays in detecting nucleic acid sequences. For instance, microarrays can be fabricated by spotting nucleic acid molecules, *e.g.* genes, oligonucleotides, *etc.*, onto substrates or fabricating oligonucleotide sequences in situ on a substrate. Spotted or fabricated nucleic acid molecules can be applied in a high density matrix pattern of up to about

30 non-identical nucleic acid molecules per square centimeter or higher, *e.g.* up to about 100 or even 1000 per square centimeter. Useful substrates for arrays include nylon, glass and silicon.

See, for instance, US Patents 5,202,231; 5,445,934; 5,525,464; 5,700,637; 5,744,305; 5,800,992,

the entirety of the disclosures of all of which are incorporated herein by reference. Sequences

5 can be efficiently analyzed by hybridization to a large set of oligonucleotides or cDNA molecules representing a large portion of a the genes of a genome. An array consisting of oligonucleotides or cDNA molecules complementary to subsequences of a target sequence can be used to determine the identity of a target sequence, measure its amount, and detect differences between the target and a reference sequence. Nucleic acid molecule microarrays may also be
10 screened with molecules or fragments thereof to determine nucleic acid molecules that specifically bind molecules or fragments thereof.

The microarray approach may also be used with polypeptide targets (U.S. Patent No. 5,445,934; U.S. Patent No:5,143,854; U.S. Patent No. 5,079,600; U.S. Patent No. 4,923,901, all of which are herein incorporated by reference in their entirety). Essentially, polypeptides are
15 synthesized on a substrate (microarray) and these polypeptides can be screened with either protein molecules or fragments thereof or nucleic acid molecules in order to screen for either protein molecules or fragments thereof or nucleic acid molecules that specifically bind the target polypeptides.

It is understood that one or more of the molecules of the present invention, preferably one
20 or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a microarray based method. In a preferred embodiment of the present invention, one or more of the *E. nidulans* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a microarray based method. A

particular preferred microarray embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes or fragments thereof that are homologs of known genes or nucleic acid molecules that comprise genes or fragments thereof that elicit only limited or no matches to known genes. A further preferred microarray embodiment of the present invention is

5 a microarray comprising nucleic acid molecules having genes or fragments thereof that are homologs of known genes and nucleic acid molecules that comprise genes or fragment thereof that elicit only limited or no matches to known genes.

In a preferred embodiment, the microarray of the present invention comprises at least 10 nucleic acid molecules that specifically hybridize under high stringency to at least 10 nucleic acid molecules encoding *E. nidulans* protein or fragments. In a more preferred embodiment, the
10 microarray of the present invention comprises at least 100 nucleic acid molecules that specifically hybridize under high stringency to at least 100 nucleic acid molecules that encode an *E. nidulans* protein or fragment thereof. In an even more preferred embodiment, the microarray of the present invention comprises at least 1,000 nucleic acid molecules that specifically
15 hybridize under high stringency to at least 1,000 nucleic acid molecules that encode an *E. nidulans* protein or fragment thereof. In a further even more preferred embodiment, the microarray of the present invention comprises at least 2,500 nucleic acid molecules that specifically hybridize under high stringency to at least 2,500 nucleic acid molecules that encode an *E. nidulans* protein or fragment thereof. While it is understood that a single nucleic acid
20 molecule may encode more than one protein or fragment thereof, in a preferred embodiment, at least 50%, preferably at least 70%, more preferably at least 80%, even more preferably at least 90% of the nucleic acid molecules that comprise the microarray encode one protein homolog or

fragment thereof. It is, of course, understood that these nucleic acid molecules can be non-identical.

In a preferred embodiment, the microarray of the present invention comprises at least 10 nucleic acid molecules that specifically hybridize under high stringency to at least 10 ENUs selected from the group having SEQ ID NO: 16207 through SEQ ID NO: 28905 or fragment thereof or complement of either. In a more preferred embodiment, the microarray of the present invention comprises at least 100 nucleic acid molecules that specifically hybridize under high stringency to at least 100 ENUs selected from the group having SEQ ID NO: 16207 through SEQ ID NO: 28905 or fragment thereof or complement of either. In an even more preferred embodiment, the microarray of the present invention comprises at least 1,000 nucleic acid molecules that specifically hybridize under high stringency to at least 1,000 ENUs selected from the group having SEQ ID NO: 16207 through SEQ ID NO: 28905 or fragment thereof or complement of either.. In a further even more preferred embodiment, the microarray of the present invention comprises at least 2,500 nucleic acid molecules that specifically hybridize under high stringency to at least 2,500 ENUs selected from the group having SEQ ID NO: 16207 through SEQ ID NO: 28905 or fragment thereof or complement of either. While it is understood that a single nucleic acid molecule may encode more than one protein homolog or fragment thereof, in a preferred embodiment, at least 50%, preferably at least 70%, more preferably at least 80%, even more preferably at least 90% of the nucleic acid molecules that comprise the microarray encode one protein or fragment thereof.

Nucleic acid molecules of the present invention may be used in site directed mutagenesis. Site-directed mutagenesis may be utilized to modify nucleic acid sequences, particularly as it is a technique that allows one or more of the amino acids encoded by a nucleic acid molecule to be

altered (*e.g.* a threonine to be replaced by a methionine). Three basic methods for site-directed mutagenesis are often employed, *i.e.* (a) cassette mutagenesis, (b) primer extension and (c) methods based on PCR. *See* also US Patent 5,880,275, US Patent 5,380,831, and US Patent 5,625,136, the entirety of all of which is incorporated herein by reference.

5 Any of the nucleic acid molecules of the present invention may either be modified by site-directed mutagenesis or used as, for example, nucleic acid molecules that are used to target other nucleic acid molecules for modification. It is understood that mutants with more than one altered nucleotide can be constructed using techniques that practitioners skilled in the art are familiar with such as isolating restriction fragments and ligating such fragments into an
10 expression vector.

 Preferred aspects of this invention comprise collections of genes, nucleic acid molecules, polypeptides and/or primers of this invention ranging in size from about 10 non-identical members or more, *e.g.* at least about 100 or 270 or higher, more preferably at least about 300 or 350, most preferably at least 500 or higher, up to about 1000, or 2000 or even higher, say about
15 5000, or more non-identical members. As used herein a non-identical member is a member that differs in nucleic acid or amino acid sequence. For example, a non-identical nucleic acid molecule is a nucleic acid molecule that differs in nucleic acid sequence from the nucleic acid molecule to which it is being compared to. For example a nucleic acid molecule having the sequence 5' CCC 3' is not identical – *i.e.* non-identical – to a nucleic acid molecule having the
20 sequence 5' CCG 3'. In one aspect a collection may comprise all of the genes, nucleic acid molecules, polypeptides and/or primers of this invention. Such collections can be located or organized in a variety of forms, *e.g.* on microarrays, in solutions, in bacterial clone libraries, *etc.*

As used herein, an "organized" collection is a collection where the nucleic acid or amino acid sequence of a member of such a collection can be determined based on its physical location.

Preferred collections of nucleic acid molecules can be selected from the following groups: SEQ ID NO: 16207 through SEQ ID NO: 27905 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 26804 or complements thereof; SEQ ID NO: 26000 through SEQ ID NO: 26804 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 25999 or complements thereof; SEQ ID NO: 24035 through SEQ ID NO: 25999 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 24034 or complements thereof; SEQ ID NO: 22710 through SEQ ID NO: 24034 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 22709 or complements thereof; SEQ ID NO: 17681 through SEQ ID NO: 22709 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17680 or complements thereof; SEQ ID NO: 17618 through SEQ ID NO: 17680 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17617 or complements thereof; SEQ ID NO: 17295 through SEQ ID NO: 17617 or complements thereof; SEQ ID NO: 16207 through SEQ ID NO: 17294 or complements thereof; SEQ ID NO: 28166 through SEQ ID NO: 44345 or complements thereof. Other preferred nucleic acid collections include any of the above groups but where such groups also include fragments of such sequences.

It is understood that all these preferred collections may also range in size from about 10 or more, *e.g.* at least about 100 or 270 or higher, more preferably at least about 300 or 350, most preferably at least 500 or higher, up to about 1000, or 2000 or even higher, say about 5000, or more non-identical members.

Another aspect of this invention provides the genes, nucleic acid molecules, polypeptides and/or primers in a substantially pure form. For instance, by use of the primers of this invention, any of the ENUs can be produced in substantially pure form by PCR.

Another aspect of this invention is to provide methods for determining gene expression, *e.g.* identifying homologous genes expressed by non-*E. nidulans* organism. Such methods comprise collecting mRNA from tissue of such organism, using the mRNA as a template for producing a quantity of labeled nucleic acid, and contacting the labeled nucleic acid molecule with a collection of purified nucleic acid molecules, *e.g.* on a microarray.

Computer Media

One or more of the nucleotide sequence provided in SEQ ID NO: 1, through SEQ ID NO: 44345 or complements or fragments of either can be "provided" in a variety of media to facilitate use. Such a medium can also provide a subset thereof in a form that allows a skilled artisan to examine the sequences. In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc, storage medium, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; optical scanner readable medium such as printed paper; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate media comprising the nucleotide sequence information of the present invention. In addition, a variety of data processor
5 programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.* text file or database) in order to obtain
10 computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing one or more of nucleotide sequences of the present invention, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information
15 provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST and/or BLAZE search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the sequences of the present invention and are useful in producing commercially important proteins
20 such as enzymes used in amino acid biosynthesis, metabolism, transcription, translation, RNA processing, nucleic acid and a protein degradation, protein modification, and DNA replication, restriction, modification, recombination, and repair.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the nucleic acid molecule of the present invention. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequence of the present invention that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTIN and BLASTIX (NCBIA). One of the available algorithms or

implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

The most preferred sequence length of a target sequence is from about 30 to 300 nucleotide residues or from about 10 to 100 of the corresponding amino acids. However, it is well recognized that during searches for commercially important fragments of the nucleic acid molecules of the present invention, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, *cis* elements, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequences of the present invention sequence identified using a search means as described above, and an output means for outputting the identified homologous sequences. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the sequence of the present invention by varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various

amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Example 1

This example serves to illustrate the generation of the 16206 nucleic acid sequences listed in Table 1 as as contigs having SEQ ID NO: 1 through SEQ ID NO: 16206. About 390,000 genomic nucleotide sequence traces are derived from 11 different M13 and double stranded libraries. The two basic methods for the DNA sequencing are the chain termination method of Sanger *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 74:5463-5467 (1977) and the chemical degradation method of Maxam and Gilbert, *Proc. Natl. Acad. Sci. (U.S.A.)* 74:560-564 (1977) using automated fluorescence-based sequencing as reported by Craxton, *Method*, 2:20-26 (1991); Ju *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 92:4347-4351 (1995); and Tabor and Richardson, *Proc. Natl. Acad. Sci. (U.S.A.)* 92:6339-6343 (1995) and high speed capillary gel electrophoresis, *e.g.* as disclosed by Swerdlow and Gesteland, *Nucleic Acids Res.* 18:1415-1419 (1990); Smith, *Nature* 349:812-813 (1991); Luckey *et al.*, *Methods Enzymol.* 218:154-172 (1993); Lu *et al.*, *J. Chromatog. A.* 680:497-501 (1994); Carson *et al.*, *Anal. Chem.* 65:3219-3226 (1993); Huang *et al.*, *Anal. Chem.* 64:2149-2154 (1992); Kheterpal *et al.*, *Electrophoresis* 17:1852-1859 (1996); Quesada and Zhang, *Electrophoresis* 17:1841-1851 (1996); Baba, *Yakugaku Zasshi* 117:265-281 (1997). For instance, genomic nucleotide sequence traces are generated using a 377 DNA Sequencer (Perkin-Elmer Corp., Applied Biosystems Div., Foster City, CA) allowing for rapid electrophoresis and data collection. With these types of automated systems, fluorescent dye-

labeled sequence reaction products are detected and chromatograms are subsequently viewed, stored in computer and analyzed using corresponding apparatus-related software programs. These methods are known to those of skill in the art and have been described and reviewed (Birren *et al.*, *Genome Analysis: Analyzing DNA*, 1, Cold Spring Harbor, New York.

- 5 Over 390,000 quality genomic sequence traces are assembled generally as follows:
 - (a) all traces are quality clipped using *yc_qual_clip.pl* (with a minimum PHRED score of 12.5 and maximum length of 50 bp);
 - (b) all traces are segregated according to library construction method;
 - (c) all traces are “vector-trimmed” *i.e.*, 5’ and 3’ vector and linker sequences are
 - 10 removed;
 - (d) all traces are re-united in one file;
 - (e) all traces are then clustered with PANGAEA’s clustering tool (available from Pangea Corp., Pittsburgh, PA). A cluster includes 2 or more traces of sequences with 90% similarity over 60 bp. After clustering the set of traces includes clusters and
 - 15 non-clustered traces referred to as “singletons”.
 - (f) A high stringency PHRAP assembly is run on each cluster to separate from clusters singlet traces which do not meet stringency criteria. The arguments to high stringency PHRAP are: minmatch 25 , minscore 50, penalty -4 ;
 - (g) Contigs and the singleton (including singlet) traces and their corresponding
 - 20 quality files are united; and, then are assembled with a low stringency PHRAP (using default PHRAP arguments) to generate a “final” assembly; and
 - (h) the final set of 16,144 nucleic acid sequences (identified in Table 1 by contig identification number “ANI61xxxx” and by the corresponding SEQ ID NO: 1 through

SEQ ID NO:16144) and 52 nucleic acid sequences (identified in Table 1 by contig identification number "ANI50xxxx" and by corresponding SEQ ID NO: 16145 through SEQ ID NO:16206) are run through the annotation and gene selection processes. Contigs in SEQ ID NO:1 through SEQ ID NO:16144 are recognized as those sequences whose designations begin with ANI61C or ANI50C. Singleton sequences are recognized as those having designations which begin with ANI61S or ANI50S.

The genomic sequence traces and many of the contigs and singleton traces are disclosed in copending provisional applications for patent identified by serial nos. 60/ 101,665; 60/101,666; 60/102,358; 60/113,361; 60/126,265; 60/130,189; 60/130,190; 60/132,861; 60/138,103; 60/149,882.

Example 2

This example illustrates the identification of ENUs within 16206 contigs assembled in Example 1. The genes and partial genes embedded in such contigs are identified through a series of informatic analyses. The tools to define genes fall into two categories: homology-based and predictive-based methods. Homology-based searches (*e.g.*, GAP2, NAP, BLASTX and TBLASTX) detect conserved sequences during comparisons of DNA sequences or hypothetically translated protein sequences to public and/or proprietary DNA and protein databases. Existence of a *E. nidulans* gene is inferred if significant sequence similarity extends over the majority of the target gene. Since homology-based methods may overlook genes unique to *E. nidulans*, for which homologous nucleic acid molecules have not yet been identified in databases, gene prediction programs are also used. Predictive methods employed in the definition of the *E. nidulans* genes included the use of the GenScan gene predictive software

program which is available from Stanford University (*e.g.* at the web site

<http://gnomic.stanford.edu/GENSCANW.html>). GenScan, in general terms, infers the presence and extent of a gene through a search for “gene-like” grammar.

The homology-based methods used to define the *E. nidulans* gene set included GAP2,

- 5 BLASTX supplemented by NAP, and TBLASTX. For a description of BLASTX and TBLASTX *see* Coulson, *Trends in Biotechnology* 12:76-80 (1994) and Birren *et al.*, *Genome Analysis*, 1:543-559 (1997). GAP2 and NAP are part of the Analysis and Annotation Tool (AAT) for Finding Genes in Genomic Sequences which was developed by Xiaoqiu Huang at Michigan Tech University and is available at the web site <http://genome.cs.mtu.edu/>. The AAT package
- 10 includes two sets of programs, one set (DPS/NAP) for comparing the query sequence with a protein database, and the other set (DDS/GAP2) for comparing the query sequence with a cDNA database. Each set contains a fast database search program and a rigorous alignment program. The database search program quickly identifies regions of the query sequence that are similar to a database sequence. Then the alignment program constructs an optimal alignment for each region
- 15 and the database sequence. The alignment program also reports the coordinates of exons in the query sequence. *See* Huang, *et al.*, *Genomics* 46: 37-45 (1997).

The GAP2 program computes an optimal global alignment of a genomic sequence and a cDNA sequence without penalizing terminal gaps. A long gap in the cDNA sequence is given a constant penalty. The DNA-DNA alignment by GAP2 adjusts penalties to accommodate introns.

- 20 The GAP2 program makes use of splice site consensus in alignment computation. GAP2 delivers the alignment in linear space, so long sequences can be aligned. *See* Huang, *Computer Applications in the Biosciences* 10 227-235 (1994). The GAP2 program aligned the *E. nidulans*

contigs with the *A. nidulans*/*E. nidulans* EST library in the microorganism databank maintained by Bruce Roe's laboratory at the University of Oklahoma.

The NAP program computes a global alignment of a DNA sequence and a protein sequence without penalizing terminal gaps. NAP handles frameshifts and long introns in the DNA sequence. The program delivers the alignment in linear space, so long sequences can be aligned. It makes use of splice site consensus in alignment computation. Both strands of the DNA sequence are compared with the protein sequence and one of the two alignments with the larger score is reported. See Huang, and Zhang, "*Computer Applications in the Biosciences* 12(6), 497-506 (1996).

NAP takes a nucleotide sequence, translates it in three forward reading frames and three reverse complement reading frames, and then compares the six translations against a protein sequence database (e.g. the non-redundant protein (i.e., nr-aa) database maintained by the National Center for Biotechnology Information as part of GenBank and available at the web site: <http://www.ncbi.nlm.nih.gov>). TBLASTX compared six possible frame translations of the *E. nidulans* contigs against six frame translations of *Aspergillus fumigatus*, *Fusarium graminearum*, *Saccharomyces cerevisiae*, and *Candida albicans* genomic sequences.

The first homology-based search for genes in the *E. nidulans* contigs is effected using the GAP2 program and the University of Oklahoma *A. nidulans*/*E. nidulans* EST database. A collection of about 14000 *A. nidulans*/*E. nidulans* EST sequences from the database with known 5' and 3' orientations and mate information are clustered into about 3500 distinct sets or "clusters". These clusters are then mapped onto an assembly of *E. nidulans* contigs represented by SEQ ID NO. 1 through SEQ ID NO. 16206 using the GAP2 program. GAP2 standards for selecting a DNA-DNA match were $\geq 96\%$ sequence identity with the following parameters:

gap extension penalty = 1

match score = 2

gap open penalty = 6

gap length for constant penalty = 20

5 mismatch penalty = -2

minimum exon length = 21

DNA matches with ESTs fell into three categories. Firstly, ENUs are identified when a 5'-3' EST pair aligned to the sequences on the same contig. Since EST's are necessarily derived from genes, no corroborating evidence is required to validate the gene prediction. Certain ENUs are identified by 5'-3' EST pair match on a single contig. These ENUs are identified by "EST" in the selection basis column of Table 2 and include SEQ ID NO. 16207 through SEQ ID NO. 17294.

Another group of ENUs identified by DNA match with EST's is selected because of alignment of a 5'-3' EST pair which spanned two contigs supported by BLASTX similarity or clonemate information. These ENUs are identified by "MCEST" in the selection basis column of Table 2 and include SEQ ID NO. 17618 through SEQ ID NO. 17680.

Another group of ENUs identified by DNA match with EST's is selected solely from a 3' EST match of at least 300 bp using EST's which are not previously aligned. These ENUs are identified by "TPEST" in the selection basis column of Table 2 and include SEQ ID NO. 17295 through SEQ IS NO. 17617.

The second homology-based method used for gene discovery is BLASTX hits extended with the NAP software package. BLASTX is run with the *E. nidulans* contigs represented by SEQ ID NO. 1 through SEQ ID NO. 16206 as queries against the GenBank non-redundant

protein data library identified as “nr-aa”. NAP is used to better align the amino acid sequences as compared to the genomic sequence. NAP extends the match in regions where BLASTX has identified high-scoring-pairs (HSPs), predicts introns, and then links the exons into a single ORF prediction. Experience suggests that NAP tends to mis-predict the first exon. *E. nidulans* introns

are almost without exception short (<150 bp), and NAP routinely predicts very long (>400 bp) introns leading to a very short, and biologically unmeaningful, 5' exon. The NAP-predicted ORFs containing long introns (>175 bp) are first segregated and truncated (the long intron and the nonsense 5' exon removed) and the remaining portion of the ORF established as a gene.

Selection in a first pass is for sequences with (a) <600 bp from the 3' end with >50% coverage,

(b) <600 bp from the 3' end with > 300 bp coverage and (c) >1000 bp from the 3' end with 500

bp coverage. Selection in a second pass is for sequences with (a) <300 bp from the 3' end with

,500 bp coverage and >80% coverage or (b) <300 bp from the 3' end and > 500 bp coverage.

The NAP parameters are:

gap extension penalty = 1

gap open penalty = 15

gap length for constant penalty = 25

min exon length (in aa) = 7

The ENUs identified by NAP with (a) >300 bp and >10% homology or (b) >175 bp and > 50% coverage are identified by “NAP” in the selection basis column of Table 2 and include SEQ ID NO. 17681 through SEQ ID NO. 22709.

For NAP alignments with large introns GenScan are used to locate the terminal exon and extend the 5' end of the terminal exon. When there is no GenScan indication of a terminal exon,

the gene is identified using the longest exon cluster without a large intron. The ENUs identified from large intron alignments are identified by "LINAP" in the selection basis column of Table 2 and include SEQ ID NO. 22710 through SEQ ID NO. 24034.

In the final homology-based method, TBLASTX, is used with genome information from three fungal genome sequencing projects: *Aspergillus fumigatus*, *Fusarium graminearum*, *Saccharomyces cerevisiae* and *Candida albicans*. As a general rule, non-coding regions of DNA accumulate mutations much more rapidly than coding regions. With this knowledge, we use TBLASTX, which compares hypothetical translations, to identify regions of DNA that code for highly similar amino acid strings in both *E. nidulans* and the four other fungal genomes. As with EST matches, the TBLASTX hits fall into three categories of defined genes: matches that fall within an *E. nidulans* contig, matches that convincingly bridge contigs, and long matches that contain sufficient portions of a gene for use in transcriptional profiling. Unlike GAP2 and BLASTX/NAP analyses, we have comparatively little experience in interpreting TBLASTX scores as a tool for defining the unigene set. For this reason, conservative standards for inclusion of TBLASTX hits into the gene set are utilized. These standards are a minimal E value of $1E-20$, and for terminal exons, a minimal match of 200 bp within the 1000 most 5' and 3' ends of an *E. nidulans* contig. In addition to these criteria, in part due to conflicting data from TBLASTX analyses (where different TBLASTX matches will suggest two or more mutually exclusive possibilities) and to concerns that repeat regions may be sufficiently similar to confound the method, TBLASTX predicted genes bridging two contigs are included when corroborating evidence in the form of GenScan predictions and/or clone mate evidence from double stranded clones is available.

The GenScan program is “trained” with *E. nidulans* characteristics. Though better than the “off-the-shelf” version, the GenScan trained to identify *E. nidulans* genes proved more proficient at predicting exons than predicting full-length genes. Predicting full-length genes is compromised by point mutations in the unfinished contigs, as well as by the short length of the contigs relative to the typical length of a gene. Due to the errors found in the full-length gene predictions by GenScan, inclusion of GenScan-predicted genes is limited to those genes and exons whose probabilities are above a conservative probability threshold. When used with TBLASTX the GenScan parameters are:

mean GenScan P value > 0.3

mean GenScan T value > 0

mean GenScan Coding score > 50

length > 200 bp

minimum TBLASTX E value < 1E-20

Significant TBLASTX hits to single contigs that are greater than 300 bp contributed 805 genes to the unigene set. The high E value threshold limited the vast majority (99%) of the TBLASTX hits to the fungal genome comparisons. The TBLASTX hits with GenScan corroboration identified 1965 ENUs identified by “GTBX” in the selection basis column of Table 2 and include SEQ ID NO. 24035 through SEQ ID NO. 25999.

To identify ENUs solely by TBLASTX, the TBLASTX E values is set at 1E-30 with a length of > 200 bp. The ENU’s identified solely by TBLASTX are identified by “TBX” in the selection basis column of Table 2 and include SEQ ID NO. 26000 through SEQ ID NO. 26804.

A final set of genes is predicted using the GenScan program “trained” with *E. nidulans* characteristics and the mean GenScan P value parameters changed to > 0.4. The ENUs identified

solely by GenScan are identified by "GSP" in the selection basis column of Table 2 and include SEQ ID NO. 26805 through SEQ ID NO. 27905.

To insure that the same nucleic acid molecule is not inferred two or more times with different methods, an all-versus-all BLASTN analysis of the all the identified ENUs is
 5 conducted. There are instances where sequencing and assembly errors will confound the identification of duplicates, but such instances are comparatively rare.

The confidence in accuracy of the identified ENUs is highest for those identified by a match of a 5'-3' EST to a single contig (identified by EST) and lowest for those identified solely the GenScan predictive algorithm (identified by GSP). The order of confidence for the ENUs is
 10 in the following order:

<u>Selection Basis</u>	<u>Confidence</u>
EST	highest
TPEST	
15 MCEST	
NAP	
LINAP	
GTBX	
TBX	
20 GSP	lowest

In Table 2 the ENUs of this invention are identified in the sequence identification (seq. id.) column the name ENU (Emericella nidulans unigene) and begins with ENU00001 for SEQ ID NO. 16207.

25 Other modifications of the above described embodiments of the invention which are obvious to those of skill in the area of molecular biology and related disciplines are intended to be within the scope of the following claims.

Example 3

This example serves to illustrate the design of primers of this invention which are useful, for instance, for initiating synthesis of nucleic acid molecules of this invention, specifically substantial parts of certain ENU's of this invention. The primers specifically disclosed herein, *i.e.* in Table 3 by SEQ ID NO. 28166 through SEQ ID NO. 44345, are designed with the program Primer3 (obtained from the MIT-Whitehead Genome Center) with a "perl-oracle" wrapper. The criteria applied to design a primer included:

Primer annealing temperature (minimum 65°C, optimum 70°C, maximum 75 °C)

Primer length (minimum 18bp, optimum 20bp, maximum 28 bp)

G+C content (minimum 20%, maximum 80%)

Position of the primer relative to the gene

Length of the amplified region (500 to 800 bp)

PHRED quality score of the gene template (minimum of 20)

Whether the gene was defined from one or two contigs

Maximum mismatch = 12.0 (weighted score from Primer3 program)

Pair Max Misprime = 24.0 (weighted score from Primer3 program)

Maximum N's = 0

Maximum poly-X = 5

The primary goal of the design process is the creation of groups of primer pairs with a common annealing temperature (T_m). When the program could identify a primer pair for any gene that fit the criteria, the gene is removed from the bin of genes needing primer design.

Genes remaining in the bin are subjected to additional rounds of primer-picking, with the gradual and simultaneous relaxation of the criteria (*i.e.*, lowering the annealing temperature, increasing

the size of the window where primers could be predicted, expanding the range of permitted size and G+C content, removing the need for a G/C clamp), until primers are picked for about 8,000 of the about 12,000 ENUs of this invention. After the *E. nidulans* specific portion of the primers is selected, an additional common primer tail sequence (universal primer) is added to the 5' ends.

5 For the forward primers, the additional common bases added are:

(5'-GAATTCAGTGGCCGCGCATG-3'); for the reverse primers the additional common bases added are: (5'-GTTCTCGAGACGAGCGATCGC-3'). The universal primer tail sequences are added so that subsequent reamplifications of any primer pair can be done with a single set of primers. In addition, the primer tail sequences contain restriction digestion sites for
 10 8 bp cutters (NotI and SgfI) and 6 bp cutters (EcoRI and XhoI) to facilitate cloning of ENUs into vectors. The forward primers contains EcoRI and NotI restriction sites; the reverse primers contains XhoI and SgfI restriction sites.

Reference is also made to Tables 2 and 3 for identification of the primers and reference to the ENU for which they are designed. The primer pair for a particular ENU is identified in Table
 15 2 by indication of the complementary or identical nucleotides in the particular ENU under the columns "Primer 5 pos" and "Primer 3 pos". The primer sequence numbers in Table 3 correspond to an ENU identified in the "Seq id" column. For example, the primer pair ENU00001p5 and ENU00001p3 represent the sequences for the 5' and 3' primer, respectively for ENU00001. The primer sequences provided in the sequence listing all contain the universal
 20 tail sequence described above as the first 21 nucleotides. It is noted that primer pairs are not required to contain the universal tail sequence, the relevant portion for amplification and/or hybridization probes being the *E. nidulans* specific sequences designated in the "Primer 5 pos" and "Primer 3 pos" columns in Table 2.

Table 1

Seq num	Contig_id
1	ANI61C99
2	ANI61C100
3	ANI61C101
4	ANI61S41
5	ANI61C102
6	ANI61C104
7	ANI61C107
8	ANI61C108
9	ANI61C110
10	ANI61S1595
11	ANI61S1596
12	ANI61S1597
13	ANI61C3499
14	ANI61C3500
15	ANI61S1599
16	ANI61C3502
17	ANI61S1603
18	ANI61C3504
19	ANI61S1606
20	ANI61C3511
21	ANI61C3512
22	ANI61C3513
23	ANI61C3514
24	ANI61C3515
25	ANI61C3516
26	ANI61S1613
27	ANI61C3518
28	ANI61S1615
29	ANI61C3521
30	ANI61C3534
31	ANI61C3535
32	ANI61C3537
33	ANI61C3539
34	ANI61S1620
35	ANI61S1621
36	ANI61C3543
37	ANI61C3546
38	ANI61S1624
39	ANI61C3549
40	ANI61S1635
41	ANI61C3559
42	ANI61C3561
43	ANI61C3563
44	ANI61C3565
45	ANI61C3567
46	ANI61S1636
47	ANI61C3572
48	ANI61S1637
49	ANI61S1639
50	ANI61S1647
51	ANI61S1648
52	ANI61S1649
53	ANI61S1650

54	ANI61S1651
55	ANI61S1652
56	ANI61S1653
57	ANI61S1654
58	ANI61S1655
59	ANI61C3599
60	ANI61C3622
61	ANI61C3624
62	ANI61C3627
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64	ANI61C3633
65	ANI61C3636
66	ANI61C3640
67	ANI61C3644
68	ANI61C3648
69	ANI61C3652
70	ANI61C3677
71	ANI61C3679
72	ANI61C3682
73	ANI61C3685
74	ANI61C3688
75	ANI61C3691
76	ANI61C3695
77	ANI61C3699
78	ANI61C3703
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84	ANI61S1679
85	ANI61C3738
86	ANI61C3742
87	ANI61C3746
88	ANI61C3750
89	ANI61S1680
90	ANI61S1691
91	ANI61S1692
92	ANI61C3789
93	ANI61C3793
94	ANI61S1693
95	ANI61S1694
96	ANI61S1696
97	ANI61C3806
98	ANI61S1698
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102	ANI61C10066
103	ANI61C10067
104	ANI61C10068
105	ANI61C10069
106	ANI61C10070
107	ANI61C10071
108	ANI61C10072
109	ANI61C10073

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111	ANI61C10086
112	ANI61C10088
113	ANI61C10089
114	ANI61C10090
115	ANI61C10091
116	ANI61C10092
117	ANI61C10093
118	ANI61C10094
119	ANI61S4148
120	ANI61S4153
121	ANI61S4154
122	ANI61S4155
123	ANI61C10111
124	ANI61S4156
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127	ANI61C10114
128	ANI61C10115
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130	ANI61C10123
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132	ANI61C10125
133	ANI61C10126
134	ANI61C10127
135	ANI61S4161
136	ANI61C10128
137	ANI61S4162
138	ANI61C10129
139	ANI61C10130
140	ANI61C10134
141	ANI61S4170
142	ANI61C10135
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145	ANI61C10138
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156	ANI61C10152
157	ANI61C10153
158	ANI61S4178
159	ANI61S4179
160	ANI61S4181
161	ANI61C10154
162	ANI61C10156
163	ANI61S4184
164	ANI61C10158
165	ANI61C10160

166	ANI61S4185
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169	ANI61C10165
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171	ANI61C10168
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173	ANI61C10170
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175	ANI61C10172
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189	ANI61C10193
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197	ANI61C10208
198	ANI61S4211
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202	ANI61C10804
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216	ANI61C10831
217	ANI61C10832
218	ANI61C10833
219	ANI61C10834
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221	ANI61S4413

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235	ANI61S4427
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238	ANI61C10863
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242	ANI61S4435
243	ANI61C10871
244	ANI61S4436
245	ANI61S4437
246	ANI61S4438
247	ANI61S4439
248	ANI61C10872
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253	ANI61S4451
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255	ANI61C10877
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257	ANI61C10879
258	ANI61C10880
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260	ANI61C10883
261	ANI61C10884
262	ANI61C10886
263	ANI61C10888
264	ANI61C10889
265	ANI61S4455
266	ANI61C10891
267	ANI61C10893
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270	ANI61C10895
271	ANI61C10896
272	ANI61S4462
273	ANI61C10897
274	ANI61S4465
275	ANI61C10899
276	ANI61C10900
277	ANI61C10901

278	ANI61C10902
279	ANI61C10903
280	ANI61C10904
281	ANI61C10906
282	ANI61S4472
283	ANI61C10907
284	ANI61C10908
285	ANI61C10909
286	ANI61C10911
287	ANI61S4476
288	ANI61C10913
289	ANI61C10914
290	ANI61C10917
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293	ANI61C10924
294	ANI61S4484
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312	ANI61C71
313	ANI61C72
314	ANI61C73
315	ANI61C74
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317	ANI61C75
318	ANI61C76
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321	ANI61C90
322	ANI61C92
323	ANI61S30
324	ANI61C93
325	ANI61C94
326	ANI61C95
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329	ANI61C98
330	ANI61C103
331	ANI61C106
332	ANI61S43
333	ANI61C109

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335	ANI61C113
336	ANI61C114
337	ANI61C116
338	ANI61C117
339	ANI61C119
340	ANI61C125
341	ANI61C126
342	ANI61C127
343	ANI61C128
344	ANI61S58
345	ANI61C129
346	ANI61C130
347	ANI61C131
348	ANI61C132
349	ANI61C134
350	ANI61C139
351	ANI61C140
352	ANI61C142
353	ANI61C143
354	ANI61S72
355	ANI61C146
356	ANI61C147
357	ANI61C148
358	ANI61C149
359	ANI61S76
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361	ANI61C158
362	ANI61C160
363	ANI61C163
364	ANI61C164
365	ANI61S90
366	ANI61C167
367	ANI61C168
368	ANI61C171
369	ANI61C173
370	ANI61C177
371	ANI61C179
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373	ANI61C183
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376	ANI61C187
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378	ANI61C190
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380	ANI61C196
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383	ANI61C201
384	ANI61S130
385	ANI61C203
386	ANI61C206
387	ANI61C207
388	ANI61C208
389	ANI61C211

390	ANI61C221
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392	ANI61C223
393	ANI61S150
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403	ANI61S428
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406	ANI61C905
407	ANI61C906
408	ANI61C907
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411	ANI61C919
412	ANI61C921
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430	ANI61C947
431	ANI61C948
432	ANI61C949
433	ANI61C950
434	ANI61C952
435	ANI61C953
436	ANI61C955
437	ANI61C956
438	ANI61C957
439	ANI61S437
440	ANI61C960
441	ANI61C961
442	ANI61C963
443	ANI61C964
444	ANI61C966
445	ANI61C967

446	ANI61C969
447	ANI61C971
448	ANI61S441
449	ANI61C974
450	ANI61C975
451	ANI61C976
452	ANI61C977
453	ANI61C978
454	ANI61C979
455	ANI61C980
456	ANI61C982
457	ANI61C984
458	ANI61C985
459	ANI61C987
460	ANI61C990
461	ANI61S460
462	ANI61C993
463	ANI61C995
464	ANI61S463
465	ANI61C999
466	ANI61C1000
467	ANI61C1002
468	ANI61C1003
469	ANI61C1006
470	ANI61S480
471	ANI61C1009
472	ANI61C1010
473	ANI61C1012
474	ANI61C1013
475	ANI61C1015
476	ANI61C1017
477	ANI61C1020
478	ANI61C1021
479	ANI61C1022
480	ANI61C1027
481	ANI61C1030
482	ANI61C1031
483	ANI61C1033
484	ANI61C1035
485	ANI61C1036
486	ANI61C1037
487	ANI61C1038
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490	ANI61C1049
491	ANI61C1051
492	ANI61C1054
493	ANI61S526
494	ANI61C1059
495	ANI61C1062
496	ANI61S530
497	ANI61C1066
498	ANI61C1068
499	ANI61C1069
500	ANI61C1722
501	ANI61S749

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504	ANI61C1728
505	ANI61C1729
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507	ANI61C1731
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515	ANI61C1748
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526	ANI61C1769
527	ANI61S751
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533	ANI61C1774
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535	ANI61C1777
536	ANI61C1779
537	ANI61C1780
538	ANI61C1782
539	ANI61S758
540	ANI61C1784
541	ANI61C1785
542	ANI61C1787
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544	ANI61C1790
545	ANI61C1791
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552	ANI61C1798
553	ANI61C1799
554	ANI61S772
555	ANI61C1800
556	ANI61C1802
557	ANI61C1803

558	ANI61C1804
559	ANI61C1805
560	ANI61C1807
561	ANI61C1810
562	ANI61C1812
563	ANI61C1814
564	ANI61S782
565	ANI61C1815
566	ANI61C1817
567	ANI61C1819
568	ANI61C1820
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591	ANI61C1857
592	ANI61C1859
593	ANI61S829
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612	ANI61C2467
613	ANI61S1039

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615	ANI61C2472
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617	ANI61S1043
618	ANI61C2474
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624	ANI61C2491
625	ANI61C2492
626	ANI61C2494
627	ANI61C2495
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632	ANI61S1056
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644	ANI61C2528
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651	ANI61S1075
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661	ANI61S1091
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667	ANI61C2570
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669	ANI61C2574

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671	ANI61C2578
672	ANI61C2580
673	ANI61C2582
674	ANI61C2584
675	ANI61C2586
676	ANI61C2587
677	ANI61C2588
678	ANI61C2590
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686	ANI61C2609
687	ANI61C2611
688	ANI61C2612
689	ANI61C2614
690	ANI61C2616
691	ANI61C2618
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697	ANI61C2634
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722	ANI61C3308
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724	ANI61C3312
725	ANI61C3314

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727	ANI61C3316
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732	ANI61C3323
733	ANI61C3326
734	ANI61C3329
735	ANI61C3331
736	ANI61C3333
737	ANI61C3335
738	ANI61C3337
739	ANI61C3339
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742	ANI61C3345
743	ANI61C3347
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749	ANI61C3359
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757	ANI61C3371
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761	ANI61C3378
762	ANI61C3381
763	ANI61C3383
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765	ANI61C3387
766	ANI61C3390
767	ANI61C3392
768	ANI61C3393
769	ANI61C3395
770	ANI61C3397
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774	ANI61C3403
775	ANI61C3406
776	ANI61C3408
777	ANI61C3410
778	ANI61C3413
779	ANI61C3415
780	ANI61C3419
781	ANI61C3420

782	ANI61C3424
783	ANI61C3427
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786	ANI61C3433
787	ANI61C3434
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792	ANI61C3449
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794	ANI61C3456
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797	ANI61C3461
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799	ANI61C3465
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807	ANI61C4220
808	ANI61C4222
809	ANI61C4223
810	ANI61C4233
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812	ANI61C4237
813	ANI61C4240
814	ANI61C4242
815	ANI61C4244
816	ANI61C4245
817	ANI61C4246
818	ANI61C4248
819	ANI61C4250
820	ANI61C4259
821	ANI61C4261
822	ANI61C4263
823	ANI61C4266
824	ANI61C4267
825	ANI61C4269
826	ANI61C4270
827	ANI61C4272
828	ANI61C4274
829	ANI61C4275
830	ANI61C4276
831	ANI61C4278
832	ANI61C4281
833	ANI61C4283
834	ANI61C4285
835	ANI61C4287
836	ANI61C4289
837	ANI61C4291

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839	ANI61C4295
840	ANI61C4299
841	ANI61C4300
842	ANI61C4301
843	ANI61C4302
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845	ANI61C4306
846	ANI61C4309
847	ANI61C4310
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849	ANI61C4312
850	ANI61C4315
851	ANI61C4316
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855	ANI61C4326
856	ANI61C4327
857	ANI61C4329
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861	ANI61C4342
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863	ANI61C4345
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872	ANI61C4363
873	ANI61C4367
874	ANI61C4368
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877	ANI61C4377
878	ANI61C4380
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891	ANI61C4409
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901	ANI61C5162
902	ANI61C5164
903	ANI61C5165
904	ANI61C5168
905	ANI61C5169
906	ANI61C5172
907	ANI61C5175
908	ANI61C5177
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16199	ANI50C8867_3
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16206	ANI50S6383

Table 2

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16207	ENU000001	ANI61C5803: 2968..3252	38-57	261-280	EST	"j3h09a1.rl, l3h09a1.fl"		32	32	1			probable 60S ribosomal protein C2E11.04; (AL031181) 60S ribosomal protein L28 [Schizosaccharomyces pombe]; (AL035064) 60S ribosomal protein L28 [Schizosaccharomyces pombe]
16208	ENU000002	ANI61C4566: 5066..5474	40-59	375-406	EST	"y6a02a1.rl, y6a02a1.fl"		33	33	1.1			(AL021841) PE_PGRS [Mycobacterium tuberculosis] (AF130355) Pad-1 [Neurospora crassa]
16209	ENU000003	ANI61C486:1 033..8	86-113	1034-1069	EST	"c9d02a1.rl, c9d02a1.fl"		269	269	2E-71			(U31653) particulate methane monooxygenase [Methylobacterium methanica]
16210	ENU000004	ANI61C7400: 91..607	112-131	560-585	EST	"w4b01a1.rl, w4b01a1.fl"		32	32	3.6			(Z95397) unknown [Schizosaccharomyces pombe] (AL031786) hypothetical protein. [Schizosaccharomyces pombe] (AE001251) exoribonuclease II (mb) [Treponema pallidum]
16211	ENU000005	ANI61C5660: 106..672	110-128	613-634	EST	"o9f10a1.rl, o9f10a1.fl"		56	56	0.000000			prostaglandin transporter (PGT) (matrin F/G); prostaglandin transporter - rat
16212	ENU000006	ANI61C1405: 3433..3638	120-139	259-283	EST	"w4c07a1.rl, w4c07a1.fl"		63	63	2E-10			prostaglandin transporter (PGT) (matrin F/G); prostaglandin transporter - rat
16213	ENU000007	ANI61C9317: 4348..4148	40-59	720-740	EST	"c5c05a1.rl, c5c05a1.fl"		33	33	2			prostaglandin transporter (PGT) (matrin F/G); prostaglandin transporter - rat
16214	ENU000008	ANI61C9324: 54..253	38-59	171-195	EST	"d5e06a1.rl, d5e06a1.fl"		30	30	2.5			prostaglandin transporter (PGT) (matrin F/G); prostaglandin transporter - rat
16215	ENU000009	ANI61C9324: 61..260	45-64	180-202	EST	"c8f05a1.rl, c8f05a1.fl"		29	29	3.3			prostaglandin transporter (PGT) (matrin F/G); prostaglandin transporter - rat
16216	ENU000010	ANI61C9324: 54..253	38-59	171-195	EST	"l0g12a1.rl, l0g12a1.fl"		30	30	2.5			prostaglandin transporter (PGT) (matrin F/G); prostaglandin transporter - rat
16217	ENU000011	ANI61C9324: 41..240	25-48	159-182	EST	"y6b07a1.rl, y6b07a1.fl"		30	30	2.5			prostaglandin transporter (PGT) (matrin F/G); prostaglandin transporter - rat
16218	ENU000012	ANI61C4812: 437..636	44-63	182-201	EST	"z3d11a1.rl, z3d11a1.fl"		143	143	1E-34			(D87063) chitinase [Emericella nidulans]
16219	ENU000013	ANI61C9324: 54..253	38-59	171-195	EST	"z4a05a1.rl, z4a05a1.fl"		30	30	2.5			prostaglandin transporter (PGT) (matrin F/G); prostaglandin transporter - rat
16220	ENU000014	ANI61C4718: 1244..1453	38-57	186-205	EST	"y3h12a1.rl, y3h12a1.fl"		32	32	0.5			ubiquitin 1 - Tetrahymena pyriformis (SGC5) (fragment); (M24081) ubiquitin [Tetrahymena pyriformis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16221	ENU00015	ANI61C4718: 38-57 1244..1453	38-57	186-205	EST	"g3c04a1.rl, g3c04a1.fl"		32	32	0.5		ubiquitin 1 - Tetrahymena pyriformis (SGC5) (fragment) ; (M24081)
16222	ENU00016	ANI61C4812: 22-42 414..625	22-42	172-191	EST	"r1d06a1.rl, r1d06a1.fl"		154	154	9E-38		ubiquitin [Tetrahymena pyriformis] (D87063) chitinase [Emericella nidulans]
16223	ENU00017	ANI61C4812: 22-42 414..625	22-42	172-191	EST	"r1b07a1.rl, r1b07a1.fl"		154	154	9E-38		(D87063) chitinase [Emericella nidulans]
16224	ENU00018	ANI61C6468: 70-89 2109..1879	70-89	240-258	EST	"z4g03a1.rl, z4g03a1.fl"		31	31	1.9		translational activator GCN1 ; translation activator GCN1 - yeast (Saccharomyces cerevisiae) ; (L12467)
16225	ENU00019	ANI61C3987: 61-80 1271..1504	61-80	233-252	EST	"r4e03a1.rl, r4e03a1.fl"		32	32	0.66		translational activator [Saccharomyces cerevisiae] ; (X91837) translational activator GCN1 [Saccharomyces cerevisiae] ; (Z72717) ORF YGL195w [Saccharomyces cerevisiae]
16226	ENU00020	ANI61C7278: 64-83 2805..3039	64-83	236-256	EST	"j0a09a1.rl, j0a09a1.fl"		28	28	9.8		phospholipase A2 (EC 3.1.1.4) precursor - Chinese habu "asparaginyl-TRNA synthetase, mitochondrial precursor (asparagine-TRNA ligase) (ASNRS) ; hypothetical protein YCR024c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR024c, len:492 [Saccharomyces cerevisiae] "
16227	ENU00021	ANI61S3058: 24-42 312..50	24-42	225-244	EST	"n8d06a1.rl, n8d06a1.fl"		151	151	9E-37		"60S ribosomal protein L13A (RP22) ; ribosomal protein L16.e.A, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 199, CAI: 0.62, predicted to be spliced, similar to A44367 A44367 P23=tumor-specific transplantation antigen and ribosomal proteins [Saccharomyces cerevisiae] "
16228	ENU00022	ANI61C6046: 28-47 484..171	28-47	278-299	EST	"clb10a1.rl, clb10a1.fl"		29	29	8.4		Apical endosomal glycoprotein precursor ; apical endosomal protein precursor - rat ; (L37380) apical endosomal glycoprotein [Rattus norvegicus]
16229	ENU00023	ANI61C1658: 55-74 1936..2297	55-74	355-374	EST	"r7d05a1.rl, r7d05a1.fl"		31	31	4.8		(AJ131708) gamma response I protein [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16230	ENU000024	ANI61C584:8 20..1208	56-75	382-401	EST	"y8g11a1.rl, y8g11a1.fl"			131	2E-30			nucleoside diphosphate kinase (NDK) (NDP kinase) ; nucleoside-diphosphate kinase (EC 2.7.4.6) - yeast (Saccharomyces cerevisiae) ; (X75780) A153 [Saccharomyces cerevisiae] ; (D13562) nucleoside diphosphate kinase [Saccharomyces cerevisiae] ; (Z28067) ORF YKL067w [Saccharomyces cerevisiae] ; nucleoside diphosphate kinase [Saccharomyces cerevisiae] protein-glutamine glutamyltransferase E3 precursor (TGase E3) (transglutaminase 3) ; (L10385) transglutaminase E3 [Mus musculus] (L36960) glycerol-3-phosphate dehydrogenase [Ceratitis capitata]
16231	ENU000025	ANI61C137:3 810..4223	70-89	415-441	EST	"10b10a1.rl, 10b10a1.fl"		31	5.9				hypothetical 93.9 KD protein T20B12.6 in chromosome III ; (U10401) T20B12.6 gene product [Caenorhabditis elegans] hydroxyproline-rich glycoprotein (clone Hyp2.13) - kidney bean (fragment) ; (M18095) hydroxyproline-rich glycoprotein [Phaseolus vulgaris] (AJ002531) nosL [Bradyrhizobium japonicum] (AF093142) aconitase [Aspergillus terreus] (U88184) F36H5.3 gene product [Caenorhabditis elegans] (Z99112) similar to hypothetical proteins [Bacillus subtilis] (AJ002291) penicillin-binding protein 1b [Streptococcus pneumoniae]
16232	ENU000026	ANI50S1275: 466..39	26-45	389-411	EST	"t2e03a1.rl, t2e03a1.fl"		76	9E-14				
16233	ENU000027	ANI61C6109: 2589..2139	61-80	445-469	EST	"o8d08a1.rl, o8d08a1.fl"		50	0.000008				
16234	ENU000028	ANI61C7998: 3381..3855	32-51	447-464	EST	"z4g12a1.rl, z4g12a1.fl"		43	0.001				
16235	ENU000029	ANI61C412:2 192..2691	59-78	497-516	EST	"c8c12a1.rl, c8c12a1.fl"		32	3.3				
16236	ENU000030	ANI61C9735: 6052..6639	23-42	548-568	EST	"i2c01a1.rl, i2c01a1.fl"		157	1E-38				
16237	ENU000031	ANI61C1708: 1586..2176	61-78	589-609	EST	"m5c06a1.rl, m5c06a1.fl"		33	2.2				
16238	ENU000032	ANI61C1110 4-2085..1446	71-90	634-668	EST	"i8g03a1.rl, i8g03a1.fl"		36	0.25				
16239	ENU000033	ANI61C5131: 985..335	60-80	649-668	EST	"j4e04a1.rl, j4e04a1.fl"		34	1.3				
16240	ENU000034	ANI61C4335: 86..752	55-76	660-679	EST	"m0h05a1.rl, m0h05a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16241	ENU00035	ANI61C630:1 41..850	64-83	701-731	EST	"y8a11a1.r1, y8a11a1.fl"		34	34	1.1		(L47321) glycoprotein 150 [Murine herpesvirus 68]; (Y09060) serine threonine rich glycoprotein [murine herpesvirus 68]; (U97553) glycoprotein 150 [murine herpesvirus 68]
16242	ENU00036	ANI61C2371: 60-79 3954..3212	60-79	736-760	EST	"g3g02a1.r1, g3g02a1.fl"		33	33	2		(AL031027) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=160.71; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:Q05586; 2-match_description=glutamate (NMDA) receptor subun...
16243	ENU00037	ANI61C2371: 51-70 3953..3207	51-70	733-755	EST	"o6e10a1.r1, o6e10a1.fl"		33	33	2		(AL031027) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=160.71; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:Q05586; 2-match_description=glutamate (NMDA) receptor subun...
16244	ENU00038	ANI61C4718: 52-71 1772..1419	52-71	779-800	EST	"d1f09a1.r1, d1f09a1.fl"		322	322	e-115		(Z22614) ubiquitin [Tetrahymena pyriformis]
16245	ENU00039	ANI61C8257: 29-48 3012..2209	29-48	771-790	EST	"c6h07a1.r1, c6h07a1.fl"		46	46	0.0003		dimethylalanine monooxygenase (N-oxide forming) 1 (hepatic flavin-containing monooxygenase 1) (FMO 1) (dimethylANline oxidase 1); (D16215) flavin-containing monooxygenase [Mus musculus]; (U87456) flavin-containing monooxygenase 1 [Mus musculus] (M17921) latency associated transcript (LAT) ORF-2 [Herpes simplex virus type 1]
16246	ENU00040	ANI61C8085: 69-88 1801..984	69-88	818-844	EST	"d5g04a1.r1, d5g04a1.fl"		34	34	1.3		(AF054174) histone macroH2A1.2 [Homo sapiens]
16247	ENU00041	ANI61C7232: 45-66 2859..3689	45-66	814-833	EST	"w6d05a1.r1, w6d05a1.fl"		33	33	3		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16248	ENU00042	ANI61C5969: 25-44 106..1208	1066- 1085	EST		"w6b10a1.r1, w6b10a1.fl"		37	0.22			"Glutenin, high molecular weight subunit PW212 precursor; glutenin, high molecular weight chain precursor - wheat; (X03346) glutenin [Triticum aestivum]"
16249	ENU00043	ANI61C1087: 41-62 482..678	1317- 1351	EST		"r7f11a1.r1, r7f11a1.fl"		122	7E-27			(U81790) PIG8 [Uromyces fabae]
16250	ENU00044	ANI61C7027: 46-65 1396..15	1365- 1385	EST		"w8c04a1.r1, w8c04a1.fl"		490	e-138			Carboxypeptidase Y precursor (carboxypeptidase YSCY)
16251	ENU00045	ANI61C8717: 25-44 4377..2914	1425- 1445	EST		"m2h12a1.r1, m2h12a1.fl"		42	0.012			(AF080683) PITSLRE protein kinase alpha SV5 isoform [Homo sapiens]
16252	ENU00046	ANI61C4015: 26-47 1137..938	149-183	EST		"j4f02a1.r1, j4f02a1.fl"		29	4.4			putative iron alcohol dehydrogenase; probable alcohol dehydrogenase (EC 1.1.1.1) - fission yeast (Schizosaccharomyces pombe); (Z49811) iron containing alcohol dehydrogenase [Schizosaccharomyces pombe]
16253	ENU00047	ANI61C3597: 46-64 1117..924	186-203	EST		"d5b05a1.r1, d5b05a1.fl"		31	0.86			(Z95150) hypothetical protein Rv3127 [Mycobacterium tuberculosis]
16254	ENU00048	ANI61C8436: 35-54 715..921	170-199	EST		"p0h09a1.r1, p0h09a1.fl"		29	4.3			(Z81050) Similarity to C.elegans ligand-gated ion channels [Caenorhabditis elegans]
16255	ENU00049	ANI61C6647: 67-86 4466..4249	220-243	EST		"h4c04a1.r1, h4c04a1.fl"		30	1.9			(U63336) MHC Class I region proline rich protein [Homo sapiens]
16256	ENU00050	ANI61C8167: 62-84 1190..961	216-249	EST		"r7c12a1.r1, r7c12a1.fl"		36	0.056			(Z99295) citrate lyase [Schizosaccharomyces pombe]
16257	ENU00051	ANI61C9308: 38-59 786..997	214-233	EST		"e9c05a1.r1, e9c05a1.fl"		35	0.1			nucleic acid-binding protein E5.1 - human; (L37368) RNA-binding protein [Homo sapiens]
16258	ENU00052	ANI61C2422: 32-53 1029..1270	204-231	EST		"j9f12a1.r1, j9f12a1.fl"		29	6.3			(AE001279) hypothetical protein [Chlamydia trachomatis]
16259	ENU00053	ANI61C6468: 26-47 1816..2056	196-229	EST		"w9f11a1.r1, w9f11a1.fl"		29	6.6			(U89708) unknown [Leptospira interrogans serovar lai]
16260	ENU00054	ANI61C6468: 25-48 2170..1924	207-229	EST		"z4g06a1.r1, z4g06a1.fl"		29	7.2			(X85254) polymerase [Hepatitis B virus]
16261	ENU00055	ANI61C1061: 65-86 1698..1953	248-278	EST		"z5f07a1.r1, z5f07a1.fl"		38	0.019			(U65409) Sla2p [Yarrowia lipolytica]
16262	ENU00056	ANI61C3434: 22-55 2506..2249	208-237	EST		"c6c12a1.r1, c6c12a1.fl"						

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16263	ENU000057	ANI61C2786: 381..121	52-75	240-270	EST	"y3g09a1.rl, y3g09a1.fl"			31	1.5		(AL023635) hypothetical protein MLCB1243.36 [Mycobacterium leprae] ubiquitin S2 [Drosophila melanogaster]
16264	ENU000058	ANI61C4718: 1697..1183	45-66	261-296	EST	"w7a05a1.rl, w7a05a1.fl"			46	0.00009		(AB007770) translation elongation factor 1 alpha [Aspergillus oryzae]
16265	ENU000059	ANI61C1794: 3511..3217	22-47	239-274	EST	"s8f04a1.rl, s8f04a1.fl"			97	3E-20		(X08013) ubiquitin (752 is 2nd base in codon) [Cricetulus sp.]
16266	ENU000060	ANI61C4718: 2247..1211	42-61	261-296	EST	"i8h04a1.rl, i8h04a1.fl"			69	1E-11		(X08013) ubiquitin (752 is 2nd base in codon) [Cricetulus sp.]
16267	ENU000061	ANI61C4718: 2247..1211	42-61	261-296	EST	"q0g06a1.rl, q0g06a1.fl"			69	1E-11		(X08013) ubiquitin (752 is 2nd base in codon) [Cricetulus sp.]
16268	ENU000062	ANI61C4718: 2247..1211	42-61	261-296	EST	"f1d09a1.rl, f1d09a1.fl"			69	1E-11		(AF060232) monoubiquitin/carboxy extension protein fusion [Botryotinia fuckeliana]
16269	ENU000063	ANI61C4718: 2247..1208	22-41	244-279	EST	"a0f02a1.rl, a0f02a1.fl"			69	1E-11		(AF060232) monoubiquitin/carboxy extension protein fusion [Botryotinia fuckeliana]
16270	ENU000064	ANI61C4718: 2247..1208	42-61	264-299	EST	"r4e11a1.rl, r4e11a1.fl"			69	1E-11		(AJ001272) manganese resistance 1 protein [Saccharomyces cerevisiae]
16271	ENU000065	ANI61C8760: 272..574	45-64	268-303	EST	"q0e09a1.rl, q0e09a1.fl"			41	0.000000		"DARPP-32=dopamine and cAMP- regulated phosphoprotein [human, brain, Peptide, 204 aa]; phosphoprotein ARPP-32 [Homo sapiens]"
16272	ENU000066	ANI61C1010 1:2112..1798	30-53	283-303	EST	"o6g04a1.rl, o6g04a1.fl"			31	3.1		hypothetical protein o259a - Escherichia coli ; (U14003) ORF_o259a [Escherichia coli]; (AE000492) FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli]
16273	ENU000067	ANI61C1147 7:3288..3617	22-52	286-309	EST	"w4a04a1.rl, w4a04a1.fl"			31	3.1		(AL022103) mannose-6-phosphate isomerase [Schizosaccharomyces pombe]
16274	ENU000068	ANI61C1368: 737..1068	29-48	294-318	EST	"d3f05a1.rl, d3f05a1.fl"			31	3.1		(AF035434) elongation factor 3 [Aspergillus fumigatus]
16275	ENU000069	ANI61C5614: 150..486	22-54	288-316	EST	"z3d01a1.rl, z3d01a1.fl"			36	0.12		
16276	ENU000070	ANI61C2246: 20..357	39-58	311-334	EST	"t2c05a1.rl, t2c05a1.fl"			183	3E-46		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16277	ENU00071	ANI61C2013: 476..820	35-66	302-337	EST	"w4a02a1.rl, w4a02a1.fl"			36	0.099			(AL031852) putative metal homeostasis factor
16278	ENU00072	ANI61C7988: 66-85 1302..1651	66-85	348-373	EST	"z4f05a1.rl, z4f05a1.fl"			127	4E-35			[Schizosaccharomyces pombe] putative proteasome component C9/Y13 (macropain subunit) (multicatalytic endopeptidase complex subunit); hypothetical protein SPA13C5.01c - fission yeast (Schizosaccharomyces pombe); (Z50112) proteasome A- type subunit [Schizosaccharomyces pombe] (D83992) similar to gpi: SCU43281_10 Lpg10p (56.7% identity in 60 aa overlap)
16279	ENU00073	ANI61S1034: 48-67 45..401	48-67	343-362	EST	"z2b09a1.rl, z2b09a1.fl"			40	0.007			[Schizosaccharomyces pombe] ribosomal protein L37a; 60S ribosomal protein L37A; ribosomal protein L37a - rat; ribosomal protein L37a - human; ribosomal protein L37a - mouse; (X66699) ribosomal protein L37a [Homo sapiens]; (X14069) ribosomal protein L37a (AA 1 - 92) [Rattus rattus]; (L06499) ribosomal protein L37a [Homo sapiens]; (X73331) ribosomal protein L37a [Mus musculus]
16280	ENU00074	ANI50S2543: 54-73 37..408	54-73	363-383	EST	"y8h12a1.rl, y8h12a1.fl"			30	0.28			40S ribosomal protein S14 (CRP2); (X53734) ribosomal protein crp-2 [Neurospora crassa]
16281	ENU00075	ANI61C5524: 22-47 1660..1284	22-47	321-356	EST	"y4f05a1.rl, y4f05a1.fl"			46	0.000000 001			aeruginosa (AC002387) putative reverse transcriptase [Arabidopsis thaliana] (U95045) velvet A [Emmericella nidulans] (AF007193) mucin [Homo sapiens]
16282	ENU00076	ANI61S2489: 22-55 12..391	22-55	327-359	EST	"m8c07a1.rl, m8c07a1.fl"			31	3			hypothetical protein YDR313c - yeast (Saccharomyces cerevisiae); (U28374) YDR313C gene product [Saccharomyces cerevisiae]
16283	ENU00077	ANI61C7366: 61-80 1189..818	61-80	373-398	EST	"t2g04a1.rl, t2g04a1.fl"			34	0.46			
16284	ENU00078	ANI61C8333: 29-50 1658..1278	29-50	339-368	EST	"l0h12a1.rl, l0h12a1.fl"			66	8E-11			
16285	ENU00079	ANI61C3987: 22-49 947..559	22-49	344-368	EST	"f2h12a1.rl, f2h12a1.fl"			32	1.8			
16286	ENU00080	ANI61C1031 24-46 7:492..102	24-46	338-371	EST	"z4a10a1.rl, z4a10a1.fl"			54	0.000000 4			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvtg	Description
16287	ENU00081	ANI61C1069 1:2879..3271	69-88	400-419	EST	"x7d07a1.r1, x7d07a1.fl"		183	5E-46				signal recognition particle 54 KD protein homolog ; signal recognition particle 54K protein homolog - Aspergillus niger ; (L38317) srpA gene product [Aspergillus niger] ; srpA gene [Aspergillus niger]
16288	ENU00082	ANI61C1067 4:424..30	62-82	393-414	EST	"i0a04a1.r1, i0a04a1.fl"		55	0.000000	2			(AL031966) hypothetical HIT-family protein [Schizosaccharomyces pombe]
16289	ENU00083	ANI61C1067 4:424..30	62-82	393-414	EST	"t2d07a1.r1, t2d07a1.fl"		55	0.000000	2			(AL031966) hypothetical HIT-family protein [Schizosaccharomyces pombe]
16290	ENU00084	ANI61C1053 6:482..86	49-68	384-403	EST	"y8f11a1.r1, y8f11a1.fl"		31	5.5				(X82877) sodium-D-glucose cotransporter [Homo sapiens]
16291	ENU00085	ANI61C3270: 208..604	22-44	357-376	EST	"x5g08a1.r1, x5g08a1.fl"		31	5.5				(D84678) omega-3 fatty acid desaturase [Triticum aestivum]
16292	ENU00086	ANI61C5867: 1364..953	34-53	384-403	EST	"g6b11a1.r1, g6b11a1.fl"		34	0.39				(Z97208) putative Na/H exchanger [Schizosaccharomyces pombe]
16293	ENU00087	ANI61S716:4 41..25	28-47	378-402	EST	"e4b03a1.r1, e4b03a1.fl"		31	6				(AF061025) leucine zipper-EF-hand containing transmembrane protein 1 [Homo sapiens]
16294	ENU00088	ANI61C4704: 435..1	55-74	428-447	EST	"x8e05a1.r1, x8e05a1.fl"		179	8E-45				"fructose-1,6-bisphosphatase (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) ; fructose-bisphosphatase (EC 3.1.3.11) - yeast (Saccharomyces cerevisiae) ; (Y00754) fructose-1,6-bisphosphatase (AA 1-348) [Saccharomyces cerevisiae] ; (J03207) fructose-1,6-bisphosphatase [Saccharomyces cerevisiae] ; (U19103) Fbp 1p: fructose-1,6-bisphosphatase [Saccharomyces cerevisiae]"
16295	ENU00089	ANI61C8447: 1183..737	45-66	414-449	EST	"j9d02a1.r1, j9d02a1.fl"		32	2.2				(Z81095) predicted using Genefinder; cDNA EST EMBL:D71338 comes from this gene; cDNA EST EMBL:D74010 comes from this gene; cDNA EST EMBL:D74852 comes from this gene; cDNA EST EMBL:C07354 comes from this gene; cDNA EST EMBL:C086...

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16296	ENU00090	ANI61C2075: 23-42 137..584	23-42	404-428	EST	"g3b07a1.rl, g3b07a1.fl"		101	101	3E-21			24 KD metalloproteinase precursor (deuterolysin) ; metalloproteinase (EC 3.4.-.) 23K - Aspergillus flavus ; (L37524) metalloproteinase [Aspergillus flavus]
16297	ENU00091	ANI61C2075: 23-42 137..584	23-42	404-428	EST	"o9d11a1.rl, o9d11a1.fl"		101	101	3E-21			24 KD metalloproteinase precursor (deuterolysin) ; metalloproteinase (EC 3.4.-.) 23K - Aspergillus flavus ; (L37524) metalloproteinase [Aspergillus flavus]
16298	ENU00092	ANI61C7813: 50-69 1049..1498	50-69	438-457	EST	"y4h05a1.rl, y4h05a1.fl"		36	36	0.12			shed acute-phase antigen - Trypanosoma cruzi ; (X57235) shed-acute-phase-antigen [Trypanosoma cruzi]
16299	ENU00093	ANI61C1368: 22-53 613..1068	22-53	411-435	EST	"e0g12a1.rl, e0g12a1.fl"		31	31	5.2			hypothetical protein o259a - Escherichia coli ; (U14003) ORF_o259a [Escherichia coli] ; (AE000492) FKBP-type 22KD peptidyl-prolyl cis-trans isomerase (rotamase) [Escherichia coli]
16300	ENU00094	ANI61C1032 71-91 2:2226..1766	71-91	470-489	EST	"w8d12a1.rl, w8d12a1.fl"		73	73	1E-26			ADP-ribosylation factor ; ADP-ribosylation factor - Ajellomyces capsulata ; (L25117) ADP-ribosylation factor [Histoplasma capsulatum]
16301	ENU00095	ANI50C1088 27-49 6_1:855..391	27-49	417-449	EST	"x7d04a1.rl, x7d04a1.fl"		32	32	2.4			(M19828) apolipoprotein B-100 precursor [Homo sapiens]
16302	ENU00096	ANI61C6652: 39-58 1047..571	39-58	454-473	EST	"a0h02a1.rl, a0h02a1.fl"		33	33	1.4			transcription factor MBP1 (MBF subunit P120) ; transcription factor MBP1 - yeast (Saccharomyces cerevisiae) ; (X74158) mbp1 transcription factor [Saccharomyces cerevisiae] ; (Z74104) ORF YDL056w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16303	ENU00097	ANI61C1710: 229..706	58-77	471-493	EST	"g5d09a1.r1, g5d09a1.fl"		32	32	1.9			(Z93377) cDNA EST EMBL:D65765 comes from this gene; cDNA EST EMBL:D69319 comes from this gene; cDNA EST yk235a4.3 comes from this gene; cDNA EST yk235a4.5 comes from this gene; cDNA EST yk414g2.5 comes from this gene [Caenorhab...; (Z81513) cDNA EST EMBL:D65765 comes from this gene; cDNA EST EMBL:D69319 comes from this gene; cDNA EST yk235a4.3 comes from this gene; cDNA EST yk235a4.5 comes from this gene; cDNA EST yk414g2.5 comes from this gene [Caenorhab... comes from this gene [O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (AF017151) oxidoreductase [Aspergillus parasiticus] v-ski avian sarcoma viral oncogene homolog ; SKI oncogene (C-SKI) ; transforming protein ski - human ; (X15218) ski protein (AA 1 - 728) [Homo sapiens] "(AL031532) yeast gtr2 homolog, novel small GTPase subfamily protein [Schizosaccharomyces pombe]" "hypothetical 81.4 KD protein in GREB-FEOA intergenic region ; (AE000416) orf, hypothetical protein [Escherichia coli]" Versican core protein precursor (large fibroblast proteoglycan) (chondroitin sulfate proteoglycan core protein 2) (PG-M) ; chondroitin sulfate proteoglycan PG-M core protein - chicken ; (D13542) proteoglycan [Gallus gallus]
16304	ENU00098	ANI61C6116: 129..612	44-69	456-485	EST	"y8f01a1.r1, y8f01a1.fl"		125	125	2E-28			
16305	ENU00099	ANI61C2195: 502..1	32-51	459-489	EST	"c7c05a1.r1, c7c05a1.fl"		32	32	2			
16306	ENU00100	ANI50C2350 0_1:322..845	23-45	480-504	EST	"i3a07a1.r1, i3a07a1.fl"		187	187	6E-47			
16307	ENU00101	ANI61C8673: 1620..2154	22-51	495-514	EST	"j0b04a1.r1, j0b04a1.fl"		32	32	3.8			
16308	ENU00102	ANI61C9863: 2554..2771	33-52	491-526	EST	"w8g10a1.r1, w8g10a1.fl"		40	40	0.01			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16309	ENU00103	ANI61C9440: 614..71	22-52	492-523	EST	"r1b12a1.rl, r1b12a1.fl"			114	2E-32			proteasome component PRE3 precursor (macropain subunit PRE3) (proteinase YSCE subunit PRE3) (multicatalytic endopeptidase complex subunit PRE3) ; multicatalytic endopeptidase complex (EC 3.4.99.46) chain PRE3 - yeast (Saccharomyces cerevisiae) ; (Z49276) ORF YJL001w [Saccharomyces cerevisiae]
16310	ENU00104	ANI61C1077 4:4466..3910	33-58	524-545	EST	"g3g03a1.rl, g3g03a1.fl"		50		0.00001			(U88181) similar to bovine PKR inhibitor P58 (GB:U04631); contains similarity to DNAL-like domain [Caenorhabditis elegans]
16311	ENU00105	ANI61C1044 5:38..594	55-74	549-569	EST	"r8f06a1.rl, r8f06a1.fl"		32		4			3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase type IV (3beta-HSD IV) (3-beta-hydroxy-delta(5)-steroid dehydrogenase (3-beta-hydroxy-5-ene steroid dehydrogenase) (progesterone reductase) / steroid delta-isomeras... ; 3beta-hydroxysteroid-Delta5-steroid dehydrogenase multifunctional protein IV - rat ; (L17138) 3 hydroxysteroid dehydrogenase [Rattus norvegicus] (Z81579) Similarity to Schistosoma eggshell protein (SW:EGGS_SCHMA); cDNA EST EMBL:T01280 comes from this gene; cDNA EST EMBL:D69189 comes from this gene [Caenorhabditis elegans]
16312	ENU00106	ANI61C5291: 2703..2141	35-59	520-555	EST	"g3c03a1.rl, g3c03a1.fl"		33		1.4			"Glucosylase 1 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan GLUCOHydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) GAM1 - yeast (Schwanniomyces occidentalis) ; (M60207) glucosylase [Schwanniomyces occidentalis] " [Schwanniomyces occidentalis] " (D86051) carbonic anhydrase [Porphyridium purpureum]
16313	ENU00107	ANI61C4823: 3940..3364	28-55	529-561	EST	"i0g04a1.rl, i0g04a1.fl"		66		3E-10			
16314	ENU00108	ANI61C6961: 1292..1868	48-68	561-582	EST	"y8d10a1.rl, y8d10a1.fl"		129		1E-37			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16315	ENU00109	ANI61C2075: 1..584	22-46	539-563	EST	"v7h01a1.r1, v7h01a1.fl"		157	157	6E-38			24 KD metalloproteinase precursor (deuterolysin) ; metalloproteinase (EC 3.4.-.-) 23K - Aspergillus flavus ; (L37524) metalloproteinase [Aspergillus flavus]
16316	ENU00110	ANI61C5881: 3049..2462	34-54	557-579	EST	"g4a11a1.r1, g4a11a1.fl"		43	43	0.002			probable membrane protein YOL084w - yeast (Saccharomyces cerevisiae) ; (X83121) orf 00953 [Saccharomyces cerevisiae] ; (Z74826) ORF YOL084w [Saccharomyces cerevisiae]
16317	ENU00111	ANI61C5908: 1519..2119	46-69	575-604	EST	"t2d10a1.r1, t2d10a1.fl"		107	107	8E-23			(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]
16318	ENU00112	ANI61C3455: 1338..1952	61-84	603-633	EST	"c7g02a1.r1, c7g02a1.fl"		191	191	4E-48			glutathione peroxidase homolog YBR244W ; probable glutathione peroxidase (EC 1.11.1.9) - yeast (Saccharomyces cerevisiae) ; (Z36113) ORF YBR244w [Saccharomyces cerevisiae]
16319	ENU00113	ANI61C1031 7:721..106	61-80	602-633	EST	"j9f07a1.r1, j9f07a1.fl"		59	59	0.000000 02			hypothetical protein YDR313c - yeast (Saccharomyces cerevisiae) ; (U28374) YDR313C gene product [Saccharomyces cerevisiae]
16320	ENU00114	ANI61C1037 9:4710..4080	53-71	614-641	EST	"d5c05a1.r1, d5c05a1.fl"		36	36	0.19			(AB000276) DAP-1 beta [Homo sapiens]
16321	ENU00115	ANI61C3140: 785..156	28-53	589-618	EST	"g3g05a1.r1, g3g05a1.fl"		31	31	6.3			(D31844) cut9+ [Schizosaccharomyces pombe]
16322	ENU00116	ANI61C1046 4:3335..2700	50-75	616-643	EST	"j9f08a1.r1, j9f08a1.fl"		36	36	0.0001			"alpha-actinin, skeletal muscle isoform (F-actin cross linking protein) ; alpha-actinin 2, skeletal muscle splice form SK - chicken ; (X59247) alpha-actinin [Gallus gallus] ; (X13874) pectoralis alpha actinin [Gallus gallus] "
16323	ENU00117	ANI61C7547: 1827..2465	34-56	601-630	EST	"c8d04a1.r1, c8d04a1.fl"		63	63	0.000000 002			(Y17393) prefoldin subunit 2 [Mus musculus]
16324	ENU00118	ANI61C7842: 820..174	32-51	618-636	EST	"o8e07a1.r1, o8e07a1.fl"		87	87	1E-16			(AB009078) L-2,3-butanediol dehydrogenase [Brevibacterium saccharolyticum]
16325	ENU00119	ANI61C1119 4:1467..807	22-50	621-640	EST	"b0a07a1.r1, b0a07a1.fl"		155	155	2E-49			60S ribosomal protein L15 ; (Y15321) putative ribosomal protein L15 [Aspergillus niger]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvtg	Description
16326	ENU00120	ANI61C4903: 24-46 1797..2461	619-646	619-646	EST	"l3a11a1.rl, l3a11a1.fl"		65	4E-20				"phosphoribosylglycinamide formyltransferase (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase) ; ADE8 protein - yeast (Saccharomyces cerevisiae) ; (M36585) ADE8 gene product [Saccharomyces cerevisiae] ; (U32274) Ade8p: glycinamide ribotide transformylase, EC number 2.1.2.2; YDR408C; CAI: 0.12 [Saccharomyces cerevisiae] ; ADE8 gene [Saccharomyces cerevisiae] ; ADE8 gene [Saccharomyces cerevisiae]"
16328	ENU00122	ANI61C9641: 22-42 57..738	634-661	634-661	EST	"r7f10a1.rl, r7f10a1.fl"		33	2.3				[Saccharomyces cerevisiae]" (U78968) surface lipoprotein DppA [Streptococcus pyogenes]
16329	ENU00123	ANI61C6008: 22-46 1..694	639-673	639-673	EST	"z1f02a1.rl, z1f02a1.fl"		103	1E-40				"ATP synthase subunit 4, mitochondrial precursor ; (AF019222) F1Fo-ATP synthase subunit 4 [Kluyveromyces lactis]"
16330	ENU00124	ANI61C1136: 29-48 8921..8224	662-684	662-684	EST	"fle10a1.rl, fle10a1.fl"		37	0.12				suppressor of hairy wing protein ; suppressor of hairy wing - fruit fly (Drosophila virilis) ; (Z25520) Hairy-wing protein [Drosophila virilis]
16331	ENU00125	ANI61C3096: 47-68 2180..1452	700-735	700-735	EST	"i8b09a1.rl, i8b09a1.fl"		268	2E-71				Peroxisomal hydratase-dehydrogenase-epimerase (HDE) (multifunctional beta-oxidation protein) [contains: 2-enoyl-CoA hydratase ; D-3-hydroxyacyl CoA dehydrogenase] ; multifunctional beta-oxidation protein - Neurospora crassa ; (X80052) multifunctional beta-oxidation protein [Neurospora crassa]
16332	ENU00126	ANI61C580:2 22-50 87..1022	691-715	691-715	EST	"m0c07a1.rl, m0c07a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16333	ENU00127	ANI61C3096: 2180..1444	47-68	708-743	EST	"c8d05al.r1, c8d05al.fl"		268	268	2E-71			Peroxisomal hydratase-dehydrogenase-epimerase (HDE) (multifunctional beta-oxidation protein) [contains: 2-enoyl-CoA hydratase ; D-3-hydroxyacyl CoA dehydrogenase] ; multifunctional beta-oxidation protein - Neurospora crassa ; (X80052) multifunctional beta-oxidation protein [Neurospora crassa] (U91983) phosphatidylserine synthase [Triticum aestivum] putative signal recognition particle receptor beta subunit (SR-beta) ; probable purine nucleotide-binding protein YKL154w - yeast (Saccharomyces cerevisiae) ; (Z28154) ORF YKL154w [Saccharomyces cerevisiae]
16334	ENU00128	ANI61C5234: 1..759	22-54	719-738	EST	"g9f05al.r1, g9f05al.fl"		118	118	2E-53			
16335	ENU00129	ANI61C4904: 1320..556	22-52	720-744	EST	"r1f06al.r1, r1f06al.fl"		59	59	0.000000			
16336	ENU00130	ANI61C7349: 2376..1588	25-56	751-771	EST	"o0d07al.r1, o0d07al.fl"		34	34	1.7			Segment polarity protein dishevelled homolog DVL-1 (dishevelled-1) (DSH homolog 1) ; (U46461) cytoplasmic phosphoprotein [Homo sapiens] (AL022304) 40s ribosomal protein s16. [Schizosaccharomyces pombe] (AL022304) 40s ribosomal protein s16. [Schizosaccharomyces pombe] hypothetical protein H19-3' - mouse ; (X58196) 3' ORF [Mus musculus] (Z49908) cDNA EST yk198d12.5 comes from this gene [Caenorhabditis elegans]
16337	ENU00131	ANI61C8418: 59..872	72-91	808-842	EST	"z4f02al.r1, z4f02al.fl"		106	106	9E-31			
16338	ENU00132	ANI61C6065: 831..3	72-91	835-858	EST	"d5g06al.r1, d5g06al.fl"		106	106	9E-31			
16339	ENU00133	ANI61C6065: 835..3	72-92	839-862	EST	"m2f09al.r1, m2f09al.fl"		32	32	4			
16340	ENU00134	ANI61C4936: 866..20	23-44	807-826	EST	"c9c04al.r1, c9c04al.fl"		32	32	4.2			
16341	ENU00135	ANI61C7423: 3162..4046	68-87	891-910	EST	"r1g10al.r1, r1g10al.fl"		37	37	0.22			adenylate cyclase (ATP pyrophosphate-lyase) (adenylate cyclase) ; adenylyate cyclase (EC 4.6.1.1) - Podospora anserina ; (L43413) adenylyate cyclase [Podospora anserina]
16342	ENU00136	ANI61C7349: 1398..2303	22-55	862-885	EST	"i0a02al.r1, i0a02al.fl"							
16343	ENU00137	ANI61C6519: 674..1581	22-41	862-887	EST	"s9a11al.r1, s9a11al.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16344	ENU00138	ANI61C6671: 3857..2945	60-79	896-930	EST	"z5e07a1.rl, z5e07a1.fl"		39	39	0.045			(Z66499) T01B7.8 [Caenorhabditis elegans]
16345	ENU00139	ANI61C2152: 1783..856	22-48	878-906	EST	"y8b10a1.rl, y8b10a1.fl"		34	34	2			(U94333) C1qR(p) [Homo sapiens]
16346	ENU00140	ANI61C1035 9:1825..2753	22-52	888-908	EST	"d1a10a1.rl, d1a10a1.fl"							tRNA nucleotidyltransferase precursor (tRNA adenylyltransferase) (CCA-adding enzyme) ; tRNA
16347	ENU00141	ANI61C1049 7:4698..5643	43-72	927-946	EST	"y3a09a1.rl, y3a09a1.fl"			33	2.7			nucleotidyltransferase - yeast (Saccharomyces cerevisiae) ; (M59870) transfer RNA nucleotidyltransferase [Saccharomyces cerevisiae] ; (U18922) Cca1p: tRNA
16348	ENU00142	ANI61C2394: 2671..1698	68-88	965-999	EST	"o6d04a1.rl, o6d04a1.fl"			229	2E-79			nucleotidyltransferase(tRNA CCA-pyrophosphorylase) [Saccharomyces cerevisiae]
16349	ENU00143	ANI61C4760: 993..18	43-65	957-976	EST	"d4a04a1.rl, d4a04a1.fl"			199	8E-71			(U76621) short-chain alcohol dehydrogenase [Aspergillus parasiticus]
16350	ENU00144	ANI61C1038 0:3175..4169	22-54	950-973	EST	"z3d02a1.rl, z3d02a1.fl"			61	0.000000			"(AL034352) yeast reduced viability upon starvation protein 161 homolog, implicated in cell growth and cytoskeletal or ganisation [Schizosaccharomyces pombe]"
16351	ENU00145	ANI61C1038 0:3175..4169	22-54	950-973	EST	"i0h07a1.rl, i0h07a1.fl"			61	0.000000			hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region ; probable membrane protein YNR018w - yeast (Saccharomyces cerevisiae) ; (Z71633) ORF YNR018w [Saccharomyces cerevisiae]
										02			hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region ; probable membrane protein YNR018w - yeast (Saccharomyces cerevisiae) ; (Z71633) ORF YNR018w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16352	ENU00146	ANI61C1038 0:3175..4169	22-54	950-973	EST	"x8b03a1.rl", x8b03a1.fl"		61	0.000000	02			hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region ; probable membrane protein YNR018w - yeast (Saccharomyces cerevisiae) ; (Z71633) ORF YNR018w [Saccharomyces cerevisiae]
16353	ENU00147	ANI61C7944: 1993..993	26-46	965-987	EST	"r5a07a1.rl", r5a07a1.fl"		52	0.000005				hypothetical 37.8 KD protein in CLB6-SPT6 intergenic region ; hypothetical protein YGR113w - yeast (Saccharomyces cerevisiae) ; (Z72898) ORF YGR113w [Saccharomyces cerevisiae]
16354	ENU00148	ANI61C5297: 26..1067	22-46	1001-1020	EST	"g7g08a1.rl", g7g08a1.fl"		61	0.000000	02			(AL033497) unknown hypothetical protein [Candida albicans]
16355	ENU00149	ANI61C5363: 99..1143	22-49	996-1024	EST	"d3a01a1.rl", d3a01a1.fl"		109	2E-24				hypothetical 43.8 KD protein in NCE3-HHT2 intergenic region ; hypothetical protein YNL035c - yeast (Saccharomyces cerevisiae) ; (Z71311) ORF YNL035c [Saccharomyces cerevisiae]
16356	ENU00150	ANI61C1754: 4786..3743	22-51	1002-1024	EST	"y8e03a1.rl", y8e03a1.fl"		96	9E-26				(X63998) aminopeptidase yscII [Saccharomyces cerevisiae]
16357	ENU00151	ANI61C8138: 4412..3341	61-82	1060-1090	EST	"r5g03a1.rl", r5g03a1.fl"		371	e-102				"mitochondrial heat shock protein SSC1 precursor (endonuclease SCEI 75 KD subunit) ; heat shock protein 70-related protein SSC1 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (M27229) heat shock protein [Saccharomyces cerevisiae] ; (Z49545) ORF YJR045c [Saccharomyces cerevisiae] ; (L36344) ORF; putative [Saccharomyces cerevisiae] "
16358	ENU00152	ANI61C2761: 1220..113	22-57	1069-1088	EST	"x5a07a1.rl", x5a07a1.fl"		102	7E-42				(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi]
16359	ENU00153	ANI61C9617: 449..1617	33-60	1139-1159	EST	"o6e11a1.rl", o6e11a1.fl"		97	2E-19				(AL023776) hypothetical protein [Schizosaccharomyces pombe]
16360	ENU00154	ANI61C687:1 329..9	35-54	1294-1313	EST	"g6a09a1.rl", g6a09a1.fl"		45	0.001				(AF007190) intestinal mucin [Homo sapiens]

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16361	ENU00155	ANI61C4155: 111..1470	22-42	1304-1339	EST	"c5b09a1.r1, c5b09a1.fl"		64	64	0.000000			ACTIN-like protein ARP9; probable membrane protein YMR033w - yeast (Saccharomyces cerevisiae); (Z49213) unknown [Saccharomyces cerevisiae]
16362	ENU00156	ANI61C6712: 33-52	33-52	1341-1367	EST	"v7c12a1.r1, v7c12a1.fl"		405	405	e-133			hypothetical 52.9 KD protein in SAP155-YMR31 intergenic region; hypothetical protein YFR044c - yeast (Saccharomyces cerevisiae); (D50617) YFR044C [Saccharomyces cerevisiae]; (D44597) unknown [Saccharomyces cerevisiae]
16363	ENU00157	ANI61C1040 9:3271..1880	34-61	1363-1382	EST	"z3b08a1.r1, z3b08a1.fl"		206	206	5E-58			eukaryotic translation initiation factor 2 alpha subunit (EIF-2-alpha); (AL021046) translational initiation factor 2 alpha [Schizosaccharomyces pombe]
16364	ENU00158	ANI61C1082 7:117..1551	54-73	1416-1446	EST	"h4a08a1.r1, h4a08a1.fl"		102	102	2E-22			(AL049522) hypothetical DNAJ domain protein [Schizosaccharomyces pombe]
16365	ENU00159	ANI61C2461: 41-61	41-61	1653-1678	EST	"i3c07a1.r1, i3c07a1.fl"		199	199	6E-50			probable N-end-recognizing protein (ubiquitin-protein ligase E3 component) (N-recognin); (AL023859) putative ubiquitin protein ligase [Schizosaccharomyces pombe]
16366	ENU00160	ANI61C9821: 22-48	22-48	1685-1708	EST	"j7b03a1.r1, j7b03a1.fl"		37	37	0.47			extensin - almond; (X65718) extensin [Prunus dulcis]; extensin [Prunus dulcis]
16367	ENU00161	ANI61C844:2 176..380	22-45	1753-1776	EST	"i3h07a1.r1, i3h07a1.fl"		101	101	2E-39			hypothetical 79.3 KD protein C24C9.05C in chromosome I; (Z98601) hypothetical protein. [Schizosaccharomyces pombe]
16368	ENU00162	ANI61C1001 4:243..2336	66-87	2084-2116	EST	"c4f11a1.r1, c4f11a1.fl"		64	64	6E-16			DNA repair protein RAD9; rad9 protein - fission yeast (Schizosaccharomyces pombe); rad9 protein - fission yeast (Schizosaccharomyces pombe); (X58231) rad9 protein [Schizosaccharomyces pombe]; (X64648) rad9 [Schizosaccharomyces pombe]; (X77276) rad9 [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16369	ENU00163	ANI61C8606: 137..2328	33-52	2151-2182	EST	"i2c03a1.r1, i2c03a1.fl"		48	48	0.0003			(AL034382) hypothetical serine rich protein [Schizosaccharomyces pombe]
16370	ENU00164	ANI61C1204: 45-65	45-65	181-202	EST	"y6g10a1.r1, y6g10a1.fl"		29	29	4.4			Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; (Z92539) eno
16371	ENU00165	ANI61C1083 32-51	32-51	164-189	EST	"m7h01a1.r1, m7h01a1.fl"		31	31	1.1			[Mycobacterium tuberculosis] (D87063) chitinase [Emericella nidulans]
16372	ENU00166	ANI61C1204: 39-59	39-59	175-196	EST	"m5e12a1.r1, m5e12a1.fl"		29	29	4.4			Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; (Z92539) eno
16373	ENU00167	ANI61C1204: 44-64	44-64	180-201	EST	"o0g12a1.r1, o0g12a1.fl"		29	29	4.4			[Mycobacterium tuberculosis]
16374	ENU00168	ANI61C1035 22-40	22-40	155-180	EST	"x8g04a1.r1, x8g04a1.fl"		29	29	3.3			serine/threonine-protein kinase SNK (serum inducible kinase) ; serum-inducible kinase - mouse
16375	ENU00169	ANI61C4983: 129..338	27-45	170-194	EST	"y8e10a1.r1, y8e10a1.fl"		31	31	1.1			(U39501) OrfB; IS3 family OrfB proteins homolog; Method: conceptual translation supplied by author.
16376	ENU00170	ANI61C4777: 1063..849	41-60	193-213	EST	"o8c07a1.r1, o8c07a1.fl"		120	120	1E-27			[Caulobacter crescentus] "Aldehyde dehydrogenase (ALDDH) ; aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans ; (M16197) aldehyde dehydrogenase [Emericella nidulans] ; dehydrogenase,aldehyde [Emericella nidulans] "
16377	ENU00171	ANI61C4777: 1063..849	41-60	193-213	EST	"r5b09a1.r1, r5b09a1.fl"		120	120	1E-27			"Aldehyde dehydrogenase (ALDDH) ; aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans ; (M16197) aldehyde dehydrogenase [Emericella nidulans] ; dehydrogenase,aldehyde [Emericella nidulans] "
16378	ENU00172	ANI61C1083 60-79	60-79	218-242	EST	"a0f05a1.r1, a0f05a1.fl"		66	66	3E-11			(D87063) chitinase [Emericella nidulans]

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16379	ENU00173	ANI61C3868: 1613..1836	50-69	212-232	EST	"g2b07a1.rl, g2b07a1.fl"		31	31	1.7		(AF130745) regulator of G-protein signalling LOCO C1 [Drosophila melanogaster]
16380	ENU00174	ANI61C8080: 949..1178	56-75	219-243	EST	"x7g02a1.rl, x7g02a1.fl"		31	31	1.9		asparagine/glutamine permease; probable membrane protein YCL025c - yeast (Saccharomyces cerevisiae); (X59720) YCL025c: len:633 [Saccharomyces cerevisiae]
16381	ENU00175	ANI61C2092: 491..258	58-77	229-249	EST	"h4c02a1.rl, h4c02a1.fl"		31	31	1.1		hypothetical 41.6 KD protein in CSIE-GLYA intergenic region; (AE000340) MFS (major facilitator superfamily) transporter [Escherichia coli]; (D90883) similar to [SwissProt Accession Number P44629] [Escherichia coli]; (D90884) similar to [SwissProt Accession Number P44629] [Escherichia coli]
16382	ENU00176	ANI61C3827: 560..317	52-71	233-253	EST	"l0d10a1.rl, l0d10a1.fl"		49	49	0.000005		Cutinase precursor (L1); (D38311) Cutinase [Aspergillus oryzae]
16383	ENU00177	ANI61C2572: 331..574	45-65	227-246	EST	"l0c11a1.rl, l0c11a1.fl"		31	31	1.3		putative 3-methyladenine DNA glycoylase; (Z95117) hypothetical protein MLC1351.17c [Mycobacterium leprae]
16384	ENU00178	ANI61C8119: 779..536	39-58	219-240	EST	"p0g10a1.rl, p0g10a1.fl"		31	31	1.6		(Z74033) F38B7.4 [Caenorhabditis elegans]
16385	ENU00179	ANI61C7674: 5430..5186	54-87	232-256	EST	"l3a10a1.rl, l3a10a1.fl"		29	29	5		Chitin synthase 1 (chitin-UDP acetyl-glucosaminyl transferase 1); chitin synthase (EC 2.4.1.16) - yeast (Saccharomyces cerevisiae); (M14045) chitin synthase [Saccharomyces cerevisiae]; (Z71468) ORF YNL192w [Saccharomyces cerevisiae]
16386	ENU00180	ANI61C3796: 1875..1628	22-50	208-227	EST	"z4b03a1.rl, z4b03a1.fl"		32	32	0.59		hypothetical 8.9 KD protein in INT-C1 intergenic region (ORF3) (ORF17); hypothetical protein 17 - phage HP1; hypothetical protein 3 - phage HP1; (U24159) orf3 [Bacteriophage HP1] Cutinase precursor (L1); (D38311) Cutinase [Aspergillus oryzae]
16387	ENU00181	ANI61C3827: 560..310	52-71	240-260	EST	"j9c08a1.rl, j9c08a1.fl"		49	49	0.000006		"(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum]"
16388	ENU00182	ANI61C3054: 2259..2511	63-82	244-273	EST	"m2e09a1.rl, m2e09a1.fl"		40	40	0.004		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
16389	ENU00183	ANI61C8048: 627..882	41-61	220-254	EST	"z1e09a1.rl, z1e09a1.fl"		29	29	7.2			(AF025847) (p)ppGpp synthetase [Myxococcus xanthus]
16390	ENU00184	ANI50C3665 52-71	52-71	256-275	EST	"m8d06a1.rl, m8d06a1.fl"		32	32	1.2			(U39501) OrfB; IS3 family OrfB proteins homolog; Method: conceptual translation supplied by author. [Caulobacter crescentus]
16391	ENU00185	ANI61C4983: 63-82	63-82	266-290	EST	"r5c08a1.rl, r5c08a1.fl"		31	31	3.1			Alkanal monooxygenase alpha chain (bacterial luciferase alpha chain); alkanal monooxygenase (FMN-linked) (EC 1.14.14.3) alpha chain - flashlight fish symbiont bacterium; (M36597) luciferase-alpha subunit
16392	ENU00186	ANI61C4523: 22-41	22-41	232-266	EST	"r6a08a1.rl, r6a08a1.fl"		29	29	9.2			[Kryptophanaron alfredi symbiont] (U86920) similar to variola A13L and vaccinia A12L [Molluscum contagiosum virus subtype 1]
16393	ENU00187	ANI61C175:3 23-42	23-42	239-267	EST	"c5b11a1.rl, c5b11a1.fl"		33	33	0.66			(AF052248) fork head domain protein FKD5 [Danio rerio]
16394	ENU00188	ANI61C9221: 68-88	68-88	283-315	EST	"t2e10a1.rl, t2e10a1.fl"		36	36	0.1			metallothionein-like protein 1; metallothionein - barley; (X58540) ids-1 [Hordeum vulgare]
16395	ENU00189	ANI61C1688: 27-46	27-46	259-281	EST	"y6c12a1.rl, y6c12a1.fl"		36	36	0.1			metallothionein-like protein 1; metallothionein - barley; (X58540) ids-1 [Hordeum vulgare]
16396	ENU00190	ANI61C5649: 25-44	25-44	265-284	EST	"c8f03a1.rl, c8f03a1.fl"		36	36	0.1			metallothionein-like protein 1; metallothionein - barley; (X58540) ids-1 [Hordeum vulgare]
16397	ENU00191	ANI61C5649: 25-44	25-44	265-284	EST	"c5b02a1.rl, c5b02a1.fl"		36	36	0.11			metallothionein-like protein 1; metallothionein - barley; (X58540) ids-1 [Hordeum vulgare]
16398	ENU00192	ANI61C5649: 25-44	25-44	271-290	EST	"z1c03a1.rl, z1c03a1.fl"		33	33	0.87			(AF003140) weak similarity to the drosophila hyperplastic disc protein (GB:L14644) [Caenorhabditis elegans]
16399	ENU00193	ANI61C7214: 72-89	72-89	320-339	EST	"w6d12a1.rl, w6d12a1.fl"							
16400	ENU00194	ANI61C1065 34-53	34-53	304-327	EST	"x9h11a1.rl, x9h11a1.fl"							
16401	ENU00195	ANI61C6234: 43-62	43-62	324-347	EST	"r5c03a1.rl, r5c03a1.fl"							
16402	ENU00196	ANI61C8131: 23-42	23-42	312-331	EST	"g5a04a1.rl, g5a04a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16403	ENU00197	ANI61C992:1	69-87	366-385	EST	"g6g12a1.r1, g6g12a1.fl"		34	0.43				(AE000831) conserved protein [Methanobacterium thermoautotrophicum]
16404	ENU00198	ANI61C9858: 562..1920 ANI61C9858: 58-77 169..538	58-77	366-385	EST	"k0b04a1.r1, k0b04a1.fl"							
16405	ENU00199	ANI61C2656: 59-78 1399..1494	59-78	369-388	EST	"j7h07a1.r1, j7h07a1.fl"							
16406	ENU00200	ANI61C8448: 22-43 488..116	22-43	332-352	EST	"w8g03a1.r1, w8g03a1.fl"							
16407	ENU00201	ANI61C9663: 66-85 2362..1988	66-85	368-398	EST	"r2d02a1.r1, r2d02a1.fl"		34	0.44				cold-regulated protein cor15b precursor - Arabidopsis thaliana ; (AC007087)
16408	ENU00202	ANI61C2177: 71-90 429..51	71-90	388-407	EST	"n0g07a1.r1, n0g07a1.fl"		35	0.26				cold-regulated protein cor15b precursor [Arabidopsis thaliana]
16409	ENU00203	ANI61C6321: 55-74 729..1115	55-74	377-399	EST	"q0h02a1.r1, q0h02a1.fl"		31	4.1				N-methyl-D-aspartate receptor subunit NR2C - mouse ; (L35029) N-methyl-D-aspartate receptor subunit NR2C [Mus musculus]
16410	ENU00204	ANI61C7538: 55-74 1408..1019	55-74	381-402	EST	"d1a12a1.r1, d1a12a1.fl"		55	0.000000	2			(D14289) MTG8 protein [Homo sapiens]
16411	ENU00205	ANI61C346:2 40-59 429..2826	40-59	373-394	EST	"p0g07a1.r1, p0g07a1.fl"		32	1.4				PTS2-containing proteins Pex7p [Pichia pastoris]
16412	ENU00206	ANI61C1677: 23-43 8849..8450	23-43	357-380	EST	"o6a03a1.r1, o6a03a1.fl"		31	3.3				(AF061837) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]
16413	ENU00207	ANI61C1064 59-78 9:793..391	59-78	399-419	EST	"r6c07a1.r1, r6c07a1.fl"							(U70038) ICP0B [Human herpesvirus 1]
16414	ENU00208	ANI61C8117: 41-60 520..924	41-60	383-403	EST	"w7f07a1.r1, w7f07a1.fl"		94	6E-19				(D89340) dipeptidyl peptidase III [Rattus norvegicus]
16415	ENU00209	ANI61C2656: 26-45 1033..1440	26-45	372-391	EST	"o4b07a1.r1, o4b07a1.fl"		32	2				(AL030978) GH3 like protein [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16416	ENU00210	ANI61C3182: 58-79 4557..4965		404-424	EST	"j4b05a1.rl, j4b05a1.fl"			157	5E-38		cystathionine gamma-lyase (gamma-cystathionase) ; cystathionine gamma-lyase (EC 4.4.1.1) - yeast (Saccharomyces cerevisiae) ; (L05146) Cys3p: cystathionine gamma-lyase [Saccharomyces cerevisiae] ; (D14135) cystathionine gamma-lyase [Saccharomyces cerevisiae] ; (L04459) cystathionine gamma-lyase [Saccharomyces cerevisiae] (U40790) vascular protein tyrosine phosphatase 1 [Rattus norvegicus] (AL049498) putative transcription factor [Schizosaccharomyces pombe] hypothetical 112.0 KD protein C1F3.03 in chromosome I ; (Z70690) unknown [Schizosaccharomyces pombe] (Z99120) yurE [Bacillus subtilis] (U56098) FacB [Aspergillus oryzae] (U80844) strong similarity to amino-terminal 80 aa of aldehyde reductases [Caenorhabditis elegans] Fimbrin-like protein FIM1 ; fimbrial protein Fim1 - Salmonella typhi ; (X74064) Fim1 protein [Salmonella typhi] Periodic tryptophan protein 1 ; PWPI1 protein - yeast (Saccharomyces cerevisiae) ; (M37578) periodic tryptophan protein [Saccharomyces cerevisiae] ; (U14913) Pwplp [Saccharomyces cerevisiae] ; periodic Ttp protein [Saccharomyces cerevisiae]
16417	ENU00211	ANI61C9024: 41-60 5175..5584		381-408	EST	"g9h09a1.rl, g9h09a1.fl"			31	3.4		
16418	ENU00212	ANI61C8749: 56-75 1001..591		399-424	EST	"c4f09a1.rl, c4f09a1.fl"			32	1.5		
16419	ENU00213	ANI61C9005: 68-87 1114..692		427-448	EST	"l3a12a1.rl, l3a12a1.fl"			41	0.004		
16420	ENU00214	ANI61C746:1 68-91 493..1065		434-454	EST	"e0d12a1.rl, e0d12a1.fl"			31	6.2		
16421	ENU00215	ANI61C9771: 23-42 3408..2966		389-423	EST	"o0e05a1.rl, o0e05a1.fl"			32	2.9		
16422	ENU00216	ANI61C3900: 71-92 332..777		456-475	EST	"b0b10a1.rl, b0b10a1.fl"			30	8.6		
16423	ENU00217	ANI61C9823: 26-46 7232..6813		411-435	EST	"w6c11a1.rl, w6c11a1.fl"			31	3.9		
16424	ENU00218	ANI61C1113 72-91 7:459..915		466-486	EST	"y8b01a1.rl, y8b01a1.fl"			63	0.000000 001		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
16425	ENU00219	ANI61C8906: 436..893	68-87	455-483	EST	"c9d01a1.r1, c9d01a1.fl"			32	2.3			"(Z70204) predicted using Genefinder; similar to Zinc finger, C4 type (two domains); cDNA EST EMBL:T00457 comes from this gene; cDNA EST EMBL:C09248 comes from this gene; cDNA EST EMBL:C07758 comes from this gene; cDNA EST yk261..." (U66220) unknown [Nannocystis exedens] (AF044025) circumsporozoite protein [Apicomplexa sp. 72141] hypothetical 62.8 KD protein in SSE1-CAR1 intergenic region; probable membrane protein YPL109c - yeast (Saccharomyces cerevisiae); (U43503) Lph17p [Saccharomyces cerevisiae] major cold shock protein CSPA; (U82822) major cold shock protein CspA [Pseudomonas aeruginosa] major cold shock protein CSPA; (U82822) major cold shock protein CspA [Pseudomonas aeruginosa] major cold shock protein CSPA; (U82822) major cold shock protein CspA [Pseudomonas aeruginosa] major cold shock protein CSPA; (U82822) major cold shock protein CspA [Pseudomonas aeruginosa] TEF5 protein - yeast (Saccharomyces cerevisiae)
16426	ENU00220	ANI61C1067 2:467..1	30-49	426-454	EST	"o0a09a1.r1, o0a09a1.fl"			34	0.62			
16427	ENU00221	ANI61C3179: 66-85 1628..2095	66-85	471-491	EST	"w9e07a1.r1, w9e07a1.fl"			31	5.4			
16428	ENU00222	ANI61C6422: 47-66 1787..2263	47-66	461-481	EST	"c3a02a1.r1, c3a02a1.fl"			90	6E-18			
16429	ENU00223	ANI61C4792: 23-42 766..289	23-42	439-458	EST	"v7c02a1.r1, v7c02a1.fl"			60	0.000000			
16430	ENU00224	ANI61C4792: 39-58 766..289	39-58	455-474	EST	"w9h11a1.r1, w9h11a1.fl"			60	0.000000			
16431	ENU00225	ANI61C4792: 23-42 766..289	23-42	439-458	EST	"m0b05a1.r1, m0b05a1.fl"			60	0.000000			
16432	ENU00226	ANI61C4792: 25-44 766..289	25-44	441-460	EST	"q0e01a1.r1, q0e01a1.fl"			60	0.000000			
16433	ENU00227	ANI61C8456: 49-68 3363..3842	49-68	461-486	EST	"c3h01a1.r1, c3h01a1.fl"			60	0.000000			
16434	ENU00228	ANI61C7916: 48-67 1409..930	48-67	461-485	EST	"y8e09a1.r1, y8e09a1.fl"			114	3E-25			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16435	ENU00229	ANI61C6190: 231..716	37-55	460-480	EST	"h1h04a1.r1, h1h04a1.fl"		59	0.000000	03			GCY protein ; GCY1 protein - yeast (Saccharomyces cerevisiae) ; (X13228) GCY protein (AA 1-312) [Saccharomyces cerevisiae] ; (X90518) ORF O31567 [Saccharomyces cerevisiae] ; (X94335) YOR3269w [Saccharomyces cerevisiae] ; (X96740) GCY protein [Saccharomyces cerevisiae] ; (Z75028) ORF YOR120w [Saccharomyces cerevisiae] (D78151) human 26S proteasome subunit p97 [Homo sapiens] "AMP deaminase (myoadenylate deaminase) ; AMP deaminase (EC 3.5.4.6) - yeast (Saccharomyces cerevisiae) ; (Z46659) AMD1 gene, len: 810, CAl: 0.19, AMP deaminase [Saccharomyces cerevisiae]" (Z99532) putative vacuolar h(+)-atpase subunit [Schizosaccharomyces pombe] methionine aminopeptidase 2 (METAP 2) (peptidase M 2) ; (U17437) methionine aminopeptidase 2 [Saccharomyces cerevisiae] ribonucleoprotein - Arabidopsis thaliana ; (M98340) ribonucleoprotein [Arabidopsis thaliana] ; Ser/Arg-rich protein [Arabidopsis thaliana] (AF003696) cellulase A [Cellvibrio mixtus] probable membrane protein YPL162c - yeast (Saccharomyces cerevisiae) ; (Z73518) ORF YPL162c [Saccharomyces cerevisiae] ; (X96770) P2558 protein [Saccharomyces cerevisiae]
16436	ENU00230	ANI61C6237: 41..533	62-81	494-512	EST	"2e09a1.r1, 2e09a1.fl"		100	1E-23				
16437	ENU00231	ANI61C8962: 786..286	65-84	504-523	EST	"c3h03a1.r1, c3h03a1.fl"		257	3E-68				
16438	ENU00232	ANI61C9646: 671..169	46-65	486-506	EST	"n8c05a1.r1, n8c05a1.fl"		85	4E-16				
16439	ENU00233	ANI61C1040: 4:2382..1875	48-67	492-513	EST	"j0d02a1.r1, j0d02a1.fl"		82	1E-17				
16440	ENU00234	ANI61C1041: 9:1472..958	48-67	496-520	EST	"n0a05a1.r1, n0a05a1.fl"		31	8.2				
16441	ENU00235	ANI61C5819: 1019..1538	50-69	495-527	EST	"y8b12a1.r1, y8b12a1.fl"		31	4.8				
16442	ENU00236	ANI61C7241: 2240..1713	46-65	505-531	EST	"k0d10a1.r1, k0d10a1.fl"		35	0.43				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16443	ENU00237	ANI61C7054: 1373..835	55-74	532-551	EST	"z5f11a1.rl, z5f11a1.fl"			201	4E-51			"Dihydroxy-acid dehydratase precursor (DAD) (2,3-dihydroxy acid hydrolyase) ; dihydroxy-acid dehydratase (EC 4.2.1.9) - yeast (Saccharomyces cerevisiae) ; (X87611) dihydroxyacid dehydratase [Saccharomyces cerevisiae] ; (Z49516) ORF YJR016c [Saccharomyces cerevisiae] "
16444	ENU00238	ANI61C1560: 70-89	70-89	543-572	EST	"z3c05a1.rl, z3c05a1.fl"			32	3.9			(AF013294) contains similarity to gag proteins [Arabidopsis thaliana]
16445	ENU00239	ANI61C1560: 70-89	70-89	543-572	EST	"o8d01a1.rl, o8d01a1.fl"			32	3.9			(AF013294) contains similarity to gag proteins [Arabidopsis thaliana]
16446	ENU00240	ANI61C7674: 22-44	22-44	507-530	EST	"l3a10a1.rl, l3a10a1.fl"			31	8.9			(AF016833) maltase-glucoamylase [Homo sapiens]
16447	ENU00241	ANI61C8356: 5738..5188	35-54	527-553	EST	"o6f04a1.rl, o6f04a1.fl"			76	3E-28			"dismutase,Mn superoxide [Saccharomyces cerevisiae] "
16448	ENU00242	ANI61C8356: 35-54	35-54	535-557	EST	"g4h09a1.rl, g4h09a1.fl"			76	3E-28			"dismutase,Mn superoxide [Saccharomyces cerevisiae] "
16449	ENU00243	ANI61C1031 61-81	61-81	568-585	EST	"e4b04a1.rl, e4b04a1.fl"							
16450	ENU00244	ANI61C2396: 56-75	56-75	577-596	EST	"c9h09a1.rl, c9h09a1.fl"			31	9.6			major blood-stage surface antigen Pv200 - Plasmodium vivax ; (M75674)
16451	ENU00245	ANI61C7700: 63-80	63-80	579-612	EST	"j7c03a1.rl, j7c03a1.fl"			66	9E-20			Pv200 [Plasmodium vivax]
16452	ENU00246	ANI61C7916: 34-53	34-53	559-583	EST	"p0c05a1.rl, p0c05a1.fl"			63	0.000000			Rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans]
16453	ENU00247	ANI61C5247: 29-62	29-62	559-590	EST	"c5c06a1.rl, c5c06a1.fl"			37	0.13			(AF010288) synaptobrevin [Aspergillus parasiticus]
16454	ENU00248	ANI61C2967: 61-80	61-80	608-629	EST	"l0c09a1.rl, l0c09a1.fl"			35	0.53			"Myristoylated alanine-rich C-kinase substrate (MARCKS) (protein kinase C substrate, 80 KD protein, light chain) (PKCSL) (80K-L protein) ; myristoylated alanine-rich protein kinase C substrate - human ; (D10522) 80K-L protein [Homo sapiens] "
		932..1542											laminin chain A - fruit fly [Drosophila melanogaster] (fragment) ; (M75882) laminin A chain [Drosophila melanogaster]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16455	ENU00249	ANI61C3552: 812..198	53-72	597-625	EST	"c9b04a1.r1, c9b04a1.fl"		56	56	3E-15		(AF047694) glutaredoxin [Vernicia fordii]
16456	ENU00250	ANI61C6038: 23-50	594-613	594-613	EST	"r5b05a1.r1, r5b05a1.fl"		45	45	0.0004		probable membrane protein YLR326w - yeast (Saccharomyces cerevisiae) ; (U20618) Ylr326wp [Saccharomyces cerevisiae]
16457	ENU00251	ANI61C1626: 33-52	605-625	605-625	EST	"j4b03a1.r1, j4b03a1.fl"		34	34	0.95		(AF055943) NADH dehydrogenase subunit II [Anolis limifrons]
16458	ENU00252	ANI61C6038: 22-47	606-625	606-625	EST	"g9d06a1.r1, g9d06a1.fl"		45	45	0.0004		probable membrane protein YLR326w - yeast (Saccharomyces cerevisiae) ; (U20618) Ylr326wp [Saccharomyces cerevisiae]
16459	ENU00253	ANI61C6038: 22-47	606-625	606-625	EST	"r7g05a1.r1, r7g05a1.fl"		45	45	0.0004		probable membrane protein YLR326w - yeast (Saccharomyces cerevisiae) ; (U20618) Ylr326wp [Saccharomyces cerevisiae]
16460	ENU00254	ANI61C4165: 72-92	659-685	659-685	EST	"g6d05a1.r1, g6d05a1.fl"		182	182	3E-45		(AF072541) xylitol dehydrogenase; XDH [Galactocandida mastotermitis]
16461	ENU00255	ANI61C6835: 63-83	659-678	659-678	EST	"o6d01a1.r1, o6d01a1.fl"		34	34	0.76		(U58951) envelope polypeptide [Feline leukemia virus]
16462	ENU00256	ANI61C407:3 31-50	633-653	633-653	EST	"w4b06a1.r1, w4b06a1.fl"		47	47	1E-14		(AE001038) enoyl-CoA hydratase (fad-3) [Archaeoglobus fulgidus]
16463	ENU00257	ANI61C7842: 22-41	625-644	625-644	EST	"g7c10a1.r1, g7c10a1.fl"		80	80	1E-14		(AB009078) L-2,3-butanediol dehydrogenase [Brevibacterium saccharolyticum]
16464	ENU00258	ANI61C2915: 22-40	636-658	636-658	EST	"x7b08a1.r1, x7b08a1.fl"		78	78	6E-16		cytochrome C oxidase polypeptide VIB (AED) ; cytochrome-c oxidase (EC 1.9.3.1) chain VIB - yeast (Saccharomyces cerevisiae) ; (M98332) cytochrome c oxidase subunit VIB [Saccharomyces cerevisiae] ; (Z73210) ORF YLR038c [Saccharomyces cerevisiae]
16465	ENU00259	ANI61C1043 44-63	654-682	654-682	EST	"x9f03a1.r1, x9f03a1.fl"		36	36	0.35		HKR1 protein precursor - yeast (Saccharomyces cerevisiae) ; (U33007) Hkr1p; YDR420W; CAI: 0.10
16466	ENU00260	ANI61C6415: 25-44	659-678	659-678	EST	"z4e10a1.r1, z4e10a1.fl"		36	36	0.00003		[Saccharomyces cerevisiae] hypothetical protein 5 - Xanthobacter sp. ; (X79863) orf5 [Xanthobacter sp. Py2]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16467	ENU00261	ANI61C2721: 1465..738	72-91	735-756	EST	"w4a08a1.rl, w4a08a1.fl"		57	57	0.000000		(Z97185) hypothetical protein [Schizosaccharomyces pombe]
16468	ENU00262	ANI61C7657: 68-87	68-87	745-764	EST	"r7c05a1.rl, r7c05a1.fl"		34	34	1.2		(L26122) matrix protein [Mumps virus]
16469	ENU00263	ANI61C5855: 25-44	25-44	704-723	EST	"i8g07a1.rl, i8g07a1.fl"		34	34	1.5		(L13855) UL3.5 [Pseudorabies virus]
16470	ENU00264	ANI61C9566: 24-44	24-44	722-753	EST	"c1c12a1.rl, c1c12a1.fl"		122	122	2E-47		"40S ribosomal protein S18E; ribosomal protein S18.e, cytosolic - yeast (Saccharomyces cerevisiae); (Z46659) 40S ribosomal protein gene, len: 146, CAl: 0.74 [Saccharomyces cerevisiae]; (U33007) Ydr450wp [Saccharomyces cerevisiae]"
16471	ENU00265	ANI61C1704: 68-87	68-87	783-802	EST	"f0h12a1.rl, f0h12a1.fl"		38	38	0.11		mucin (clone PGM-2A) - pig; gastric mucin - pig (fragment); (U10281) gastric mucin [Sus scrofa]
16472	ENU00266	ANI61C8446: 1107..1885	39-58	750-775	EST	"i0g02a1.rl, i0g02a1.fl"		126	126	2E-28		hypothetical protein 1 - Pseudomonas cepacia; (U19883) unknown [Burkholderia cepacia]
16473	ENU00267	ANI61C3644: 32-51	32-51	750-769	EST	"m0a12a1.rl, m0a12a1.fl"		36	36	0.25		"Dynactin, 117 KD isoform; dynactin - chicken; (X62773) dynactin [Gallus sp.]"
16474	ENU00268	ANI61C6750: 2437..2657	45-64	783-802	EST	"z4h02a1.rl, z4h02a1.fl"		32	32	5		probable membrane protein YOR086c - yeast (Saccharomyces cerevisiae); (X94335) YOR3141c [Saccharomyces cerevisiae]; (Z74994) ORF YOR086c [Saccharomyces cerevisiae]
16475	ENU00269	ANI61C3540: 1573..772	27-62	767-786	EST	"r7h08a1.rl, r7h08a1.fl"		65	65	5E-10		"(D90835) H-NS-repressed protein, 30K [Escherichia coli]"
16476	ENU00270	ANI61C1048: 8:1485..2295	29-48	778-797	EST	"o6c11a1.rl, o6c11a1.fl"		35	35	0.77		nucleocapsid protein - phocine distemper virus
16477	ENU00271	ANI50C4955: 3:287..1106	59-78	815-836	EST	"i0a07a1.rl, i0a07a1.fl"		85	85	2E-22		(AL035528) putative protein [Arabidopsis thaliana]
16478	ENU00272	ANI61C4457: 164..985	23-42	784-802	EST	"d5g03a1.rl, d5g03a1.fl"		32	32	6.9		(U90878) carboxyl terminal LIM domain protein [Homo sapiens]
16479	ENU00273	ANI61C8325: 2353..1515	26-46	803-822	EST	"z3b12a1.rl, z3b12a1.fl"		34	34	1.4		(AF024502) No definition line found [Caenorhabditis elegans]
16480	ENU00274	ANI61C6322: 176..1022	49-68	834-853	EST	"g2a01a1.rl, g2a01a1.fl"						
16481	ENU00275	ANI61C7455: 307..1160	22-41	814-833	EST	"g5g12a1.rl, g5g12a1.fl"						

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16482	ENU00276	ANI61C878:2 051..1195	53-72	845-867	EST	"y6g06a1.r1, y6g06a1.fl"							(AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga menziesii] (AF093540) ribosomal protein L26 [Zea mays]
16483	ENU00277	ANI61C878:2 051..1195	44-63	836-858	EST	"y8e02a1.r1, y8e02a1.fl"							Purine Nucleoside Phosphorylase
16484	ENU00278	ANI61C878:2 051..1195	53-72	845-867	EST	"o8h12a1.r1, o8h12a1.fl"							
16485	ENU00279	ANI61C7147: 5139..6007	72-92	879-898	EST	"h4a04a1.r1, h4a04a1.fl"							
16486	ENU00280	ANI61C1473: 3691..4569	63-82	875-899	EST	"h1g02a1.r1, h1g02a1.fl"							
16487	ENU00281	ANI61C3452: 953..65	33-52	860-879	EST	"d5b06a1.r1, d5b06a1.fl"							
16488	ENU00282	ANI61C6527: 4147..3252	58-77	887-911	EST	"i2a02a1.r1, i2a02a1.fl"							
16489	ENU00283	ANI61C6529: 4358..5265	70-88	916-935	EST	"j9f03a1.r1, j9f03a1.fl"							
16490	ENU00284	ANI61C1023: 2980..2071	64-83	905-930	EST	"o6c05a1.r1, o6c05a1.fl"							
16491	ENU00285	ANI61C6339: 2287..1364	44-63	906-925	EST	"b0e10a1.r1, b0e10a1.fl"							
16492	ENU00286	ANI61C9112: 1258..2202	34-53	911-936	EST	"l3e12a1.r1, l3e12a1.fl"							
16493	ENU00287	ANI61C2746: 36..983	57-76	933-962	EST	"h4b10a1.r1, h4b10a1.fl"							
													(AF029913) unknown [Cochliobolus heterostrophus] ; (AF027687) unknown [Cochliobolus heterostrophus] (U41264) coded for by C. elegans cDNA yk20f8.5; coded for by C. elegans cDNA yk44g1.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk36g6.5; coded for by C. elegans cDNA yk20f8.5; coded for by C. elegans cDNA yk16g12.... (AE000988) coenzyme F390 synthetase (ftsA-2) [Archaeoglobus fulgidus] hypothetical 15.7 KD protein in NUP85-SSC1 intergenic region ; probable membrane protein YJR044c - yeast (Saccharomyces cerevisiae) ; (Z49544) ORF YJR044c [Saccharomyces cerevisiae] ; (L36344) ORF; putative [Saccharomyces cerevisiae] "(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus] " (Z99753) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16494	ENU00288	ANI61C7396: 5964..5008	30-49	923-944	EST	"m6h01a1.r1, m6h01a1.fl"		46	46	0.0005			cytochrome C oxidase polypeptide VIA precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain VIa precursor - yeast (Saccharomyces cerevisiae) ; (X72970) cytochrome-c oxidase [Saccharomyces cerevisiae] ; (X91837) cytochrome-C oxidase chain VIa precursor [Saccharomyces cerevisiae] ; (Z72713) ORF YGL191w [Saccharomyces cerevisiae]
16495	ENU00289	ANI61C8213: 915..1006	69-88	966-985	EST	"g4a02a1.r1, g4a02a1.fl"		133	133	2E-30			(L06279) HOG1 protein [Saccharomyces cerevisiae] hypothetical protein YOL071w - yeast (Saccharomyces cerevisiae) ; (Z74813) ORF YOL071w [Saccharomyces cerevisiae]
16496	ENU00290	ANI61C352:9 45-63 115..10082	45-63	943-970	EST	"x5e08a1.r1, x5e08a1.fl"		79	79	4E-14			"ribosomal protein L31.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (U19729) Ylr406cp: member of L31E ribosomal protein family [Saccharomyces cerevisiae] "
16497	ENU00291	ANI61C1713: 224..1196	33-51	944-963	EST	"z1f05a1.r1, z1f05a1.fl"		112	112	4E-24			[U52210] outer membrane protein; OmpH [Pasteurella multocida] (AL031262) hypothetical protein [Schizosaccharomyces pombe] probable oxidoreductase C26F1.07 in chromosome I ; (Z73100) unknown [Schizosaccharomyces pombe]
16498	ENU00292	ANI61C1510: 2838..2784	54-73	985-1006	EST	"d5f06a1.r1, d5f06a1.fl"		36	36	0.56			X-Ray Structure Of Bacteriorhodopsin From Microcrystals Grown In Lipidic Cubic Phases
16499	ENU00293	ANI61C560:1 41..1141	66-85	1004-1023	EST	"j9h05a1.r1, j9h05a1.fl"		35	35	0.97			hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe]
16500	ENU00294	ANI61C6754: 4129..5153	43-62	1002-1025	EST	"i7f03a1.r1, i7f03a1.fl"		276	276	2E-73			
16501	ENU00295	ANI61C8915: 1890..846	23-42	1006-1025	EST	"y8a06a1.r1, y8a06a1.fl"		57	57	0.0000003			
16502	ENU00296	ANI61C9104: 2033..3112	60-79	1061-1093	EST	"o6b05a1.r1, o6b05a1.fl"		68	68	3E-22			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16503	ENU00297	ANI61C1724: 2733..3814	56-77	1074-1095	EST	"o6d03a1.r1, o6d03a1.fl"			233	2E-60			"vacuolar aminopeptidase I precursor (polypeptidase) (leucine aminopeptidase IV) (LAPIV) (aminopeptidase III) (aminopeptidase YSCI) ; aminopeptidase yscI (EC 3.4.11.-) precursor, vacuolar - yeast (Saccharomyces cerevisiae) ; (M25548) aminopeptidase I [Saccharomyces cerevisiae] ; (X71133) vacuolar aminopeptidase YSC1 [Saccharomyces cerevisiae] ; (Z28103) ORF YKL103c [Saccharomyces cerevisiae] "
16504	ENU00298	ANI61C8591: 4826..3741	56-75	1078-1098	EST	"w8e01a1.r1, w8e01a1.fl"			35	1.1			"(U50191) C. elegans collagen dpy-10 gene (Levy, A.D., Yang, J. and Kramer, J.M. Mol. Biol. Cell 4, 803-17, 1993) [Caenorhabditis elegans] "
16505	ENU00299	ANI61C1649: 1879..782	57-76	1090-1112	EST	"g5e01a1.r1, g5e01a1.fl"			198	8E-50			"serine/threonine-protein kinase SAT4 ; probable protein kinase YCR008w (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (S76380) putative protein kinase=YCR101 [Saccharomyces cerevisiae, Peptide, 603 aa] [Saccharomyces cerevisiae] ; (X59720) YCR008w, len:603 [Saccharomyces cerevisiae] "
16506	ENU00300	ANI61C1085 45-64 7:3708..2609	45-64	1083-1102	EST	"g4c03a1.r1, g4c03a1.fl"			123	2E-27			Dynamin-like protein C12C2.08 ; (Z54140) dynamin-related protein [Schizosaccharomyces pombe]
16507	ENU00301	ANI61C9149: 1087..2190	27-46	1069-1088	EST	"m5b05a1.r1, m5b05a1.fl"			90	4E-46			(AF003835) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Rattus norvegicus]
16508	ENU00302	ANI61C352:8 960..10076	26-45	1066-1100	EST	"j9e11a1.r1, j9e11a1.fl"			79	5E-14			hypothetical protein YOL071w - yeast (Saccharomyces cerevisiae) ; (Z74813) ORF YOL071w [Saccharomyces cerevisiae]
16509	ENU00303	ANI61C312:2 52-71 088..960	52-71	1106-1138	EST	"g3f04a1.r1, g3f04a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16510	ENU00304	ANI61C2872: 1333..193	43-63	1122-1141	EST	"i0a05a1.r1, i0a05a1.fl"		357	357	9E-98			"glycogen (starch) synthase, isoform 2 ; UDPglucose--starch glucosyltransferase (EC 2.4.1.11) 2 - yeast (Saccharomyces cerevisiae) ; (U17244) Gsy2p: Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae] "
16511	ENU00305	ANI61C1373: 2625..3780	69-88	1153-1182	EST	"z7b06a1.r1, z7b06a1.fl"		32	32	7.6			hypothetical ABC transporter ATP-binding protein CY3G12.08 ; (Z79702) hypothetical protein Rv2326c [Mycobacterium tuberculosis]
16512	ENU00306	ANI61C9941: 1716..542	46-65	1156-1178	EST	"h4a11a1.r1, h4a11a1.fl"		224	224	6E-87			dolichyl-phosphate-mannose--protein mannosyltransferase 2 ; hypothetical protein YAL023 - yeast (Saccharomyces cerevisiae) ; (L05146) Pmt2p: protein O-D-mannosyltransferase [Saccharomyces cerevisiae] ; (L05027) ORF YAL23 [Saccharomyces cerevisiae]
16513	ENU00307	ANI61C2872: 1385..193	42-64	1173-1192	EST	"c6c08a1.r1, c6c08a1.fl"		378	378	e-104			"glycogen (starch) synthase, isoform 2 ; UDPglucose--starch glucosyltransferase (EC 2.4.1.11) 2 - yeast (Saccharomyces cerevisiae) ; (U17244) Gsy2p: Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae] "
16514	ENU00308	ANI61C9181: 6707..5501	40-59	1182-1204	EST	"g4c08a1.r1, g4c08a1.fl"		169	169	3E-49			ORM1 protein ; probable membrane protein YGR038w - yeast (Saccharomyces cerevisiae) ; (Z72823) ORF YGR038w [Saccharomyces cerevisiae]
16515	ENU00309	ANI61C8866: 224..1436	23-42	1171-1193	EST	"k5h03a1.r1, k5h03a1.fl"		76	76	6E-13			(AF047004) dimethylglycine dehydrogenase-like protein isoform 1; putative sarcosine dehydrogenase [Homo sapiens]
16516	ENU00310	ANI61C6281: 155..1393	35-53	1209-1229	EST	"y6c08a1.r1, y6c08a1.fl"		169	169	8E-47			splicing factor U2AF homolog - mouse ; (X64587) orf [Mus musculus]
16517	ENU00311	ANI61C9556: 7091..5789	29-48	1270-1289	EST	"d3d03a1.r1, d3d03a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16518	ENU00312	ANI61C1004 0:1354..50	24-44	1267-1286	EST	"d3d05a1.rl, d3d05a1.fl"		120	2E-26				U84404) E6-associated protein E6-AP/ubiquitin-protein ligase [Homo sapiens]; (AF016708) E6-AP ubiquitin-protein ligase [Homo sapiens] probable membrane protein YPL006w - yeast (Saccharomyces cerevisiae); (Z48483) unknown [Saccharomyces cerevisiae]; (U33335) Lpa1 lp [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae] (AC003027) lc prt_seq No definition line found [Arabidopsis thaliana] (AF010145) hexose transporter [Aspergillus parasiticus] Spermidine synthase (putrescine aminopropyltransferase) (SPDSY); (Z54140) putrescine aminopropyltransferase [Schizosaccharomyces pombe] (AL032632) predicted using Genefinder; similar to Myosin head (motor domain); cDNA EST yk209b12.5 comes from this gene; cDNA EST yk248g5.3 comes from this gene; cDNA EST yk248g5.5 comes from this gene; cDNA EST yk398h10.3 comes...
16519	ENU00313	ANI61C7887: 32-51 750..2077	32-51	1296-1317	EST	"p0h07a1.rl, p0h07a1.fl"		255	4E-67				
16520	ENU00314	ANI61C3862: 57-76 2878..1528	57-76	1336-1365	EST	"d4c06a1.rl, d4c06a1.fl"		212	6E-54				
16521	ENU00315	ANI61C903:1 56-73 507..133	56-73	1362-1388	EST	"o0f08a1.rl, o0f08a1.fl"		300	e-135				
16522	ENU00316	ANI61C4572: 54-73 1186..2561	54-73	1365-1387	EST	"h4a05a1.rl, h4a05a1.fl"		129	1E-40				
16523	ENU00317	ANI61C6258: 48-67 1889..511	48-67	1364-1384	EST	"r1e10a1.rl, r1e10a1.fl"		32	7.1				
16524	ENU00318	ANI61C5156: 37-58 2879..1478	37-58	1375-1396	EST	"y8e05a1.rl, y8e05a1.fl"		343	2E-93				(AL033503) phenylalanyl-tRNA synthetase [Candida albicans]
16525	ENU00319	ANI61C2972: 51-70 4998..3543	51-70	1435-1463	EST	"y6f05a1.rl, y6f05a1.fl"		242	e-104				"Succinic semialdehyde dehydrogenase"; (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens]; (AL031230) dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24)) [Homo sapiens] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16526	ENU00320	ANI61C6489: 8615..7108	50-69	1482-1515	EST	"g7h07a1.r1, g7h07a1.fl"		73	73	2E-34			hypothetical 42.3 KD protein in YTA2-DIT1 intergenic region ; hypothetical protein YDR400w - yeast (Saccharomyces cerevisiae) ; (U32274) Ydr400wp; CAI: 0.14 [Saccharomyces cerevisiae]
16527	ENU00321	ANI61C41:22 27..705	40-60	1489-1520	EST	"i7c04a1.r1, i7c04a1.fl"		316	316	2E-85			glucosamine-6-phosphate isomerase (glucosamine-6-phosphate deaminase) ; glucosamine-6-phosphate deaminase protein (nagB) homolog - Haemophilus influenzae (strain Rd KW20) ; (U32700) glucosamine-6-phosphate isomerase (nagB) [Haemophilus influenzae Rd]
16528	ENU00322	ANI61C5260: 516..2046	40-59	1504-1528	EST	"c4h09a1.r1, c4h09a1.fl"		347	347	8E-95			gamma-glutamyl phosphate reductase (GPR) (glutamate-5-semialdehyde dehydrogenase) (glutamyl-gamma-semialdehyde dehydrogenase) ; glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41) - yeast (Saccharomyces cerevisiae) ; (X90565) orf 06155 [Saccharomyces cerevisiae] ; (U43565) gamma-glutamyl phosphate reductase [Saccharomyces cerevisiae] ; (Z75231) ORF YOR323c [Saccharomyces cerevisiae]
16529	ENU00323	ANI61C7453: 1689..3255	50-69	1555-1574	EST	"y4d12a1.r1, y4d12a1.fl"		155	155	5E-37			pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 ; (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster] (AB000281) krev-1 [Neurospora crassa]
16530	ENU00324	ANI61C1897: 3224..1593	70-89	1635-1658	EST	"m6h05a1.r1, m6h05a1.fl"		158	158	9E-38			(AJ000504) Meis2a homeodomain protein [Mus musculus]
16531	ENU00325	ANI61C715:5 48..2259	70-89	1718-1737	EST	"y4b11a1.r1, y4b11a1.fl"		81	81	3E-14			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16532	ENU00326	ANI61C6741: 22-41 2777..4487			EST	"m5f01a1.r1, m5f01a1.fl"			134	9E-37			acid protease precursor ; acid proteinase (EC 3.4.23.-) PEP1 precursor - yeast (Saccharomycopsis fibuligera) ; (D00313) open reading frame of PEP1 (putative secretable acid protease) [Saccharomycopsis fibuligera] ; acid protease PEP1 [Saccharomycopsis fibuligera]
16533	ENU00327	ANI61C7453: 50-69 1689..3454		1754- 1773	EST	"g6g01a1.r1, g6g01a1.fl"			155	6E-37			pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 ; (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster] (Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]
16534	ENU00328	ANI61C146:5 31-50 780..5675		1855- 1876	EST	"m5h10a1.r1, m5h10a1.fl"			52	0.00001			probable sterigmatocystin biocynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emericella nidulans] "(Z98762) SPAC4A8.06c, unknown, len:578aa, some similarity eg. to BAH_STRHY, Q01109, acetyl- hydrolase, (299aa), fasta sco res, opt:259, E():8.2e-17, (35.6% identity in 118 aa overl ap) [Schizosaccharomyces pombe]"
16535	ENU00329	ANI61C7950: 53-72 2442..624		1937- 1957	EST	"g6d12a1.r1, g6d12a1.fl"			97	5E-19			
16536	ENU00330	ANI61C292:5 27-46 926..8002		2037- 2060	EST	"c6c10a1.r1, c6c10a1.fl"			134	3E-30			
16537	ENU00331	ANI61C8138: 22-45 1813..1614		149-179	EST	"o0g08a1.r1, o0g08a1.fl"			29	3.3			(Z68879) Similarity to alcohol-steroid dehydrogenases; cDNA EST yk275a9.3 comes from this gene; cDNA EST yk275a9.5 comes from this gene [Caenorhabditis elegans] ; (Z68880) Similarity to alcohol-steroid dehydrogenases; cDNA EST yk275a9.3 comes from this gene; cDNA EST yk275a9.5 comes from this gene [Caenorhabditis elegans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16538	ENU00332	ANI61C8543: 1308..1109	32-55	167-189	EST	"g8d02a1.r1, g8d02a1.fl"		29	29	4.4			coenzyme PQQ synthesis protein C (coenzyme PQQ synthesis protein I); gene I protein - Acinetobacter calcoaceticus ; (X06452) gene I [Acinetobacter calcoaceticus]
16539	ENU00333	ANI61C8580: 27-46 3853..4053	27-46	158-185	EST	"c1a1l1a1.r1, c1a1l1a1.fl"							
16540	ENU00334	ANI61C6714: 22-48 4109..3905	22-48	165-184	EST	"p0b08a1.r1, p0b08a1.fl"							
16541	ENU00335	ANI61C1027 22-53 7:4906..5110	22-53	149-184	EST	"w4g12a1.r1, w4g12a1.fl"							
16542	ENU00336	ANI61C3347: 26-47 2768..2973	26-47	154-189	EST	"t2b02a1.r1, t2b02a1.fl"							
16543	ENU00337	ANI61C1049 31-51 7:1475..1683	31-51	178-197	EST	"c9e10a1.r1, c9e10a1.fl"		66	66	2E-15			(AF022972) similar to C. elegans olfactory receptor ODR-10 (GB:U49449) [Caenorhabditis elegans] "probable T-complex protein 1, ETA subunit (TCP-1-ETA) (CCT-ETA) ; (Z95397) Cct7p [Schizosaccharomyces pombe] "
16544	ENU00338	ANI61C6193: 25-48 1220..1011	25-48	165-192	EST	"y8a10a1.r1, y8a10a1.fl"		29	29	5.7			(AF032464) unknown [Leishmania mexicana mexicana] (Y10616) SMTA-2 protein [Sordaria macrospora]
16545	ENU00339	ANI61C9537: 61-80 418..628	61-80	205-229	EST	"y8d05a1.r1, y8d05a1.fl"		32	32	0.38			"3',5'-cyclic-nucleotide phosphodiesterase (PDEase) ; probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) pde1 - fission yeast (Schizosaccharomyces pombe) ; (S64907) Dictyostelium discoideum phosphodiesterase homolog [Schizosaccharomyces pombe=fission yeast, Peptide, 346 aa] [Schizosaccharomyces pombe] ; (AL031545) 3',5'-cyclic-nucleotide phosphodiesterase [Schizosaccharomyces pombe] ; pde1 gene [Schizosaccharomyces pombe] "
16546	ENU00340	ANI61C8199: 68-87 3060..2848	68-87	203-238	EST	"z1c08a1.r1, z1c08a1.fl"		28	28	7.4			"(AF016659) contains similarity to ankyrin repeats; partial CDS, this gene probably begins in the next clone [Caenorhabditis elegans] "
16547	ENU00341	ANI61C9708: 22-50 2531..2744	22-50	157-192	EST	"o6a04a1.r1, o6a04a1.fl"		30	30	1.9			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16548	ENU00342	ANI61C7957: 1675..1463	22-41	157-192	EST	"c9d07a1.rl, c9d07a1.fl"		32	0.65				(Z81050) Similarity to Shrimp amylase (TR:Q26193); cDNA EST EMBL:Z14343 comes from this gene [Caenorhabditis elegans] carboxy-terminal proteinase (EC 3.4.21.-) prc - Escherichia coli ; (D00674) ORF of prc gene [Escherichia coli] (AJ002204) polyamine oxidase [Zea mays] (Z49073) similarity to the OV-17 antigen precursor from onchocerca volvulus (Swiss Prot accession number P36991) [Caenorhabditis elegans] (Z49073) similarity to the OV-17 antigen precursor from onchocerca volvulus (Swiss Prot accession number P36991) [Caenorhabditis elegans] DNA binding protein - Emericella nidulans ; (Z47081) DNA binding protein [Emericella nidulans] (AE001208) conserved hypothetical protein [Treponema pallidum] neutral proteinase II - Aspergillus oryzae neutral proteinase II - Aspergillus oryzae "(Y12655) 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase component [Pseudomonas putida] " "growth factor-responsive protein, vascular smooth muscle - rat ; (U06713) SM-20 [Rattus norvegicus] " (Z99532) conserved hypothetical protein [Schizosaccharomyces pombe] protein-tyrosine kinase (EC 2.7.1.112) - human ; (L13738) activated p21cdc42Hs kinase [Homo sapiens] ; non-receptor Tyr kinase [Homo sapiens]
16549	ENU00343	ANI61C5524: 1497..1284	63-82	199-234	EST	"j0a01a1.rl, j0a01a1.fl"		29	4.3				
16550	ENU00344	ANI50C4357 1:203..416	38-60	190-209	EST	"m8b11a1.rl, m8b11a1.fl"		45	0.000000				
16551	ENU00345	ANI61C5958: 318..105	27-47	180-199	EST	"z2fl2a1.rl, z2fl2a1.fl"		29	5.6				
16552	ENU00346	ANI61C5958: 318..105	29-49	182-201	EST	"s8h07a1.rl, s8h07a1.fl"		29	5.6				
16553	ENU00347	ANI61C7015: 7018..6798	50-70	209-228	EST	"c5d05a1.rl, c5d05a1.fl"		31	0.84				
16554	ENU00348	ANI61C6213: 2661..2441	22-44	165-200	EST	"o6fl2a1.rl, o6fl2a1.fl"		30	2.5				
16555	ENU00349	ANI61C3157: 382..578	70-89	222-249	EST	"x9f02a1.rl, x9f02a1.fl"		37	0.015				
16556	ENU00350	ANI61C3157: 382..578	70-89	222-249	EST	"x9f01a1.rl, x9f01a1.fl"		37	0.015				
16557	ENU00351	ANI61C7797: 2467..2244	52-72	211-232	EST	"x7d03a1.rl, x7d03a1.fl"		30	2.5				
16558	ENU00352	ANI61C475:1 851..2074	71-90	223-252	EST	"r1e07a1.rl, r1e07a1.fl"		30	2.3				
16559	ENU00353	ANI61C5180: 690..914	55-74	215-237	EST	"w8h01a1.rl, w8h01a1.fl"		30	3				
16560	ENU00354	ANI61C3752: 1462..1687	38-57	200-221	EST	"e4b01a1.rl, e4b01a1.fl"		31	1				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16561	ENU00355	ANI61C4777: 1066..840	38-57	193-222	EST	"h0b08a1.r1", h0b08a1.fl"			122	4E-28			"Aldehyde dehydrogenase (ALDDH); aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans; (M16197) aldehyde dehydrogenase [Emericella nidulans]; dehydrogenase,aldehyde [Emericella nidulans] "
16562	ENU00356	ANI61C4718: 1183..1410	22-57	187-207	EST	"r6b04a1.r1", r6b04a1.fl"			28	9.1			peroxisome biogenesis factor 13; peroxisomal membrane protein PEX13 (peroxin-13); (AF048755) HsPex13p [Homo sapiens]; (U71374) HsPex13p [Homo sapiens]
16563	ENU00357	ANI61C5532: 64..292	32-57	188-218	EST	"y8h06a1.r1", y8h06a1.fl"			29	4.1			hypothetical 16.2 KD protein in PFK1-TDS4 intergenic region; hypothetical protein YGR243w - yeast (Saccharomyces cerevisiae); (Z73028) ORF YGR243w [Saccharomyces cerevisiae]
16564	ENU00358	ANI61C971:9 74..746	22-43	188-208	EST	"x9h10a1.r1", x9h10a1.fl"			29	4.1			(U80842) ZC239.9 gene product [Caenorhabditis elegans]
16565	ENU00359	ANI61S4572: 1..230	22-54	185-209	EST	"r1f01a1.r1", r1f01a1.fl"			48	0.00001			(AL032631) predicted using Genefinder; cDNA EST yk393b10.5 comes from this gene; cDNA EST yk403h3.3 comes from this gene; cDNA EST yk403h3.5 comes from this gene; cDNA EST yk252h6.3 comes from this gene; cDNA EST yk252h6.5 come...
16566	ENU00360	ANI61C1083 4:2471..2242	39-58	195-226	EST	"q0a10a1.r1", q0a10a1.fl"			43	0.0003			(D87063) chitinase [Emericella nidulans]
16567	ENU00361	ANI61C4987: 777..545	22-49	184-212	EST	"o8h01a1.r1", o8h01a1.fl"			31	1.9			(AF026401) stearyl-CoA desaturase [Mucor rouxii]
16568	ENU00362	ANI61C5234: 844..1078	23-49	188-215	EST	"a0a05a1.r1", a0a05a1.fl"			30	3.3			gene hb protein - mouse (fragment); (X81634) hb [Mus musculus]
16569	ENU00363	ANI61C6800: 1284..1050	30-50	191-222	EST	"i3b03a1.r1", i3b03a1.fl"			32	0.5			"(AE001069) molybdopterin oxidoreductase, iron-sulfur binding subunit [Archaeoglobus fulgidus] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16570	ENU00364	ANI61C1364: 237..1	72-92	231-265	EST	"x9d10a1.rl, x9d10a1.fl"		29	29	5.9		"alpha-amylase type B isozyme precursor (1,4-alpha-D-glucan glucanOhydrolase) (cloneS GRAMY56 and 963) ; alpha-amylase (EC 3.2.1.1) B precursor (gene Amy56 and others) - barley ; (X15227) alpha amylase [Hordeum vulgare] ; high pl alpha amylase [Hordeum vulgare var. distichum] "
16571	ENU00365	ANI61C3918: 3045..3280	23-52	186-216	EST	"y8c02a1.rl, y8c02a1.fl"		29	29	4.5		"triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - dog ; (M35302) lipase precursor [Canis familiaris] "
16572	ENU00366	ANI61C1028 0:110..347	27-46	196-222	EST	"r2g06a1.rl, r2g06a1.fl"		31	31	1.2		Conidiation-specific protein 10; conidiation-specific protein - Neurospora crassa ; (M20005) conidiation-specific protein con-10 [Neurospora crassa]
16573	ENU00367	ANI61C1968: 611..372	65-84	233-262	EST	"m8a09a1.rl, m8a09a1.fl"		32	32	0.54		(AF038948) ultraviolet cone visual pigment; rhodopsin [Ambystoma tigrinum]
16574	ENU00368	ANI61C5343: 767..526	48-69	217-247	EST	"o9h08a1.rl, o9h08a1.fl"		64	64	1E-10		(AF093244) import protein Tim9p [Saccharomyces cerevisiae]
16575	ENU00369	ANI61C5354: 9..251	30-53	199-230	EST	"g9f01a1.rl, g9f01a1.fl"		29	29	4.8		(Z46276) Ig heavy chain variable region [Homo sapiens]
16576	ENU00370	ANI61C2518: 513..270	22-41	196-223	EST	"m6b02a1.rl, m6b02a1.fl"		31	31	2.3		(X98456) ORF 2 [Mus musculus]
16577	ENU00371	ANI61C8695: 4642..4889	29-55	210-234	EST	"r4c07a1.rl, r4c07a1.fl"		31	31	2.4		(AC000132) Strong similarity to Dianthus cysteine proteinase (gb U17135). [Arabidopsis thaliana]
16578	ENU00372	ANI61C1147 7:1040..790	47-66	236-255	EST	"c9e12a1.rl, c9e12a1.fl"						
16579	ENU00373	ANI61C7858: 2004..1752	47-66	234-257	EST	"m0c05a1.rl, m0c05a1.fl"						
16580	ENU00374	ANI61C6863: 1064..805	27-49	225-244	EST	"j0c04a1.rl, j0c04a1.fl"						
16581	ENU00375	ANI61C1748: 899..1158	31-53	217-248	EST	"y6c05a1.rl, y6c05a1.fl"						
16582	ENU00376	ANI61C4718: 1143..1410	35-70	240-260	EST	"x5f07a1.rl, x5f07a1.fl"						
16583	ENU00377	ANI61C1626: 1305..1037	22-52	229-248	EST	"r5a02a1.rl, r5a02a1.fl"						

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16584	ENU00378	ANI61C1253: 58-77 6182..6451	58-77	261-285	EST	"c9d06al.r1, c9d06al.fl"		31	31	1.6		(Z54206) UL52 [Bovine herpesvirus 1] ; (AJ004801) component of DNA helicase/primase complex [Bovine herpesvirus type 1.1]
16585	ENU00379	ANI61C9672: 22-55 3072..2798	22-55	234-254	EST	"dlgl0al.r1, dlgl0al.fl"		34	34	0.26		S59/4 homeotic protein - fruit fly (Drosophila melanogaster)
16586	ENU00380	ANI61C5697: 48-67 279..1	48-67	262-284	EST	"r5b08al.r1, r5b08al.fl"		31	31	2.2		(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]
16587	ENU00381	ANI61C9139: 55-77 688..410	55-77	264-291	EST	"z1f06al.r1, z1f06al.fl"		30	30	3.8		"(AL034559) predicted using hexExon; MAL3P7.37 (PFC1030w), Hypothetical protein, len: 1543 aa [Plasmodium falciparum]"
16588	ENU00382	ANI61C2195: 33-51 296..17	33-51	241-270	EST	"m8h11al.r1, m8h11al.fl"		69	69	6E-12		(AL023635) hypothetical protein MLCB1243.36 [Mycobacterium leprae]
16589	ENU00383	ANI61C1049 0:1251..1532	23-50	243-262	EST	"g6g03al.r1, g6g03al.fl"		31	31	1.7		cryptogene protein G4 - Sauroleishmania tarentolae (strain LEM125)
16590	ENU00384	ANI61C1029 6:4459..4741	22-56	236-262	EST	"i0h11al.r1, i0h11al.fl"		33	33	0.63		(AJ000871) histidine kinase [Streptococcus mitis]
16591	ENU00385	ANI61C7052: 48-74 3030..2741	48-74	262-295	EST	"g9g11al.r1, g9g11al.fl"		68	68	2E-11		Peroxisomal membrane protein PMP47A ; 47K peroxisomal membrane protein - yeast (Candida boidinii) ; (J05672) peroxisomal membrane protein [Candida boidinii]
16592	ENU00386	ANI61C1754: 22-54 347..639	22-54	246-272	EST	"y6h08al.r1, y6h08al.fl"		30	30	4.4		(AB003699) Cdc7-related kinase [Xenopus laevis]
16593	ENU00387	ANI61C7776: 45-66 3863..3567	45-66	274-299	EST	"h0h05al.r1, h0h05al.fl"		37	37	0.034		(Z99292) hypothetical protein [Schizosaccharomyces pombe]
16594	ENU00388	ANI61C319:4 907..5205	22-45	258-277	EST	"m8a02al.r1, m8a02al.fl"						
16595	ENU00389	ANI61C8590: 37-58 194..494	37-58	268-295	EST	"c5e10al.r1, c5e10al.fl"						
16596	ENU00390	ANI61C1017 1:2998..2696	22-41	257-282	EST	"y8g02al.r1, y8g02al.fl"						
16597	ENU00391	ANI61C1049 0:1227..1532	22-54	266-285	EST	"o8f10al.r1, o8f10al.fl"		69	69	7E-12		(AL023635) hypothetical protein MLCB1243.36 [Mycobacterium leprae]

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16598	ENU00392	ANI61C8580: 49-67 7053..7358	293-312	293-312	EST	"i0e02al.rl, i0e02al.fl"		31	31	3.5			glucose inhibited division protein B ; (U97573) gidB homolog [Treponema pallidum] ; (AE001263) glucose- inhibited division protein B (gidB) [Treponema pallidum] probable endoglucanase - Ruminococcus flavefaciens ; (X56082) endo-glucanase [Ruminococcus flavefaciens]
16599	ENU00393	ANI61C7799: 27-46 9..315	256-291	256-291	EST	"n3a07al.rl, n3a07al.fl"		31	31	2.1			probable endoglucanase - Ruminococcus flavefaciens ; (X56082) endo-glucanase [Ruminococcus flavefaciens]
16600	ENU00394	ANI61C9506: 32-52 1881..1574	267-297	267-297	EST	"y6e07al.rl, y6e07al.fl"		31	31	2.1			probable endoglucanase - Ruminococcus flavefaciens ; (X56082) endo-glucanase [Ruminococcus flavefaciens]
16601	ENU00395	ANI61C7799: 27-46 9..316	257-292	257-292	EST	"e9a07al.rl, e9a07al.fl"		31	31	2.1			probable endoglucanase - Ruminococcus flavefaciens ; (X56082) endo-glucanase [Ruminococcus flavefaciens]
16602	ENU00396	ANI61C9506: 32-52 1881..1574	267-297	267-297	EST	"l3b06al.rl, l3b06al.fl"		29	29	8.4			"cytochrome P450 52C2 (CYPLIIC2) (alkane-inducible P450-ALK6-A) ; cytochrome P450 ALK6-A, alkane- inducible - yeast (Candida maltosa) ; (D12718) n-alkane inducible cytochrome P-450 [Candida maltosa] "
16603	ENU00397	ANI61C1453: 54-73 283..592	295-321	295-321	EST	"b0h04al.rl, b0h04al.fl"		30	30	5.1			(AE000820) magnesium chelatase subunit [Methanobacterium thermoautotrophicum] probable clathrin heavy chain ; (Z69240) clathrin heavy chain [Schizosaccharomyces pombe]
16604	ENU00398	ANI61C4718: 23-45 1101..1410	270-290	270-290	EST	"o6h06al.rl, o6h06al.fl"		46	46	0.00006			
16605	ENU00399	ANI61C6956: 24-43 3451..3765	275-296	275-296	EST	"m5fl1al.rl, m5fl1al.fl"		30	30	5.1			
16606	ENU00400	ANI61C692:4 22-55 92..173	274-299	274-299	EST	"x7g04al.rl, x7g04al.fl"		46	46	0.00006			
16607	ENU00401	ANI61C2935: 43-62 550..231	290-320	290-320	EST	"w4e09al.rl, w4e09al.fl"		31	31	2.3			
16608	ENU00402	ANI61C9040: 22-56 1556..1876	265-300	265-300	EST	"o0b07al.rl, o0b07al.fl"		31	31	2.3			
16609	ENU00403	ANI61C124:1 24-47 235..909	280-308	280-308	EST	"y4a12al.rl, y4a12al.fl"		31	31	2.3			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16610	ENU00404	ANI61C6709: 644..314	36-56	290-324	EST	"k5e05a1.r1, k5e05a1.fl"		31	31	3.1			zinc finger protein MSN4 (multicopy suppressor of SNF1 protein 4) ; finger protein MSN4 - yeast (Saccharomyces cerevisiae) ; (L08839) zinc finger protein [Saccharomyces cerevisiae] ; (X75781) human transcription factor homologue [Saccharomyces cerevisiae] ; (Z28062) ORF YKL062w [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
16611	ENU00405	ANI61C6046: 1179..848	22-52	290-311	EST	"c1b10a1.r1, c1b10a1.fl"		32	32	1.1			hypothetical 12.8 KD protein in ARO9-SPS100 intergenic region precursor ; hypothetical protein YHR138c - yeast (Saccharomyces cerevisiae) ; (U10398) Yhr138cp [Saccharomyces cerevisiae] ; (Y13625) hypothetical protein [Saccharomyces cerevisiae] (AF066054) formaldehyde dehydrogenase [Pichia pastoris]
16612	ENU00406	ANI61C7955: 405..73	31-49	301-321	EST	"h4c10a1.r1, h4c10a1.fl"		112	112	5E-35			Intercellular adhesion molecule-1 precursor (ICAM-1) ; (U65789) intercellular adhesion molecule-1 [Bos taurus]
16613	ENU00407	ANI61C1112: 9-889..563	22-42	287-313	EST	"m0h06a1.r1, m0h06a1.fl"		32	32	1.4			(U42845) coded for by C. elegans cDNA yk83a12.5; coded for by C. elegans cDNA yk74b10.5; coded for by C. elegans cDNA yk64a6.5; coded for by C. elegans cDNA yk108g8.5; coded for by C. elegans cDNA yk90b... exodeoxyribonuclease V (EC 3.1.11.5) 67K chain - Escherichia coli ; (X04582) exonuclease V alpha subunit (AA 1-608) [Escherichia coli] (AJ005589) protein tyrosine phosphatase [Pisum sativum] (U74668) soluble transducer protein HtH [Halobacterium salinarum]
16614	ENU00408	ANI61C1029: 0-98..433	22-56	287-315	EST	"z3d09a1.r1, z3d09a1.fl"		67	67	9E-21			
16615	ENU00409	ANI61C9613: 533..872	25-45	300-322	EST	"c1h09a1.r1, c1h09a1.fl"		32	32	1.9			
16616	ENU00410	ANI61C2251: 777..1118	50-69	327-349	EST	"z4h11a1.r1, z4h11a1.fl"		36	36	0.075			
16617	ENU00411	ANI61C3279: 568..227	31-50	298-330	EST	"o1f04a1.r1, o1f04a1.fl"		31	31	2.5			
16618	ENU00412	ANI61C6812: 4365..4708	39-60	313-340	EST	"q0c10a1.r1, q0c10a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16619	ENU00413	ANI61C6812: 4365..4708	36-57	310-337	EST	"o9c11a1.r1, o9c11a1.fl"		31	31	2.5			HtH [Halobacterium salinarum] (U74668) soluble transducer protein
16620	ENU00414	ANI61C6812: 4365..4708	26-47	300-327	EST	"g6a05a1.r1, g6a05a1.fl"		31	31	2.5			HtH [Halobacterium salinarum] (U74668) soluble transducer protein
16621	ENU00415	ANI61C2656: 40-59 1399..1505	40-59	312-343	EST	"f0h06a1.r1, f0h06a1.fl"		31	31	4.3			TBF1 protein (TTAGGG repeat-binding factor 1) (TBF alpha); TTAGGG repeat-binding factor 1 - yeast (Saccharomyces cerevisiae); (U43703) Tbf1p [Saccharomyces cerevisiae]
16622	ENU00416	ANI61C6003: 65-85 398..743	65-85	349-368	EST	"b0g08a1.r1, b0g08a1.fl"		29	222	9.8			(U33940) gp46 surface membrane protein [Simian T-cell lymphotropic virus type 1] CATALase B; (U80672) catalase [Emmericella nidulans] (U16751) cold-responsive gene product [Brassica oleracea] "mitochondrial 60S ribosomal protein L24 precursor (YML24); ribosomal protein Yml24, mitochondrial - yeast (Saccharomyces cerevisiae); (Z47815) ribosomal protein [Saccharomyces cerevisiae]"
16623	ENU00417	ANI61C2752: 54-73 589..243	54-73	339-358	EST	"o8b12a1.r1, o8b12a1.fl"		34	34	0.39			
16624	ENU00418	ANI61C9663: 25-59 2057..2403	25-59	298-329	EST	"w8e04a1.r1, w8e04a1.fl"		59	59	0.000000			
16625	ENU00419	ANI61C2968: 23-56 909..563	23-56	295-327	EST	"m7e04a1.r1, m7e04a1.fl"		02	02				
16626	ENU00420	ANI61C1731: 72-94 468..114	72-94	350-384	EST	"e0d10a1.r1, e0d10a1.fl"		89	89	2E-17			Conidium-specific protein; SpoC1-C1D protein - Emmericella nidulans; (X54668) SpoC1-C1D product [Emmericella nidulans] amidase (EC 3.5.1.4) - Aspergillus oryzae; (D10492) acetamidase [Aspergillus oryzae] (U81825) pacifastin light chain precursor [Pacifastacus leniusculus] tyrA protein - Bacillus subtilis; (M80245) TyrA [Bacillus subtilis]; (Z99115) prephenate dehydrogenase [Bacillus subtilis] mucin JER57 - human
16627	ENU00421	ANI61C7024: 55-74 407..762	55-74	336-368	EST	"q0e11a1.r1, q0e11a1.fl"		35	35	0.24			
16628	ENU00422	ANI61C4014: 35-54 1146..790	35-54	330-349	EST	"y8c04a1.r1, y8c04a1.fl"		32	32	1.2			
16629	ENU00423	ANI61C713:2 45-64 337..1976	45-64	330-364	EST	"z1g01a1.r1, z1g01a1.fl"		30	30	6.2			
16630	ENU00424	ANI61C3305: 22-53 1206..842	22-53	325-344	EST	"r7d11a1.r1, r7d11a1.fl"		30	30	8.3			
16631	ENU00425	ANI61C3024: 26-46 1315..1680	26-46	321-349	EST	"y6e02a1.r1, y6e02a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16632	ENU00426	ANI61C9488: 22-47 629..263	22-47	314-346	EST	"c8c02a1.rl, c8e02a1.fl"		68	2E-11				ABC1 transporter; ABC-type ATPase [Magnaporthe grisea] (AF032443)
16633	ENU00427	ANI61C7171: 70-89 2045..2412	70-89	368-395	EST	"y8g06a1.rl, y8g06a1.fl"		33	0.74				response regulator (AF049107) homolog [Myxococcus xanthus] (AL021426) cwIM [Mycobacterium tuberculosis]
16634	ENU00428	ANI61C1077 70-89 3:2911..2542	70-89	370-397	EST	"j0g10a1.rl, j0g10a1.fl"		31	4.9				probable membrane protein YOL089c - yeast (Saccharomyces cerevisiae) ; (X83121) orf 00938 [Saccharomyces cerevisiae] ; (Z74831) ORF YOL089c [Saccharomyces cerevisiae]
16635	ENU00429	ANI61C1105 31-58 4:1301..1670	31-58	334-358	EST	"c6a01a1.rl, c6a01a1.fl"		39	0.01				
16636	ENU00430	ANI61C5376: 45-64 329..700	45-64	345-374	EST	"o8h06a1.rl, o8h06a1.fl"		36	0.15				metallothionein-like protein 1 ; metallothionein - barley ; (X58540) ids-1 [Hordeum vulgare]
16637	ENU00431	ANI61C9746: 71-91 4418..4047	71-91	372-400	EST	"z4h04a1.rl, z4h04a1.fl"		33	1				zinc finger RNA binding protein [Mus musculus] (AF071059)
16638	ENU00432	ANI61C5649: 24-53 145..519	24-53	329-356	EST	"l0a09a1.rl, l0a09a1.fl"		30	8.8				hypothetical 49.6 KD protein in OMPP 3'region precursor ; (X74278) ORF [Escherichia coli]
16639	ENU00433	ANI61C5657: 22-49 755..379	22-49	334-356	EST	"c4fl2a1.rl, c4fl2a1.fl"		30	8.8				hypothetical 49.6 KD protein in OMPP 3'region precursor ; (X74278) ORF [Escherichia coli]
16640	ENU00434	ANI61C9902: 22-45 2140..2517	22-45	331-357	EST	"g6d04a1.rl, g6d04a1.fl"		30	8.8				
16641	ENU00435	ANI61C9902: 22-45 2140..2517	22-45	331-357	EST	"x8d07a1.rl, x8d07a1.fl"		30	8.8				
16642	ENU00436	ANI61C7527: 22-51 444..66	22-51	336-358	EST	"c8g08a1.rl, c8g08a1.fl"		32	2.3				hypothetical protein HHRF4 ; HHRF4 protein - human cytomegalovirus (strain AD169) ; (X04650) HHRF4 reading frame [human herpesvirus 5] ; (X17403) HCMVUS29 [human herpesvirus 5]
16643	ENU00437	ANI61C9007: 72-91 1132..752	72-91	375-410	EST	"flb11a1.rl, flb11a1.fl"		35	0.21				transcription factor SL1 - human ; (L39059) transcription factor SL1 [Homo sapiens]
16644	ENU00438	ANI61C5627: 50-69 3687..3307	50-69	353-388	EST	"i0d03a1.rl, i0d03a1.fl"							
16645	ENU00439	ANI61C8042: 43-61 22..404	43-61	350-383	EST	"o8a10a1.rl, o8a10a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16646	ENU00440	ANI61C5175: 3158..3541	23-47	343-363	EST	"y6a11a1.r1, y6a11a1.fl"			32	2.3			"Erythronolide synthase, modules 1 and 2 (ORF 1) (6-deoxyerythronolide B synthase 1) (DEBS 1)" (L04667) resolvase [Plasmid RP4]
16647	ENU00441	ANI61C440:4 20..36	28-47	350-370	EST	"w4f08a1.r1, w4f08a1.fl"			30	9			M polyprotein - Rift Valley fever virus (strain ZH-501) (AL023634) hypothetical protein [Schizosaccharomyces pombe]; (AF095790) BAG-family molecular chaperone regulator-1B protein [Schizosaccharomyces pombe] (AF052832) unknown [Trypanosoma cruzi] ribosomal protein S14.c - Neurospora crassa (U43840) GmCK3p [Glycine max]
16648	ENU00442	ANI61C7649: 131..297	69-90	383-415	EST	"r4a02a1.r1, r4a02a1.fl"			32	1.4			
16649	ENU00443	ANI61C1012 2:2192..1803	22-47	344-369	EST	"g6b06a1.r1, g6b06a1.fl"			41	0.005			
16650	ENU00444	ANI61C1109 0:2478..2084	65-84	382-417	EST	"z3e08a1.r1, z3e08a1.fl"			34	0.64			
16651	ENU00445	ANI61C3946: 2627..3024	35-54	356-390	EST	"g6c04a1.r1, g6c04a1.fl"			55	4E-18			
16652	ENU00446	ANI61C3084: 180..577	58-80	392-413	EST	"y4f05a1.r1, y4f05a1.fl"			41	0.003			
16653	ENU00447	ANI61C1141 3:144..542	57-76	378-413	EST	"r2h05a1.r1, r2h05a1.fl"			39	0.011			(D90910) hypothetical protein [Synecchocystis sp.]
16654	ENU00448	ANI61C3310: 503..103	71-90	410-429	EST	"g8a03a1.r1, g8a03a1.fl"			33	0.85			voltage-gated potassium channel protein KV1.1 (MK1) (MBK1); potassium channel KV1.1 protein - mouse; (Y00305) potassium channel protein-1 (AA 1-495) [Mus musculus]; (M30439) potassium channel protein [Mus musculus]; K channel protein [Mus musculus]
16655	ENU00449	ANI61C2937: 761..1161	22-54	356-380	EST	"h1b05a1.r1, h1b05a1.fl"			32	2.5			(U66846) orf5 [Streptococcus pneumoniae] (AB011167) KIAA0595 protein [Homo sapiens] (U48796) taxadiene synthase [Taxus brevifolia]; taxadiene synthase [Taxus brevifolia] (U65312) RNA-dependent RNA polymerase [Avian pneumovirus]
16656	ENU00450	ANI61C1754: 2139..1738	32-51	367-391	EST	"y8g09a1.r1, y8g09a1.fl"			30	9.7			
16657	ENU00451	ANI61C8200: 3379..2978	55-74	385-414	EST	"c8f08a1.r1, c8f08a1.fl"			30	9.8			
16658	ENU00452	ANI61C3381: 758..1161	51-70	377-412	EST	"a0a01a1.r1, a0a01a1.fl"			31	3.3			
16659	ENU00453	ANI61C261:2 090..2494	29-48	362-390	EST	"r5g10a1.r1, r5g10a1.fl"							

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16660	ENU00454	ANI61C185:9 36-55 78..1380		377-397	EST	"k5c02a1.r1, k5c02a1.fl"		55	55	0.000000 004			cyclophilin-like protein wis2 - fission yeast (Schizosaccharomyces pombe) ; (X91981) wis2 [Schizosaccharomyces pombe] ; (Z98598) probable 40 kd peptidyl-prolyl cis-trans isomerase se [Schizosaccharomyces pombe] [L05903] major surface glycoprotein [Pneumocystis carinii]
16661	ENU00455	ANI61C9244: 71-100 3735..4139	414-433		EST	"f2a10a1.r1, f2a10a1.fl"		31	31	5.7			
16662	ENU00456	ANI61C2518: 22-49 680..270	363-390		EST	"m8d03a1.r1, m8d03a1.fl"		90	90	9E-18			ENP1 protein ; hypothetical protein YBR247c - yeast (Saccharomyces cerevisiae) ; (Z36116) ORF YBR247c [Saccharomyces cerevisiae] ; (U50779) Enp1p [Saccharomyces cerevisiae] (AC006592) unknown protein [Arabidopsis thaliana] "(U23782) orf3; partial hypothetical protein, similar to the 55.2 kDa hypothetical protein in the HXT8 5' region of Saccharomyces cerevisiae, Swiss-Prot Accession Number P39976 [Neisseria meningitidis] "
16664	ENU00458	ANI61C6691: 37-60 1754..2166	388-407		EST	"g7a08a1.r1, g7a08a1.fl"		32	32	1.5			
16665	ENU00459	ANI61C9739: 22-53 7766..8182	362-396		EST	"g6a06a1.r1, g6a06a1.fl"		30	30	7.9			
16666	ENU00460	ANI61C9037: 61-81 539..121	418-437		EST	"z4h06a1.r1, z4h06a1.fl"		32	32	2			hypothetical 104.8 KD protein in CTK3-COQ5 intergenic region ; hypothetical protein YML111w - yeast (Saccharomyces cerevisiae) ; (Z49210) unknown [Saccharomyces cerevisiae] hypothetical protein KIAA0391 ; (AB002389) KIAA0391 [Homo sapiens]
16667	ENU00461	ANI61C6251: 23-43 1016..598	370-399		EST	"r5e10a1.r1, r5e10a1.fl"		30	30	7.8			membrane glycoprotein CLA-1 protein long form precursor - human ; (Z22555) CLA-1 [Homo sapiens] (AC004877) sco-spondin-mucin-like; similar to P98167 (PID:g1711548); details of intron/exon structure uncertain [Homo sapiens] (U00055) R02F2.8 gene product [Caenorhabditis elegans]
16668	ENU00462	ANI61C1904: 22-48 223..642	380-399		EST	"n3b03a1.r1, n3b03a1.fl"		31	31	6			
16669	ENU00463	ANI61C9741: 44-63 1156..1576	403-422		EST	"h1c11a1.r1, h1c11a1.fl"		32	32	2.7			
16670	ENU00464	ANI61C9676: 72-91 1902..2323	422-451		EST	"z3e05a1.r1, z3e05a1.fl"		31	31	3.5			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16671	ENU00465	ANI61C1027 7:83..506	71-90	427-452	EST	"y8e07a1.r1, y8e07a1.fl"		47	47	0.00007			(AB017603) ribosomal protein L37 homolog [Schizosaccharomyces pombe]
16672	ENU00466	ANI61C9948: 988..561	34-59	399-419	EST	"z3c09a1.r1, z3c09a1.fl"		36	36	0.14			"PTB-associated splicing factor (PSF) ; PTB-associated splicing factor, long form - human ; (X70944) PTB-associated splicing factor [Homo sapiens]"
16673	ENU00467	ANI61C1097 4:3415..3842	27-47	377-412	EST	"y6f10a1.r1, y6f10a1.fl"		31	31	3.6			(X95665) cDNA6 [Brugia pahangi]
16674	ENU00468	ANI61C1100 4:9438..9866	24-43	384-410	EST	"i7d03a1.r1, i7d03a1.fl"		56	56	0.000000 1			serine palmitoyltransferase 2 (long chain Base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe]
16675	ENU00469	ANI61C1051 7:1114..1182	44-63	406-430	EST	"x9a08a1.r1, x9a08a1.fl"		32	32	2.1			(U33937) FbpB [Neisseria gonorrhoeae] ; fbpB gene [Neisseria gonorrhoeae]
16676	ENU00470	ANI61C4808: 898..1326	52-72	412-438	EST	"b0h08a1.r1, b0h08a1.fl"		71	71	3E-12			probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emericella nidulans]
16677	ENU00471	ANI61C804:5 94..1030	45-64	420-439	EST	"y8c09a1.r1, y8c09a1.fl"		30	30	8.6			(U28940) coded for by C. elegans cDNA yk36b8.3; coded for by C. elegans cDNA cm14e5; coded for by C. elegans cDNA yk36b8.5; similar to ATPases [Caenorhabditis elegans]
16678	ENU00472	ANI61C7530: 1846..1400	72-91	441-476	EST	"v7f12a1.r1, v7f12a1.fl"		99	99	2E-20			40S ribosomal protein S27 ; ribosomal protein S27 - African clawed frog ; (X71350) ribosomal protein S27 homologue [Xenopus laevis]
16679	ENU00473	ANI61C3327: 119..565	59-78	435-463	EST	"r4a03a1.r1, r4a03a1.fl"							
16680	ENU00474	ANI61C1036 3:568..1014	22-48	392-426	EST	"c4e08a1.r1, c4e08a1.fl"							

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16681	ENU00475	ANI61C1079 9:807..361	55-76	435-459	EST	"r2f01al.r1, r2f01al.fl"		30	104	8.6			(U08029) NADH:nitrate reductase [Spinacia oleracea] "6-phosphofructo-2-kinase 1 (phosphofructokinase 2 I) (6PF-2-K 1) ; 6-phosphofructo-2-kinase (EC 2.7.1.105) - yeast (Saccharomyces cerevisiae) ; (Z38125) len: 827, CAl: 0.17, A41136 A41136; 6- phosphofructo-2-kinase [Saccharomyces cerevisiae] "
16682	ENU00476	ANI61C5287: 59-78 2720..2270	59-78	444-467	EST	"x7h08al.r1, x7h08al.fl"		104	3E-22				"6-phosphofructo-2-kinase 1 (phosphofructokinase 2 I) (6PF-2-K 1) ; 6-phosphofructo-2-kinase (EC 2.7.1.105) - yeast (Saccharomyces cerevisiae) ; (Z38125) len: 827, CAl: 0.17, A41136 A41136; 6- phosphofructo-2-kinase [Saccharomyces cerevisiae] "
16683	ENU00477	ANI61C5287: 59-78 2720..2270	59-78	444-467	EST	"m8ellal.r1, m8ellal.fl"		104	3E-22				"6-phosphofructo-2-kinase 1 (phosphofructokinase 2 I) (6PF-2-K 1) ; 6-phosphofructo-2-kinase (EC 2.7.1.105) - yeast (Saccharomyces cerevisiae) ; (Z38125) len: 827, CAl: 0.17, A41136 A41136; 6- phosphofructo-2-kinase [Saccharomyces cerevisiae] "
16684	ENU00478	ANI61C4063: 72-94 250..702	72-94	461-482	EST	"y4d05al.r1, y4d05al.fl"		68	3E-11				hypothetical 102.5 KD protein in KRE1-HXT14 intergenic region ; probable membrane protein YNL321w - yeast (Saccharomyces cerevisiae) ; (Z46259) NO339 [Saccharomyces cerevisiae] ; (Z71597) ORF YNL321w [Saccharomyces cerevisiae] (AF091234) putative transcription factor [Mus musculus] (X98931) heat shock protein 70 [Emeticella nidulans] (AC004684) myb-related protein [Arabidopsis thaliana] (AL035064) caax prenyl protease 2 [Schizosaccharomyces pombe]
16685	ENU00479	ANI61C946:1 124..1576	27-46	412-437	EST	"d5g05al.r1, d5g05al.fl"		34	0.59				(U41063) P-type ATPase [Tetrahymena thermophila] (L20099) envelope glycoprotein [Simian immunodeficiency virus]
16686	ENU00480	ANI61C1054 8:1251..799	69-88	460-480	EST	"x7a06al.r1, x7a06al.fl"		148	6E-61				
16687	ENU00481	ANI61C1253: 28-48 1..401	28-48	422-440	EST	"c4a10al.r1, c4a10al.fl"		33	1				
16688	ENU00482	ANI61C6228: 22-43 495..37	22-43	407-437	EST	"i3h05al.r1, i3h05al.fl"		121	3E-27				
16689	ENU00483	ANI61C8193: 22-41 1030..1490	22-41	421-440	EST	"w4a11al.r1, w4a11al.fl"		32	2.4				
16690	ENU00484	ANI61C9369: 22-55 848..1040	22-55	416-441	EST	"h4b05al.r1, h4b05al.fl"		31	5.3				
16691	ENU00485	ANI61C4221: 35-58 882..420	35-58	420-455	EST	"g5h02al.r1, g5h02al.fl"							
16692	ENU00486	ANI61C3695: 23-50 1088..1552	23-50	426-445	EST	"x8d02al.r1, x8d02al.fl"							

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16693	ENU00487	ANI61C5753: 886..1354	41-61	442-467	EST	"g6f04al.r.l, g6f04al.fl"		34	34	0.82			(AB004535) ATP-dependent RNA helicase MSS116 precursor [Schizosaccharomyces pombe]
16694	ENU00488	ANI61C8865: 596..1066	30-59	438-458	EST	"m8a03al.r.l, m8a03al.fl"		219	219	7E-57			(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe] (Z79754) similar to DEAH-type helicase; cDNA EST EMBL:D37033 comes from this gene; cDNA EST
16695	ENU00489	ANI61C13:74 1..1215	22-41	425-453	EST	"v7gl2al.r.l, v7gl2al.fl"		30	30	9.5			EMBL:D34035 comes from this gene; cDNA EST yk421c9.3 comes from this gene; cDNA EST yk421c9.5 comes from this gene; cDNA EST yk277h10.3... ; (Z83224) similar to DEAH-type helicase; cDNA EST EMBL:D37033 comes from this gene; cDNA EST EMBL:D34035 comes from this gene; cDNA EST yk421c9.3 comes from this gene; cDNA EST yk421c9.3 comes from this gene; cDNA EST yk421c9.5 comes from this gene; cDNA EST yk277h10.3... ; (Z83224) similar to DEAH-type helicase; cDNA EST EMBL:D37033 comes from this gene;
16696	ENU00490	ANI61C766:1 726..2199	48-67	454-479	EST	"c8c07al.r.l, c8c07al.fl"		134	134	3E-31			cDNA EST yk277h10.3... "40S ribosomal protein S24e (RP50); ribosomal protein S24.e - yeast (Saccharomyces cerevisiae); (Z38060) spliced ribosomal protein, len: 135, CAI: 0.76, similar to RS24_HUMAN P16632 40S ribosomal protein S24 (S19) [Saccharomyces cerevisiae]; (U18814) Rps24cap: 40S ribosomal protein S24E (RP50) [Saccharomyces cerevisiae]"
16697	ENU00491	ANI61C766:1 726..2199	48-67	454-479	EST	"d3b02al.r.l, d3b02al.fl"		134	134	3E-31			"40S ribosomal protein S24E (RP50); ribosomal protein S24.e - yeast (Saccharomyces cerevisiae); (Z38060) spliced ribosomal protein, len: 135, CAI: 0.76, similar to RS24_HUMAN P16632 40S ribosomal protein S24 (S19) [Saccharomyces cerevisiae]; (U18814) Rps24cap: 40S ribosomal protein S24E (RP50) [Saccharomyces cerevisiae]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16698	ENU00492	ANI61C766:1 726..2199	48-67	454-479	EST	"j7g09a1.rl, j7g09a1.fl"		134	134	3E-31			"40S ribosomal protein S24E (RP50) ; ribosomal protein S24.e - yeast (Saccharomyces cerevisiae) ; (Z38060) spliced ribosomal protein, len: 135, CAI: 0.76, similar to RS24_HUMAN P16632 40S ribosomal protein S24 (S19) [Saccharomyces cerevisiae] ; (U18814) Rps24eap: 40S ribosomal protein S24E (RP50) [Saccharomyces cerevisiae] "
16699	ENU00493	ANI61C766:1 726..2199	48-67	454-479	EST	"c8c03a1.rl, c8c03a1.fl"		134	134	3E-31			"40S ribosomal protein S24E (RP50) ; ribosomal protein S24.e - yeast (Saccharomyces cerevisiae) ; (Z38060) spliced ribosomal protein, len: 135, CAI: 0.76, similar to RS24_HUMAN P16632 40S ribosomal protein S24 (S19) [Saccharomyces cerevisiae] ; (U18814) Rps24eap: 40S ribosomal protein S24E (RP50) [Saccharomyces cerevisiae] "
16700	ENU00494	ANI61C7522: 24-46 4086..3612	24-46	437-456	EST	"h1b06a1.rl, h1b06a1.fl"		36	36	0.16			(D28529) protein tyrosine phosphatase DPZPTP [Mus musculus]
16701	ENU00495	ANI61C3801: 72-100 85..559	72-100	473-504	EST	"p0d11a1.rl, p0d11a1.fl"		125	125	2E-28			rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans]
16702	ENU00496	ANI61C7089: 22-43 1..475	22-43	421-454	EST	"y8b04a1.rl, y8b04a1.fl"		32	32	1.9			nodulation protein NOLB ; nolB protein - Rhizobium fredii ; (L12251) nodulation protein [Rhizobium fredii]
16703	ENU00497	ANI61C7891: 52-71 516..41	52-71	458-485	EST	"h1c04a1.rl, h1c04a1.fl"		32	32	1.9			nodulation protein NOLB ; nolB protein - Rhizobium fredii ; (L12251) nodulation protein [Rhizobium fredii]
16704	ENU00498	ANI61C1557: 27-62 6717..6239	27-62	430-463	EST	"r4a11a1.rl, r4a11a1.fl"		203	203	5E-52			"carbamoyl-phosphate synthase, arginine-specific, small chain precursor (arginine-specific carbamoyl-phosphate synthetase, glutamine chain) (CPS-A) ; (AF001029) carbamoyl phosphate synthetase, small subunit [Trichoderma virens] "
16705	ENU00499	ANI61C2811: 70-90 64..542	70-90	482-506	EST	"d3g03a1.rl, d3g03a1.fl"		203	203	5E-52			"carbamoyl-phosphate synthase, arginine-specific, small chain precursor (arginine-specific carbamoyl-phosphate synthetase, glutamine chain) (CPS-A) ; (AF001029) carbamoyl phosphate synthetase, small subunit [Trichoderma virens] "

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16706	ENU00500	ANI61C1128 2:645..166	22-47	440-459	EST	"f0c08a1.r1, f0c08a1.fl"		56	56	0.000000	1		(U44750) NAD-dependent 15-hydroxyprostaglandin dehydrogenase [Rattus norvegicus] (AF034606) chordin [Danio rerio]
16707	ENU00501	ANI61C3972: 22-52	428-463	EST		"i7c08a1.r1, i7c08a1.fl"		33	33	1.1			acetyl-coenzyme A synthetase (acetate-CoA ligase) (acyl-activating enzyme) ; acetate--CoA ligase (EC 6.2.1.1) - Emericella nidulans ; (X16990) acetate--CoA ligase [Emericella nidulans] (AC007109) unknown protein [Arabidopsis thaliana] (AF006492) FOG [Mus musculus]
16709	ENU00503	ANI61C1479: 22-49	448-470	EST		"i0d02a1.r1, i0d02a1.fl"		56	56	0.000000			
16710	ENU00504	ANI61C9694: 54-73	477-502	EST		"y4c12a1.r1, y4c12a1.fl"		36	36	0.17			
16711	ENU00505	ANI61C9253: 22-46	439-471	EST		"h8g04a1.r1, h8g04a1.fl"		102	102	5E-25			probable chorismate mutase (CM) ; (Z98529) putative chorismate mutase [Schizosaccharomyces pombe]
16712	ENU00506	ANI61C8431: 29-50	459-481	EST		"m5b08a1.r1, m5b08a1.fl"		43	43	0.001			MSF1 protein ; MSF1 protein - yeast (Saccharomyces cerevisiae) ; (X70279) MSF1 protein [Saccharomyces cerevisiae] ; (U17246) Mslp' [Saccharomyces cerevisiae]
16713	ENU00507	ANI61C4749: 25-52	459-478	EST		"c4e09a1.r1, c4e09a1.fl"							
16714	ENU00508	ANI61C1132 22-54	448-476	EST		"f0g05a1.r1, f0g05a1.fl"		34	34	0.53			(AF139463) early growth response 2 protein [Homo sapiens]
16715	ENU00509	ANI61C1051 48-67	483-505	EST		"m5d02a1.r1, m5d02a1.fl"		31	31	4.6			(U87864) neuralized homolog [Homo sapiens] ; (AF029729) neuralized [Homo sapiens]
16716	ENU00510	ANI61C1094 39-58	477-496	EST		"o8g03a1.r1, o8g03a1.fl"		32	32	3.5			(AL021841) PE_PGRS [Mycobacterium tuberculosis]
16717	ENU00511	ANI61C3429: 55-74	484-516	EST		"h1a12a1.r1, h1a12a1.fl"		85	85	3E-16			(Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi]
16718	ENU00512	ANI61C941:6 27-48	454-489	EST		"a0b04a1.r1, a0b04a1.fl"							
16719	ENU00513	ANI61C5252: 23-52	452-485	EST		"j4d06a1.r1, j4d06a1.fl"							

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16720	ENU00514	ANI61C8314: 1118..1625	36-57	482-501	EST	"r5a05a1.rl, r5a05a1.fl"		34	34	0.54			DNA damage tolerance protein RAD31 ; (Y08805) rad31 ; [Schizosaccharomyces pombe] ; (Z98560) superoxide dismutase [Schizosaccharomyces pombe] (AE001403) predicted secreted protein [Plasmodium falciparum] (D89782) thymidylate synthetase [Theileria sp.] (M77661) putative pol polyprotein [Magnaporthe grisea] (AF035770) ribosomal protein L37 [Schistosoma mansoni]
16721	ENU00515	ANI61C3915: 513..1	32-52	473-502	EST	"w4a01a1.rl, w4a01a1.fl"		31	31	6.2			
16722	ENU00516	ANI61C1099 8:3077..3589	42-61	477-512	EST	"z3f05a1.rl, z3f05a1.fl"		31	31	8.1			
16723	ENU00517	ANI61C5345: 70..585	39-59	479-512	EST	"d3c04a1.rl, d3c04a1.fl"		31	31	4.8			
16724	ENU00518	ANI61C3288: 3396..2881	35-54	489-508	EST	"l3e05a1.rl, l3e05a1.fl"		63	63	1E-17			
16725	ENU00519	ANI61C4412: 2074..2592	22-43	476-498	EST	"s9c09a1.rl, s9c09a1.fl"		43	43	0.001			larval glue protein Lgp-1 precursor - fruit fly (Drosophila virilis) ; glue protein lgp-1 - fruit fly (Drosophila virilis) ; (X76203) major larval glue protein [Drosophila virilis] ; (Z29565) glue protein [Drosophila virilis] ; glue protein [Drosophila virilis] hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] hypothetical protein YHR004c-a - yeast (Saccharomyces cerevisiae) ; (Z80875) Mrs11p [Saccharomyces cerevisiae] ; (U10555) Mrs11p [Saccharomyces cerevisiae] hypothetical 23.1 KD protein in BSAA-ILVD intergenic region ; (L77246) putative [Bacillus subtilis] ; (Z99115) similar to hypothetical proteins [Bacillus subtilis] transcription factor shn - fruit fly (Drosophila melanogaster)
16726	ENU00520	ANI61C4714: 41..565	23-48	484-505	EST	"q0d03a1.rl, q0d03a1.fl"		87	87	1E-16			
16727	ENU00521	ANI61C9255: 158..685	57-86	523-542	EST	"s9b03a1.rl, s9b03a1.fl"		64	64	2E-17			
16728	ENU00522	ANI61C6137: 3737..4265	37-55	504-523	EST	"i8c05a1.rl, i8c05a1.fl"		80	80	8E-15			
16729	ENU00523	ANI61C1372: 1269..738	70-89	528-559	EST	"r7g08a1.rl, r7g08a1.fl"		34	34	0.58			
16730	ENU00524	ANI61C1114: 2012..2544	70-89	537-560	EST	"k0b01a1.rl, k0b01a1.fl"							

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16731	ENU00525	ANI61C5175: 684..164	32-61	500-522	EST	"n8d07al.r1, n8d07al.fl"		70	9E-12			[Z82286] predicted using Genefinder [Caenorhabditis elegans]
16732	ENU00526	ANI61C1010: 0:1378..1912	58-79	527-550	EST	"h0g08al.r1, h0g08al.fl"		34	0.58			[U39645] repeated leucine-rich (LRR) [Caenorhabditis elegans]
16733	ENU00527	ANI61C8798: 1288..749	33-54	504-530	EST	"j9al1al.r1, j9al1al.fl"		66	2E-10			[AL035602] putative protein [Arabidopsis thaliana]
16734	ENU00528	ANI61C5214: 1839..2379	22-48	501-520	EST	"g9f09al.r1, g9f09al.fl"		31	5.1			[AE000524] carboxynorspermidine decarboxylase (nspC) [Helicobacter pylori 26695]
16735	ENU00529	ANI61C8429: 1285..743	22-42	492-522	EST	"o0h06al.r1, o0h06al.fl"		43	0.002			hypothetical protein YOR297c - yeast (Saccharomyces cerevisiae) ; (Z75205)
16736	ENU00530	ANI61C7324: 6273..5731	72-95	546-572	EST	"h0h11al.r1, h0h11al.fl"		43	0.002			ORF YOR297c [Saccharomyces cerevisiae]
16737	ENU00531	ANI61C7324: 6273..5731	72-95	546-572	EST	"t2b05al.r1, t2b05al.fl"		43	0.002			hypothetical protein YOR297c - yeast (Saccharomyces cerevisiae) ; (Z75205)
16738	ENU00532	ANI61C1077: 4:3391..3935	42-62	522-545	EST	"o6d07al.r1, o6d07al.fl"		143	9E-34			ORF YOR297c [Saccharomyces cerevisiae]
16739	ENU00533	ANI61C7767: 561..16	22-53	506-525	EST	"g3b08al.r1, g3b08al.fl"		35	0.46			protein-L-isoaspartate O-methyltransferase (protein-beta-aspartate methyltransferase) (PIMT) (protein L-isoaspartyl methyltransferase) (L-isoaspartyl protein carboxyl methyltransferase) ; (L07941) L-isoaspartyl methyltransferase [Triticum aestivum]
16740	ENU00534	ANI61C5800: 2619..3167	22-55	502-528	EST	"n0e05al.r1, n0e05al.fl"		32	2.3			titin - human
16741	ENU00535	ANI61C598:3: 5..586	23-44	500-532	EST	"dlal1al.r1, dlal1al.fl"		125	2E-28			(AJ235271) cell surface antigen (sca3) [Rickettsia prowazekii]
16742	ENU00536	ANI61C3057: 326..868	22-46	512-531	EST	"m0g08al.r1, m0g08al.fl"		125	2E-28			probable ARP2/3 complex 34 KD subunit (P34-ARC) ; (Z98981) probable Arp2-3 complex subunit [Schizosaccharomyces pombe]
16743	ENU00537	ANI61C3057: 326..868	22-46	512-531	EST	"q0c02al.r1, q0c02al.fl"		125	2E-28			probable ARP2/3 complex 34 KD subunit (P34-ARC) ; (Z98981) probable Arp2-3 complex subunit [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16744	ENU00538	ANI61C1043	69-88	559-583	EST	"p0c03a1.r1, p0e03a1.fl"							(Z50795) R166.3 [Caenorhabditis elegans]
16745	ENU00539	ANI61C319:2	24-46	513-545	EST	"w7e08a1.r1, w7e08a1.fl"			64	6E-10			hypothetical 9.1 KD protein C23C11.12 in chromosome I ; (Z98559) very hypothetical protein [Schizosaccharomyces pombe]
16746	ENU00540	ANI61C8718:	42-61	530-563	EST	"n8h01a1.r1, n8h01a1.fl"			34	0.62			hypothetical 9.1 KD protein C23C11.12 in chromosome I ; (Z98559) very hypothetical protein [Schizosaccharomyces pombe]
16747	ENU00541	ANI61C7165:	46-65	543-569	EST	"i0d06a1.r1, i0d06a1.fl"							(AF055904) unknown [Myxococcus xanthus]
16748	ENU00542	ANI61C7165:	46-65	543-569	EST	"k5g04a1.r1, k5g04a1.fl"			39	0.032			(U95843) pTP [Murine adenovirus type 1]
16749	ENU00543	ANI61C9738:	22-57	517-546	EST	"g6c12a1.r1, g6c12a1.fl"			31	9.3			(Z77135) similar to endothelin converting enzyme 1; cDNA EST yk452c2.5 comes from this gene; cDNA EST yk357g11.3 comes from this gene; cDNA EST yk357g11.5 comes from this gene; cDNA EST ...
16750	ENU00544	ANI61C9691:	64-83	564-590	EST	"y6f09a1.r1, y6f09a1.fl"			102	2E-21			(M16336) CD2 surface antigen [Homo sapiens]
16751	ENU00545	ANI61C5967:	46-65	547-572	EST	"c3a12a1.r1, c3a12a1.fl"							
16752	ENU00546	ANI61C1353:	30-65	537-557	EST	"z4c01a1.r1, z4c01a1.fl"			32	4.1			(AF035770) ribosomal protein L37 [Schistosoma mansoni]
16753	ENU00547	ANI61C541:2	25-56	528-553	EST	"e9f10a1.r1, e9f10a1.fl"			63	2E-17			(U51998) C12D12.1 gene product [Caenorhabditis elegans]
16754	ENU00548	ANI61C3288:	35-54	549-567	EST	"y8a07a1.r1, y8a07a1.fl"			36	0.22			
16755	ENU00549	ANI61C5479:	44-64	545-580	EST	"w6c12a1.r1, w6c12a1.fl"							
16756	ENU00550	ANI61C8257:	71-91	589-608	EST	"z5g08a1.r1, z5g08a1.fl"							
16757	ENU00551	ANI61C128:2	47-65	565-585	EST	"g9b08a1.r1, g9b08a1.fl"			33	1.4			high-sulfur keratin - human ; (X63337) high sulfur keratin [Homo sapiens]

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16758	ENU00552	ANI61C5509: 817..235	27-46	548-567	EST	"flg08a1.r1, flg08a1.fl"			201	4E-51			"hypothetical 37.2 KD protein in CHA1-PRD1 intergenic region ; hypothetical protein YCL059c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL059c, len:316 [Saccharomyces cerevisiae] "
16759	ENU00553	ANI61C597:8 01..218	72-91	594-613	EST	"n0b05a1.r1, n0b05a1.fl"			41	0.007			(U34390) protein with neutralization-sensitive epitopes [Cryptosporidium parvum] ; (Y16243) sporozoite surface antigen p23 [Cryptosporidium parvum] surfactin synthetase component II - Bacillus subtilis (fragment) ; (D13262) surfactin synthetase [Bacillus subtilis] "acidic ribosomal protein P0.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (M37326) ribosomal protein L10e [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (U19028) Rpl10ep [Saccharomyces cerevisiae] "
16760	ENU00554	ANI61C1027 7:2108..2694	42-61	560-586	EST	"i0f07a1.r1, i0f07a1.fl"			32	4.3			ribosomal protein S27 (metallopantstimulin 1) ; 40S ribosomal protein S27 (metallopantstimulin 1) (MPS-1) ; growth factor-inducible zinc finger protein MPS-1 - human ; (L19739) metallopantstimulin [Homo sapiens] ; (U57847) ribosomal protein S27 [Homo sapiens]
16761	ENU00555	ANI50C392_ 2:873..394	70-89	595-615	EST	"c9e07a1.r1, c9e07a1.fl"			223	7E-58			putative 40S ribosomal protein in SNF2-CPA1 intergenic region ; ribosomal protein S10.e.A - yeast (Saccharomyces cerevisiae) ; (Z75201) ORF YOR293w [Saccharomyces cerevisiae]
16762	ENU00556	ANI61C630:2 46..833	72-94	582-617	EST	"i8c07a1.r1, i8c07a1.fl"			34	1.1			(AF056116) LRP1 [Fugu rubripes]
16763	ENU00557	ANI61C3327: 119..707	59-78	585-605	EST	"m8f08a1.r1, m8f08a1.fl"			99	2E-20			
16764	ENU00558	ANI61C884:5 89..1	22-54	545-568	EST	"m8g04a1.r1, m8g04a1.fl"			98	2E-24			
16765	ENU00559	ANI61C5819: 615..26	22-49	547-569	EST	"z3g04a1.r1, z3g04a1.fl"			31	7.5			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16766	ENU00560	ANI61C4296: 1125..535	22-49	535-570	EST	"c7e04a1.r1, c7e04a1.fl"		60	60	0.000000	02		(AF069523) heat shock protein Hsp88 [Neurospora crassa]
16767	ENU00561	ANI61C4371: 1085..494	24-56	553-573	EST	"l3g10a1.r1, l3g10a1.fl"		62	62	0.000000	004		(D85230) hypothetical protein [Plectonema boryanum]
16768	ENU00562	ANI61C9600: 3992..4585	36-65	568-587	EST	"q0h08a1.r1, q0h08a1.fl"		147	147	3E-39			hypothetical oxidoreductase in CIT A-SSPB intergenic region ; (Y14082) hypothetical protein [Bacillus subtilis] ; (Z99109) similar to glucose 1-dehydrogenase [Bacillus subtilis]
16769	ENU00563	ANI61C5468: 594..1	32-52	550-583	EST	"m5d10a1.r1, m5d10a1.fl"		95	95	3E-19			hypothetical 49.6 KD protein in ELM1-PR12 intergenic region ; hypothetical protein YKL046c precursor - yeast (Saccharomyces cerevisiae) ; (Z28046) ORF YKL046c [Saccharomyces cerevisiae]
16770	ENU00564	ANI61C8586: 791..196	41-60	574-594	EST	"n8f01a1.r1, n8f01a1.fl"		109	109	2E-23			"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"
16771	ENU00565	ANI61C405:1 982..1384	58-77	580-613	EST	"i3b04a1.r1, i3b04a1.fl"		51	51	0.000006			eukaryotic translation initiation factor 1A (EIF-1A) (EIF-4C) ; translation initiation factor eIF-1A - yeast (Saccharomyces cerevisiae) ; (U11585) translation initiation factor 1A [Saccharomyces cerevisiae] ; (Z49260) Tif1 1p [Saccharomyces cerevisiae]
16772	ENU00566	ANI61C2419: 85..684	51-71	577-608	EST	"r4f07a1.r1, r4f07a1.fl"		160	160	9E-39			hypothetical 50.4 KD protein C1F8.04C in chromosome I ; (Z81312) unknown [Schizosaccharomyces pombe]
16773	ENU00567	ANI61C9395: 5609..5313	25-46	559-587	EST	"m0d12a1.r1, m0d12a1.fl"		39	39	0.035			(AP000001) 58aa long hypothetical protein [Pyrococcus horikoshii]
16774	ENU00568	ANI61C1253: 1..401	22-51	568-586	EST	"e9h12a1.r1, e9h12a1.fl"		46	46	0.0002			(AL034352) putative signal transduction protein
16775	ENU00569	ANI61C1110 3:4962..4355	23-43	567-588	EST	"c6d09a1.r1, c6d09a1.fl"		34	34	1.2			[Schizosaccharomyces pombe] hypothetical PXL-I protein ; trans-activating transcriptional regulatory protein - bovine leukemia virus (fragment)
16776	ENU00570	ANI61C322:7 669..8278	46-65	585-613	EST	"w9c02a1.r1, w9c02a1.fl"		31	31	6			(AF079173) ORF1 protein [TT virus]
16777	ENU00571	ANI61C9395: 6467..5856	22-56	562-591	EST	"m8g07a1.r1, m8g07a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16778	ENU00572	ANI61C6494: 4383..5000	22-45	576-597	EST	"g2e12a1.r1, g2e12a1.fl"		31	31	6.1			(Y11476) hypothetical protein [Bacteriophage 12826]
16779	ENU00573	ANI61C9771: 2155..2773	29-50	571-605	EST	"o9d08a1.r1, o9d08a1.fl"		31	31	6.1			(Y13978) thrombomucin [Gallus gallus]
16780	ENU00574	ANI61C7686: 1198..578	30-50	589-608	EST	"z6h07a1.r1, z6h07a1.fl"		87	87	1E-16			(AL034583) hypothetical protein [Schizosaccharomyces pombe]
16781	ENU00575	ANI61C3783: 1110..490	24-43	583-602	EST	"w4d02a1.r1, w4d02a1.fl"		102	102	3E-21			transcription initiation factor TFIID 90 KD subunit (TAFII-90); TATA box-binding protein-associated factor chain TAFII90 - yeast (Saccharomyces cerevisiae); (Z21487) unknown [Saccharomyces cerevisiae]; (Z36067) ORF YBR198c [Saccharomyces cerevisiae]; TATA box-binding protein-associated factor [Saccharomyces cerevisiae]
16782	ENU00576	ANI61C9540: 114..737	22-46	567-602	EST	"g3b03a1.r1, g3b03a1.fl"		34	34	0.93			(U95159) gelsolin-related protein GRP125 [Dictyostelium discoideum]
16783	ENU00577	ANI61C8836: 2937..3563	72-92	636-655	EST	"n8h06a1.r1, n8h06a1.fl"		33	33	2.1			(AB014462) neuronal leucine-rich repeat protein [Xenopus laevis]
16784	ENU00578	ANI50C2177 6_1:487..1113	37-56	592-621	EST	"f0b09a1.r1, f0b09a1.fl"		35	35	0.42			(Z78420) Weak similarity to Human transcription factor SP3 (SW:SP3_HUMAN); cDNA EST EMBL:C09666 comes from this gene; cDNA EST EMBL:C08071 comes from this gene [Caenorhabditis elegans]
16785	ENU00579	ANI61C3301: 1648..2275	23-42	589-608	EST	"o6g06a1.r1, o6g06a1.fl"		86	86	2E-16			"(U32776) L-2,4-diaminobutyrate decarboxylase [Haemophilus influenzae Rd]"
16786	ENU00580	ANI61C1106 5:6001..5372	29-48	588-616	EST	"h0c06a1.r1, h0c06a1.fl"		36	36	0.24			(U41994) similar to glycoproteins [Caenorhabditis elegans]
16787	ENU00581	ANI61C5297: 1067..435	62-81	626-651	EST	"m7h04a1.r1, m7h04a1.fl"		33	33	2.1			(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]
16788	ENU00582	ANI61C7555: 3136..3767	22-52	576-611	EST	"y8b06a1.r1, y8b06a1.fl"		102	102	3E-38			hypothetical 16.9 KD protein in ALD6-PDR12 intergenic region; hypothetical protein YPL059w - yeast (Saccharomyces cerevisiae); (U39205) Lpe13p [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16789	ENU00583	ANI61C8842: 57-76 966..1597	57-76	613-646	EST	"c9e09a1.r1, c9e09a1.fl"		34	34	0.72			(Z92782) F14F8.4 [Caenorhabditis elegans]
16790	ENU00584	ANI61C8836: 72-94 2929..3563	72-94	644-663	EST	"w4c01a1.r1, w4c01a1.fl"		33	33	2.1			(AB014462) neuronal leucine-rich repeat protein [Xenopus laevis]
16791	ENU00585	ANI61C3242: 41-60 307..949	41-60	621-641	EST	"x9c11a1.r1, x9c11a1.fl"		123	123	1E-27			hypothetical 31.5 KD protein ; (U05664) homologous to Swiss-Prot Accession Number P20435: Saccharomyces cerevisiae RNA polymerase subunit RPO26 [Sulfolobus acidocaldarius]
16792	ENU00586	ANI61C7237: 22-46 2093..1450	22-46	604-623	EST	"x5h08a1.r1, x5h08a1.fl"		32	32	4.9			"Allergen ARA H 1, clone P17 (ARA H 1) ; (L38853) Ara h I [Arachis hypogaea]"
16793	ENU00587	ANI61C1080: 36-62 1883..2530	36-62	620-641	EST	"z4f12a1.r1, z4f12a1.fl"		222	222	2E-57			(AF051914) C-4 methyl sterol oxidase [Candida albicans]
16794	ENU00588	ANI61C353:3 22-47 055..3702	22-47	594-627	EST	"a0g03a1.r1, a0g03a1.fl"		31	31	6.5			hypothetical 46.4 KD protein SLL1917 ; (D90904) oxygen independent coprophorhyrinogen III oxidase [Synechocystis sp.]
16795	ENU00589	ANI61C7994: 52-78 5677..5028	52-78	637-659	EST	"t2a09a1.r1, t2a09a1.fl"		123	123	8E-28			(AL033391) hypothetical membrane protein [Candida albicans]
16796	ENU00590	ANI61C8252: 22-42 2731..2079	22-42	597-632	EST	"r2h04a1.r1, r2h04a1.fl"		78	78	1E-18			F-actin capping protein alpha subunit ; actin-capping protein alpha chain - yeast (Saccharomyces cerevisiae) ; (X61398) Capping Protein Alpha Subunit [Saccharomyces cerevisiae] ; (Z28007) ORF YKL007w
16797	ENU00591	ANI61C2704: 62-85 358..1011	62-85	638-673	EST	"h1d05a1.r1, h1d05a1.fl"		37	37	0.15			[Saccharomyces cerevisiae] ; (S59773) CAP1 [Saccharomyces cerevisiae]
16798	ENU00592	ANI61C14:16 24-47 46..2300	24-47	608-636	EST	"t2d08a1.r1, t2d08a1.fl"							Exocyst complex component SEC3 (PSL1 protein) ; PSL1 protein - yeast (Saccharomyces cerevisiae) ; (L22204) Psl1p [Saccharomyces cerevisiae] ; (U18778) Sec3p [Saccharomyces cerevisiae]
16799	ENU00593	ANI61C4315: 62-94 4444..3788	62-94	655-676	EST	"o9f07a1.r1, o9f07a1.fl"		32	32	5			probable phosphatidylserine synthase PEL1 - yeast (Saccharomyces cerevisiae)

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16800	ENU00594	ANI61C3288: 3396..2737	35-54	625-652	EST	"y6h10al.rl, y6h10al.fl"		63	63	2E-17		(AF035770) ribosomal protein L37 [Schistosoma mansoni] (U47849) Lozenge [Drosophila melanogaster]
16801	ENU00595	ANI61C1113 22-51	22-51	612-640	EST	"r4b11al.rl, r4b11al.fl"		32	32	5.1		hypothetical 118.4 KD protein in BAT2-DAL5 intergenic region precursor ; probable membrane protein
16802	ENU00596	ANI61C3266: 22-53 3466..2805	22-53	615-641	EST	"a0h04al.rl, a0h04al.fl"		33	33	1.7		YJR151c - yeast (Saccharomyces cerevisiae) ; (Z49651) ORF YJR151c [Saccharomyces cerevisiae]
16803	ENU00597	ANI61C9578: 61-80 6806..6144	61-80	647-681	EST	"w6g09al.rl, w6g09al.fl"		40	40	0.018		(AL031031) hypothetical protein SC7C7.09 [Streptomyces coelicolor] (Z78420) Weak similarity to Human transcription factor SP3 (SW:SP3_HUMAN); cDNA EST EMBL:C09666 comes from this gene; cDNA EST EMBL:C08071 comes from this gene [Caenorhabditis elegans]
16804	ENU00598	ANI50C2177 27-52 6_1:451..1114	27-52	626-648	EST	"z3d05al.rl, z3d05al.fl"		35	35	0.45		(L26122) matrix protein [Mumps virus]
16805	ENU00599	ANI61C7657: 70-89 871..1535	70-89	662-692	EST	"d4b01al.rl, d4b01al.fl"		34	34	1		hypothetical 13.9 KD protein C2E11.03C in chromosome I ; (AL031181) very hypothetical protein [Schizosaccharomyces pombe] ; (AL035064) very hypothetical protein [Schizosaccharomyces pombe]
16806	ENU00600	ANI61C187:9 22-46 75..310	22-46	621-645	EST	"q0h12al.rl, q0h12al.fl"		61	61	0.000000 006		hypothetical 23.7 KD protein in NMD5-HOM6 intergenic region ; hypothetical protein YJR133w - yeast (Saccharomyces cerevisiae) ; (Z49633) ORF YJR133w [Saccharomyces cerevisiae]
16807	ENU00601	ANI61C5803: 22-56 2406..1760	22-56	611-646	EST	"d5f05al.rl, d5f05al.fl"		46	46	0.0002		(Z47973) ORF L0596 [Saccharomyces cerevisiae] histone H2B ; histone H2B - Emericella nidulans ; (X55547) H2B [Emericella nidulans] ; histone H2B [Emericella nidulans]
16808	ENU00602	ANI61C6798: 31-50 5067..5734	31-50	633-656	EST	"b0g07al.rl, b0g07al.fl"		53	53	0.000000 003		
16809	ENU00603	ANI61C1042 22-50 6:1247..579	22-50	629-648	EST	"r7c08al.rl, r7c08al.fl"		62	62	2E-34		
16810	ENU00604	ANI61C7674: 26-46 1339..2007	26-46	626-652	EST	"g4e06al.rl, g4e06al.fl"						

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16811	ENU00605	ANI61C1080: 1861..2530	22-49	628-649	EST	"g4f03a1.rl, g4f03a1.fl"		32	32	5.1			"Allergen ARA H 1, clone P17 (ARA H 1); (L38853) Ara h 1 [Arachis hypogaea]"
16812	ENU00606	ANI61C1100: 4016..3347	22-49	625-649	EST	"l3e08a1.rl, l3e08a1.fl"		37	37	0.001			hypothetical 15.7 KD protein in UBP1-HNT1 intergenic region; probable membrane protein YDL123w - yeast (Saccharomyces cerevisiae); (Z74171) ORF YDL123w [Saccharomyces cerevisiae]
16813	ENU00607	ANI61C2308: 79..749	22-53	631-650	EST	"g5g06a1.rl, g5g06a1.fl"		45	45	0.0004			Conidiation-specific protein 8; con-8 protein - Neurospora crassa; (X07040) con-8 [Neurospora crassa]
16814	ENU00608	ANI61C3183: 491..1165	37-56	637-669	EST	"w8f02a1.rl, w8f02a1.fl"		33	33	0.001			NADH-ubiquinone oxidoreductase B22 subunit (complex I-B22) (CI-B22); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine; (X64836) NADH-ubiquinone oxidoreductase complex B22 subunit [Bos taurus]
16815	ENU00609	ANI61C9395: 6555..5879	69-88	670-703	EST	"o8b09a1.rl, o8b09a1.fl"		31	31	6.9			(AF079173) ORF1 protein [TT virus]
16816	ENU00610	ANI61C1077: 4-2433..1757	22-45	630-656	EST	"c6a04a1.rl, c6a04a1.fl"		33	33	2.3			(U89341) phosphoglucomutase 1 [Zea mays]
16817	ENU00611	ANI61C2136: 4474..3796	22-44	635-658	EST	"g3a02a1.rl, g3a02a1.fl"		48	48	0.00005			Long-chain-fatty-acid--CoA ligase 4 (long-chain acyl-CoA synthetase 4) (fatty acid activator 4); long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) FAA4 - yeast (Saccharomyces cerevisiae); (Z48756) unknown [Saccharomyces cerevisiae]
16818	ENU00612	ANI61C3715: 10..689	31-54	638-667	EST	"j9f11a1.rl, j9f11a1.fl"		62	62	0.00000003			hypothetical 17.5 KD protein in chromosome II; (AL022103) hypothetical protein [Schizosaccharomyces pombe]
16819	ENU00613	ANI61C9064: 375..1062	50-69	660-695	EST	"l3d12a1.rl, l3d12a1.fl"		34	34	1.1			(U96771) unknown [Prevotella bryantii]
16820	ENU00614	ANI61C8444: 1586..2274	56-74	682-702	EST	"j0c06a1.rl, j0c06a1.fl"		136	136	1E-31			(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16821	ENU00615	ANI61C7805: 4521..5220	36-56	666-693	EST	"g4c12a1.r1, g4c12a1.fl"			40	0.019			hypothetical 8.2 KD protein C26A3.14C in chromosome I; (Z69240) very hypothetical protein [Schizosaccharomyces pombe]
16822	ENU00616	ANI61C884:7 03..1	26-46	663-686	EST	"g6c01a1.r1, g6c01a1.fl"			98	4E-27			putative 40S ribosomal protein in SNF2-CPA1 intergenic region; ribosomal protein S10.e.A - yeast (Saccharomyces cerevisiae); (Z75201) ORF YOR293w [Saccharomyces cerevisiae]
16823	ENU00617	ANI61C9578: 42-61 6806..6103	42-61	678-703	EST	"k0d01a1.r1, k0d01a1.fl"			40	0.019			(AL031031) hypothetical protein SC7C7.09 [Streptomyces coelicolor]
16824	ENU00618	ANI61C9152: 27-47 1281..1985	27-47	670-689	EST	"m8f07a1.r1, m8f07a1.fl"			85	4E-16			(AL049559) hypothetical protein [Schizosaccharomyces pombe]
16825	ENU00619	ANI61C8549: 22-52 2986..3690	22-52	657-684	EST	"w6e07a1.r1, w6e07a1.fl"			34	1.4			hypothetical 15.6 KD protein in CSN-ADHB intergenic region; (U933875) Yral [Bacillus subtilis]; (X92868) unknown [Bacillus subtilis]; (Z99117) similar to hypothetical proteins from B. subtilis [Bacillus subtilis]
16826	ENU00620	ANI61C9745: 42-63 4683..3978	42-63	687-705	EST	"s9f03a1.r1, s9f03a1.fl"			46	0.000000 008			small nuclear ribonucleoprotein SM D2 (SNRNP core protein D2) (SM-D2); small nuclear ribonucleoprotein chain D2 - human; (U15008) Sm D2 [Homo sapiens]; (AC007191) SMD2_HUMAN; SNRNP core protein D2; SM-D2 [Homo sapiens]
16827	ENU00621	ANI61C9745: 42-63 4683..3978	42-63	687-705	EST	"w9g09a1.r1, w9g09a1.fl"			46	0.000000 008			small nuclear ribonucleoprotein SM D2 (SNRNP core protein D2) (SM-D2); small nuclear ribonucleoprotein chain D2 - human; (U15008) Sm D2 [Homo sapiens]; (AC007191) SMD2_HUMAN; SNRNP core protein D2; SM-D2 [Homo sapiens]
16828	ENU00622	ANI50C6889 50-69 1:1625..916	50-69	686-717	EST	"d1f10a1.r1, d1f10a1.fl"			199	2E-50			probable membrane protein YPL134c - yeast (Saccharomyces cerevisiae); (U43703) Lpt11p [Saccharomyces cerevisiae]
16829	ENU00623	ANI61C7675: 43-75 5310..4598	43-75	682-713	EST	"o0c10a1.r1, o0c10a1.fl"			32	5.6			(AB001347) brain beta 3 spectrin [Rattus norvegicus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16830	ENU00624	ANI61C1679: 2377..1661	34-57	678-707	EST	"o0e10a1.rl, o0e10a1.fl"		32	32	4.3			[X03541] trik gene product (aa 1-641) [Homo sapiens] ; gene oncD [Homo sapiens]
16831	ENU00625	ANI61C7987: 29-48	29-48	683-702	EST	"t2e02a1.rl, t2e02a1.fl"		72	72	4E-12			(AL035655) 60s ribosomal protein l36 [Schizosaccharomyces pombe]
16832	ENU00626	ANI61C1126: 282..997 31..746	28-48	679-701	EST	"i0d04a1.rl, i0d04a1.fl"		92	92	2E-33			40S ribosomal protein S17 ; (M13933) ribosomal protein S17 [Cricetus griseus] ; (D25213) ribosomal protein S17 [Mus musculus]
16833	ENU00627	ANI61C6923: 1761..1045	22-45	672-696	EST	"d5g10a1.rl, d5g10a1.fl"		35	35	0.5			(AF014795) cytochrome P450 30 [Mercenaria mercenaria]
16834	ENU00628	ANI61C9637: 4095..4814	46-68	704-723	EST	"h0d10a1.rl, h0d10a1.fl"		214	214	1E-55			Peptidyl-prolyl cis-trans isomerase (PPIase) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
16835	ENU00629	ANI61C9637: 4095..4814	35-57	693-712	EST	"g6g11a1.rl, g6g11a1.fl"		214	214	1E-55			Peptidyl-prolyl cis-trans isomerase (PPIase) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
16836	ENU00630	ANI61C9637: 4095..4814	40-62	698-717	EST	"o6a07a1.rl, o6a07a1.fl"		214	214	1E-55			Peptidyl-prolyl cis-trans isomerase (PPIase) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16837	ENU00631	ANI61C7067: 869..148	24-49	674-703	EST	"i7f01a1.r1, i7f01a1.fl"		178	4E-44				Mannitol-1-phosphate 5-dehydrogenase ; mannitol-1-phosphate dehydrogenase - Bacillus subtilis (fragment) ; (D38161) mannitol-1-phosphate dehydrogenase [Bacillus subtilis] ; (D50453) homologue of mannitol-1-phosphate dehydrogenase of Streptococcus mutans [Bacillus subtilis] ; (Z99106) mannitol-1-phosphate dehydrogenase [Bacillus subtilis] ; mannitol-1-phosphate dehydrogenase [Bacillus subtilis] (AL033391) conserved hypothetical protein [Candida albicans] GAG polypeptide [contains: inner coat protein P12; core protein P15; core shell protein P30; nucleoprotein P10] ; gag polypeptide - baboon endogenous virus (strain M7) ; (X05470) gag gene product (AA 1-537) [Baboon endogenous virus] ; (D10032) polypeptide [Baboon endogenous virus] ; (M16550) gag polypeptide [Baboon endogenous virus] (Z97052) hypothetical protein [Schizosaccharomyces pombe] GAG polypeptide [contains: inner coat protein P12; core protein P15; core shell protein P30; nucleoprotein P10] ; gag polypeptide - baboon endogenous virus (strain M7) ; (X05470) gag gene product (AA 1-537) [Baboon endogenous virus] ; (D10032) polypeptide [Baboon endogenous virus] ; (M16550) gag polypeptide [Baboon endogenous virus]
16838	ENU00632	ANI61C1010 32-53	682-714	EST	"t2a12a1.r1, t2a12a1.fl"			87	6E-23				
16839	ENU00633	ANI61C6349: 51-70 940..130	714-734	EST	"k5d10a1.r1, k5d10a1.fl"			34	1.5				
16840	ENU00634	ANI61C3091: 33-52 559..1284	681-716	EST	"y3d09a1.r1, y3d09a1.fl"			42	0.000000				
16841	ENU00635	ANI61C6349: 56-75 940..130	719-739	EST	"i2e02a1.r1, i2e02a1.fl"			34	1.5				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16842	ENU00636	ANI61C1031 8:1119..849	52-75	716-737	EST	"y6a08a1.r1, y6a08a1.fl"		92	92	3E-18			"probable 60S ribosomal protein YIL052C ; ribosomal protein L34.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z38060) spliced ribosomal protein, len: 121, CAI: 0.77, RL34_RAT P11250 60S ribosomal protein L34 [Saccharomyces cerevisiae]"
16843	ENU00637	ANI61C7768: 51..778	62-81	716-747	EST	"m0g07a1.r1, m0g07a1.fl"		142	142	5E-55			(AL023518) Tallp transaldolase [Schizosaccharomyces pombe]
16844	ENU00638	ANI61C6509: 1025..295	70-90	737-758	EST	"a0f04a1.r1, a0f04a1.fl"		33	33	2			(U34781) Antho-LWamidII preprohormone [Anthopleura elegantissima] ; prepro-hormone [Anthopleura elegantissima]
16845	ENU00639	ANI61C3368: 7507..8240	44-63	709-735	EST	"y8d01a1.r1, y8d01a1.fl"		262	262	6E-75			aminopeptidase Y (EC 3.4.11.-) precursor - yeast (Saccharomyces cerevisiae)
16846	ENU00640	ANI61C1096 0:2340..3077	70-89	746-764	EST	"k0h03a1.r1, k0h03a1.fl"		37	37	0.17			(M94288) Nopp140 [Rattus norvegicus]
16847	ENU00641	ANI61C1537: 1654..917	48-68	711-742	EST	"g9f06a1.r1, g9f06a1.fl"		86	86	3E-16			(U16137) Mvp1p [Saccharomyces cerevisiae]
16848	ENU00642	ANI61C2890: 6590..5853	50-69	717-745	EST	"r5g07a1.r1, r5g07a1.fl"		32	32	4.5			"(D90129) T-cell receptor beta chain, leader sequence, variable region, diversity region and joining region [Bos taurus]"
16849	ENU00643	ANI61C9959: 1129..1867	41-62	704-737	EST	"d5h12a1.r1, d5h12a1.fl"		34	34	1.5			hypothetical 36.9k protein - Acetobacter pasteurianus plasmid AP12875 ; (U20550) protein A [Acetobacter pasteurianus]
16850	ENU00644	ANI61C9172: 1232..1971	30-49	706-727	EST	"m5d05a1.r1, m5d05a1.fl"							(Z67882) similar to p-glycoprotein (MDR) [Caenorhabditis elegans]
16851	ENU00645	ANI61C8729: 1741..2481	57-75	723-755	EST	"y8h03a1.r1, y8h03a1.fl"		35	35	0.68			(AF100656) contains weak similarity to Plasmodium yoelii rhostry protein S6 (GB:U36927) [Caenorhabditis elegans]
16852	ENU00646	ANIC9281_1: 750..1	53-72	730-760	EST	"y8e11a1.r1, y8e11a1.fl"		34	34	0.89			(AF053883) coatomer alpha subunit [Emericella nidulans]
16853	ENU00647	ANI61C1053 9:976..226	26-50	706-734	EST	"r4b09a1.r1, r4b09a1.fl"		441	441	e-123			
16854	ENU00648	ANI61C9111: 5741..6491	29-51	718-737	EST	"c5b03a1.r1, c5b03a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16855	ENU00649	ANI61C1048 3:4098..4851	22-43	714-733	EST	"g9e11a1.r1, g9e11a1.fl"		48	48	0.00005		(AL023534) hypothetical protein [Schizosaccharomyces pombe] (AF057353) translation elongation factor 3 [Thermomyces lanuginosus] (AF042103) tat protein [Human immunodeficiency virus type 1] putative mitochondrial carrier YER053C ; hypothetical protein YER053c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer053cp [Saccharomyces cerevisiae] "(U48363) alpha-NAC, muscle-specific form gp220 [Mus musculus] ; (U48364) alpha-NAC, muscle-specific form gp220 [Mus musculus] " crml+ protein - fission yeast (Schizosaccharomyces pombe) "phosphatidylinositol 3-kinase catalytic subunit, delta isoform (PI3-kinase P110 subunit delta) (PTDINS-3-kinase P110) (P13K) (P110delta) ; (U86587) phosphatidylinositol 3-kinase catalytic subunit p110 delta [Mus musculus] " "mitochondrial 60S ribosomal protein MRP49 precursor ; ribosomal protein MRP49, mitochondrial - yeast (Saccharomyces cerevisiae) ; (M81697) mitochondrial ribosomal protein [Saccharomyces cerevisiae] ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28167) ORF YKL167c [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] " (Z81523) Similarity to Bovine protooncogene C-MYB (TR:Q28080); cDNA EST EMBL:D32371 comes from this gene; cDNA EST EMBL:D34735 comes from this gene; cDNA EST EMBL:D37111 comes from this gene; cDNA EST EMBL:D71956 comes from thi...
16856	ENU00650	ANI61C4054: 248..1007	22-51	708-739	EST	"c9d08a1.r1, c9d08a1.fl"		43	43	0.003		
16857	ENU00651	ANI61C1080 1:769..6	22-52	723-743	EST	"n8f04a1.r1, n8f04a1.fl"		33	33	2.1		
16858	ENU00652	ANI61C1027 7:7366..6602	31-51	718-753	EST	"j9a02a1.r1, j9a02a1.fl"		159	159	2E-38		
16859	ENU00653	ANI61C8646: 2416..1650	34-54	729-758	EST	"g3c08a1.r1, g3c08a1.fl"		56	56	0.000000 2		
16860	ENU00654	ANI61C2324: 1280..514	65-87	766-790	EST	"r5c11a1.r1, r5c11a1.fl"		118	118	4E-26		
16861	ENU00655	ANI61C3531: 1196..418	55-82	760-791	EST	"a0c01a1.r1, a0c01a1.fl"		32	32	3.6		
16862	ENU00656	ANI61C7922: 4398..3619	22-42	738-759	EST	"p0g04a1.r1, p0g04a1.fl"		46	46	0.0003		
16863	ENU00657	ANI61C8803: 2388..1609	30-50	741-767	EST	"w9h07a1.r1, w9h07a1.fl"		35	35	0.72		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16864	ENU00658	ANI61C4078: 1227..448	57-77	767-794	EST	"o0a12a1.r1, o0a12a1.fl"		34	34	1.6			(M13790) albumin 1 [Pisum sativum]
16865	ENU00659	ANI61C6432: 1618..833	43-76	751-786	EST	"c6c05a1.r1, c6c05a1.fl"			36	0.25			hypothetical 18.9 KD protein in GCN20-CMK1 intergenic region ; hypothetical protein YFR011c - yeast (Saccharomyces cerevisiae) ; (D50617) YFR011C [Saccharomyces cerevisiae] ; (D44599) ochre suppressor tyr-tRNA (sup4) [Saccharomyces cerevisiae] (U29096) coded for by C. elegans cDNA CEES150F; coded for by C. elegans cDNA CEESU96F; similar to C. elegans proteins ZC84.1 and ZC84.6 ; also similar to serine protease inhibitors (members of BPTI/Kunitz family of inhibitors) [Caenorhabditis...]
16867	ENU00661	ANI61C4657: 1509..720	32-51	759-778	EST	"p0e06a1.r1, p0e06a1.fl"			32	4.8			"N,O-diacetylmuramidase (lysozyme CH) ; lysozyme (EC 3.2.1.17) - fungus (Chalara sp.) "
16868	ENU00662	ANI61C757:1 532..2322	56-75	780-804	EST	"g2c04a1.r1, g2c04a1.fl"			214	5E-62			hypothetical 8.2 KD protein C26A3.14C in chromosome I ; (Z69240) very hypothetical protein [Schizosaccharomyces pombe] (AF093540) ribosomal protein L26 [Zea mays]
16869	ENU00663	ANI61C7805: 4476..5266	58-77	786-806	EST	"z1d03a1.r1, z1d03a1.fl"			40	0.022			endoplasmic reticulum membrane protein SHR3 - yeast (Saccharomyces cerevisiae) ; (X99000) secretory component [Saccharomyces cerevisiae] ; (Z74260) ORF YDL212w [Saccharomyces cerevisiae]
16870	ENU00664	ANI61C1473: 3701..4495	55-76	781-807	EST	"h4a07a1.r1, h4a07a1.fl"			115	3E-25			thioredoxin H-type 2 (TRX-H2) ; thioredoxin h2 - common tobacco ; (Z11803) thioredoxin [Nicotiana tabacum] ; thioredoxin [Nicotiana tabacum]
16871	ENU00665	ANI50C2006 8_1:1456..2253	22-44	757-777	EST	"j0c07a1.r1, j0c07a1.fl"			69	4E-11			(U72240) unknown [Choristoneura fumiferana nucleopolyhedrovirus]
16872	ENU00666	ANI61C8263: 1773..976	25-44	761-781	EST	"r4a09a1.r1, r4a09a1.fl"			34	1.7			
16873	ENU00667	ANI61C5890: 298..1097	71-90	802-828	EST	"e0a12a1.r1, e0a12a1.fl"			31	8.4			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% cvrg	Description
16874	ENU00668	ANI61C9181: 2043..2843	35-58	768-793	EST	"y8e04a1.r1, y8e04a1.fl"		38	38	0.11		argBPIB [Homo sapiens] (X95677)
16875	ENU00669	ANI61C5479: 3056..3857	22-51	746-781	EST	"o6f11a1.r1, o6f11a1.fl"		36	36	0.33		U51998) C12D12.1 gene product [Caenorhabditis elegans]
16876	ENU00670	ANI61C5479: 3056..3857	22-51	746-781	EST	"m6c01a1.r1, m6c01a1.fl"		36	36	0.33		U51998) C12D12.1 gene product [Caenorhabditis elegans]
16877	ENU00671	ANI61C5479: 3052..3857	22-51	750-785	EST	"g9b05a1.r1, g9b05a1.fl"		36	36	0.33		U51998) C12D12.1 gene product [Caenorhabditis elegans]
16878	ENU00672	ANI61C5479: 3050..3857	22-50	752-787	EST	"c7f06a1.r1, c7f06a1.fl"		35	35	0.57		U51998) C12D12.1 gene product [Caenorhabditis elegans]
16879	ENU00673	ANI61C6923: 1896..1088	53-72	785-819	EST	"g8g01a1.r1, g8g01a1.fl"		131	131	6E-30		(AF014795) cytochrome P450 30 [Mercenaria mercenaria]
16880	ENU00674	ANI61C8986: 4553..3743	69-88	803-836	EST	"c9b09a1.r1, c9b09a1.fl"		35	35	0.76		(AL031798) 40s ribosomal protein s20. [Schizosaccharomyces pombe]
16881	ENU00675	ANI61C8585: 4159..3348	27-47	777-796	EST	"z2h10a1.r1, z2h10a1.fl"						Double-strand-break repair protein RAD21 ; rad21 protein - fission yeast (Schizosaccharomyces pombe) ; (M96437) putative [Schizosaccharomyces pombe] ; (AL023781) double-strand-break repair protein Rad21p [Schizosaccharomyces pombe]
16882	ENU00676	ANI61C5319: 134..949	50-70	803-823	EST	"m8c02a1.r1, m8c02a1.fl"		32	32	3.8		(AE000787) B. burgdorferi predicted coding region BBJ02 [Borrelia burgdorferi]
16883	ENU00677	ANI61C3974: 2143..1324	22-53	773-799	EST	"j9d07a1.r1, j9d07a1.fl"		62	62	3E-16		hypothetical 11.8 KD protein C1B3.02C in chromosome I ; (Z98598) hypothetical protein
16884	ENU00678	ANI61C6288: 2371..3191	46-68	794-824	EST	"m6g04a1.r1, m6g04a1.fl"		62	62	6E-18		[Schizosaccharomyces pombe] (U81827) 8 kDa cytoplasmic dynein light chain [Emmericella nidulans]
16885	ENU00679	ANI61C4570: 1255..2076	24-43	768-803	EST	"l0a12a1.r1, l0a12a1.fl"		99	99	3E-20		GTP-binding protein ypt5 - fission yeast (Schizosaccharomyces pombe)
16886	ENU00680	ANI61C8349: 495..1322	28-50	789-813	EST	"b0h11a1.r1, b0h11a1.fl"		135	135	2E-37		"(AL031856) atp synthase gamma chain, mitochondrial precursor [Schizosaccharomyces pombe] "
16887	ENU00681	ANI61C9418: 845..14	28-52	782-817	EST	"o6f03a1.r1, o6f03a1.fl"		55	55	0.000000	5	(AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16888	ENU00682	ANI61C6226: 10431..9594	22-49	794-818	EST	"j0c01a1.r1, j0c01a1.fl"		53	53	0.000003			hypothetical 31.5 KD protein C15A10.09C in chromosome I; (Z97208) hypothetical protein [Schizosaccharomyces pombe]
16889	ENU00683	ANI61C878:3 931..3092	54-76	828-851	EST	"q0d08a1.r1, q0d08a1.fl"		40	40	0.024			(Z81460) cDNA EST EMBL:D73695 comes from this gene; cDNA EST EMBL:D71097 comes from this gene; cDNA EST yk274d11.3 comes from this gene; cDNA EST yk274d11.5 comes from this gene [Caenorhabditis elegans]
16890	ENU00684	ANI61C7240: 661..1505	34-54	805-836	EST	"m7b01a1.r1, m7b01a1.fl"		33	33	3.1			hypothetical 90.8 KD protein T05H10.7 in chromosome II; (Z47811) similar to glycerophosphoryl diester phosphodiesterase domain; cDNA EST EMBL:D27842 comes from this gene; cDNA EST EMBL:D27841 comes from this gene; cDNA EST EMBL:D32990 comes from this gene; cDNA EST EMBL:D35712 comes...; (Z47812) similar to glycerophosphoryl diester phosphodiesterase domain; cDNA EST EMBL:D27842 comes from this gene; cDNA EST EMBL:D27841 comes from this gene; cDNA EST EMBL:D32990 comes from this gene; cDNA EST EMBL:D35712 comes... S59/4 homeotic protein - fruit fly (Drosophila melanogaster)
16891	ENU00685	ANI61C1144 2:601..1451	41-61	819-849	EST	"l3h06a1.r1, l3h06a1.fl"		38	38	0.071			Lipoamide acyltransferase component precursor of branched-chain alpha-keto acid dehydrogenase complex (E2) (dihydrolipoamide branched chain transacylase) (BCKAD E2 subunit); dihydrolipoamide transacylase precursor - mouse; (L42996)
16892	ENU00686	ANI61C9218: 2868..2007	36-55	825-855	EST	"z1g12a1.r1, z1g12a1.fl"		218	218	4E-56			acyltransferase [Mus musculus]; branched chain alpha-ketoacid dehydrogenase:subunit=E2 [Mus musculus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16893	ENU00687	ANI61C8190: 107..972	34-62	823-857	EST	"i0a12a1.r1, i0a12a1.fl"		50	50	0.00002			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16894	ENU00688	ANI61C8179: 28-56 768..1633	28-56	828-851	EST	"i3g02a1.r1, i3g02a1.fl"		32	32	7.1			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16895	ENU00689	ANI61S262:1 22-48 55..9	22-48	822-846	EST	"r7d07a1.r1, r7d07a1.fl"		337	337	e-105			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16896	ENU00690	ANI61C8190: 34-62 107..977	34-62	827-862	EST	"r2f06a1.r1, r2f06a1.fl"		50	50	0.00002			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16897	ENU00691	ANI61C353:2 27-56 718..3588	27-56	832-855	EST	"i0b10a1.r1, i0b10a1.fl"		307	307	9E-83			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16898	ENU00692	ANI61C7950: 44-64 4700..3828	44-64	840-873	EST	"c1d09a1.r1, c1d09a1.fl"		34	34	0.28			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16899	ENU00693	ANI61C7751: 69-89 48..919	69-89	877-898	EST	"x7e04a1.r1, x7e04a1.fl"		34	34	1.4			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16900	ENU00694	ANI61C1473: 27-46 3649..4525	27-46	830-861	EST	"t2b06a1.r1, t2b06a1.fl"		115	115	3E-25			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16901	ENU00695	ANI61C560:8 22-49 1..959	22-49	838-857	EST	"h4e06a1.r1, h4e06a1.fl"		35	35	0.83			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16902	ENU00696	ANI61C8403: 27-56 687..1574	27-56	842-872	EST	"k5c08a1.r1, k5c08a1.fl"		188	188	4E-47			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16903	ENU00697	ANI61C6874: 22-48 1796..935	22-48	847-867	EST	"c9c06a1.r1, c9c06a1.fl"		185	185	7E-69			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)
16904	ENU00698	ANI61C4183: 23-42 2..893	23-42	837-872	EST	"o8c11a1.r1, o8c11a1.fl"		35	35	0.85			Thaumatococcus-like pathogenesis-related protein 1 precursor ; (L39774)

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16905	ENU00699	ANI61C1112 8:1455..560	22-53	844-875	EST	"j9c05a1.r1, j9c05a1.fl"		37	0.22				(Z83317) cDNA EST EMBL:D36535 comes from this gene [Caenorhabditis elegans]
16906	ENU00700	ANI61C1095: 1317..418	38-58	865-895	EST	"p0c12a1.r1, p0c12a1.fl"		91	4E-19				hypothetical 16.2 KD protein C4F8.01 in chromosome I; (Z98530) hypothetical protein [Schizosaccharomyces pombe]
16907	ENU00701	ANI61C6422: 116..1018	60-79	900-920	EST	"m8h02a1.r1, m8h02a1.fl"		116	2E-25				hypothetical 62.8 KD protein in SSE1-CAR1 intergenic region; probable membrane protein YPL109c - yeast (Saccharomyces cerevisiae); (U43503) Lph17p [Saccharomyces cerevisiae]
16908	ENU00702	ANI61C1113 9:150..1055	34-53	879-897	EST	"j7d09a1.r1, j7d09a1.fl"		36	0.29				(AB002371) KIAA0373 [Homo sapiens]
16909	ENU00703	ANI61C3229: 1018..1925	22-49	856-887	EST	"s9c03a1.r1, s9c03a1.fl"		117	5E-28				ubiquitin-like protein 9 - Arabidopsis thaliana
16910	ENU00704	ANI61C1209: 14407..13498	41-60	889-908	EST	"x8e02a1.r1, x8e02a1.fl"		34	1.1				(M69057) GABA-alpha receptor [Drosophila melanogaster]
16911	ENU00705	ANI61C6421: 11040..10129	50-71	900-919	EST	"d5c07a1.r1, d5c07a1.fl"		85	9E-16				isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]
16912	ENU00706	ANI61C878.2 079..1168	22-56	860-891	EST	"j0d05a1.r1, j0d05a1.fl"		96	1E-27				(AB017593) MBF1 [Saccharomyces cerevisiae]
16913	ENU00707	ANI61C4912: 2045..2962	48-83	895-923	EST	"j7h09a1.r1, j7h09a1.fl"		34	1.5				(D31765) KIAA0061 [Homo sapiens]
16914	ENU00708	ANI61C9205: 1105..2025	59-79	910-937	EST	"e9g09a1.r1, e9g09a1.fl"		326	1E-88				heat shock protein HSP1 (65 KD IGE-binding protein); (U92465) heat shock protein [Aspergillus fumigatus]
16915	ENU00709	ANI61C5619: 1134..986	39-62	896-926	EST	"k5b07a1.r1, k5b07a1.fl"		69	4E-11				probable transcription factor YPL230w - yeast (Saccharomyces cerevisiae); (X94561) transcription factor [Saccharomyces cerevisiae]; (Z73586) ORF YPL230w [Saccharomyces cerevisiae]
16916	ENU00710	ANI61C4416: 1283..2213	63-82	918-951	EST	"o9c12a1.r1, o9c12a1.fl"		40	0.027				110 KD antigen (PK110); 110k antigen - Plasmodium knowlesi (fragment); (M19152) 110k dalton antigen [Plasmodium knowlesi]
16917	ENU00711	ANI61C1027 9:8355..9296	22-49	890-921	EST	"z5f08a1.r1, z5f08a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16918	ENU00712	ANI61C8351: 4794..5737	22-48	897-922	EST	"v9c03a1.r1, w9c03a1.fl"		92	108	3E-27			Phosphatidyl synthase (Z99295) phosphatidyl synthase [Schizosaccharomyces pombe] (AL034489) predicted using Genefinder; cDNA EST yk367h5.3 comes from this gene; cDNA EST yk367h5.5 comes from this gene; cDNA EST EMBL:Z14572 comes from this gene [Caenorhabditis elegans]
16919	ENU00713	ANI61C5444: 32-51 1810..867	32-51	914-933	EST	"g4d03a1.r1, g4d03a1.fl"				6E-23			(D49367) 4-coumarate:CoA ligase [Lithospermum erythrorhizon] hypothetical 29.3 KD protein C3F10.08C in chromosome I; (Z69369) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (sdsB region) - Pseudomonas sp (AL031013) putative secreted protein [Streptomyces coelicolor] kinetoplast-associated protein - Trypanosoma cruzi; (M25364) kinetoplast-associated protein [Trypanosoma cruzi]
16920	ENU00714	ANI61C1141 45-64 1:1207..269	45-64	929-948	EST	"m0f05a1.r1, m0f05a1.fl"		187	187	1E-46			Purine nucleoside phosphorylase (inosine phosphorylase) (PNP); purine-nucleoside phosphorylase (EC 2.4.2.1) - Escherichia coli; (M60917) purine nucleoside phosphorylase [Escherichia coli]; (U14003) purine-nucleoside phosphorylase [Escherichia coli]; (AE000508) purine-nucleoside phosphorylase [Escherichia coli] GTP-binding protein ypt5 - fission yeast (Schizosaccharomyces pombe) hypothetical 37.7 KD protein C18B11.06 in chromosome I; hypothetical protein SPAC18B11.06 - fission yeast (Schizosaccharomyces pombe); (Z50728) hypothetical protein [Schizosaccharomyces pombe]
16921	ENU00715	ANI61C1057 22-55 7:1157..269	22-55	908-925	EST	"o0e11a1.r1, o0e11a1.fl"		35	35	0.69			
16922	ENU00716	ANI61C9395: 24-43 6836..5890	24-43	895-928	EST	"d4c02a1.r1, d4c02a1.fl"		36	36	0.31			
16923	ENU00717	ANI61C8649: 69-88 4267..5218	69-88	953-978	EST	"y6c07a1.r1, y6c07a1.fl"		42	42	0.005			
16924	ENU00718	ANI61C4368: 22-44 202..1159	22-44	915-937	EST	"d5a01a1.r1, d5a01a1.fl"		34	34	1.6			
16925	ENU00719	ANI61C3644: 26-50 842..4594	26-50	919-947	EST	"l3f05a1.r1, l3f05a1.fl"		33	33	2.7			
16926	ENU00720	ANI61C4570: 33-56 1063..2039	33-56	931-966	EST	"l3g11a1.r1, l3g11a1.fl"		132	132	1E-37			
16927	ENU00721	ANI61C8257: 40-59 19..1006	40-59	964-985	EST	"o6e02a1.r1, o6e02a1.fl"		85	85	9E-16			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16928	ENU00722	ANI61C9555: 4133..5128	72-94	1004-1023	EST	"q0a07a1.r1, q0a07a1.fl"			34	1.7			interleukin 4 receptor precursor; CD124 ; interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen) ; (X52425) interleukin 4 receptor [Homo sapiens] ; (AC004525) Interleukin 4 alpha-chain precursor [Homo sapiens]
16929	ENU00723	ANI61C2666: 22-55 5004..4007	22-55	943-976	EST	"y7b01a1.r1, y7b01a1.fl"		199	2E-50				Pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) precursor - Pseudomonas aeruginosa (strain PAO) ; (M33557) delta-1-pyrroline-5-carboxylate reductase (EC 1.5.1.2) [Pseudomonas aeruginosa] (AL031740) 60s ribosomal protein l10a. [Schizosaccharomyces pombe] hypothetical 53.9 KD protein C1F5.08C in chromosome I ; (Z68136) unknown [Schizosaccharomyces pombe]
16930	ENU00724	ANI61C5218: 34-66 1629..632	34-66	971-990	EST	"c1c10a1.r1, c1c10a1.fl"		252	2E-66				probable serine/threonine-protein kinase C1D4.11C ; (Z69239) unknown [Schizosaccharomyces pombe]
16931	ENU00725	ANI61C1101 28-49 6:1959..961	28-49	964-984	EST	"n8e06a1.r1, n8e06a1.fl"		139	2E-32				
16932	ENU00726	ANI61C1027 22-46 7:6262..5262	22-46	961-980	EST	"z7f04a1.r1, z7f04a1.fl"		33	2.9				
16933	ENU00727	ANI61C5890: 55-76 467..1472	55-76	997-1018	EST	"v7c05a1.r1, v7c05a1.fl"		32	5				(AF027867) SacI methylase [Streptomyces achromogenes]
16934	ENU00728	ANI61C9978: 33-52 3494..2487	33-52	972-998	EST	"y4a06a1.r1, y4a06a1.fl"		36	0.57				(AF064070) putative epimerase/dehydratase WbiG [Burkholderia pseudomallei]
16935	ENU00729	ANI61C3947: 29-48 1493..485	29-48	967-995	EST	"x8b06a1.r1, x8b06a1.fl"		61	0.000000				hypothetical 89.2 KD protein C4H3.11C in chromosome I ; (Z69380) unknown [Schizosaccharomyces pombe]
16936	ENU00730	ANI61C9564: 41-60 1335..325	41-60	982-1009	EST	"v7g01a1.r1, v7g01a1.fl"		147	2E-46				ribosomal protein L12 ; 60S ribosomal protein L12 ; ribosomal protein L12 - human ; (L06505) ribosomal protein L12 [Homo sapiens]
16937	ENU00731	ANI50C7010 24-44 2_1:1444..432	24-44	967-994	EST	"c8f11a1.r1, c8f11a1.fl"		86	3E-17				(Z99262) putative endosomal Vps protein complex subunit [Schizosaccharomyces pombe]
16938	ENU00732	ANI61C5415: 24-52 475..1494	24-52	982-1001	EST	"c8b03a1.r1, c8b03a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16939	ENU00733	ANI61C5415: 475..1494	24-52	982-1001	EST	"o6e09a1.rl, o6e09a1.fl"		86	86	3E-17			(Z99262) putative endosomal Vps protein complex subunit [Schizosaccharomyces pombe]
16940	ENU00734	ANI61C5415: 475..1494	24-52	982-1001	EST	"g2b05a1.rl, g2b05a1.fl"		86	86	3E-17			(Z99262) putative endosomal Vps protein complex subunit [Schizosaccharomyces pombe]
16941	ENU00735	ANI61C6105: 1166..2186	22-47	974-1000	EST	"g7b11a1.rl, g7b11a1.fl"		131	131	6E-30			"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe]"
16942	ENU00736	ANI61C9555: 4102..5128	34-56	997-1016	EST	"m5c02a1.rl, m5c02a1.fl"		34	34	1.7			interleukin 4 receptor precursor; CD124; interleukin-4 receptor alpha chain precursor (IL-4R-alpha) (CD124 antigen); (X52425) interleukin 4 receptor [Homo sapiens]; (AC004525) Interleukin 4 alpha-chain precursor [Homo sapiens]
16943	ENU00737	ANI61C8351: 4698..5725	29-52	987-1013	EST	"s9d01a1.rl, s9d01a1.fl"		92	92	2E-30			(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
16944	ENU00738	ANI61C4397: 2140..1113	22-52	988-1007	EST	"j9d05a1.rl, j9d05a1.fl"		39	39	0.039			aggregation protein asp1 - Enterococcus faecalis plasmid pPDI; (X62656) aggregation substance (ASPI) [Enterococcus faecalis]
16945	ENU00739	ANI61C2666: 2876..3907	44-67	1013-1033	EST	"t2a05a1.rl, t2a05a1.fl"		32	32	5.1			light repressible receptor protein kinase - Arabidopsis thaliana; (X97774) light repressible receptor protein kinase [Arabidopsis thaliana]
16946	ENU00740	ANI61C8498: 102..1140	25-50	995-1021	EST	"r1d01a1.rl, r1d01a1.fl"		243	243	2E-63			(AL035216) probable involvement in ergosterol biosynthesis [Schizosaccharomyces pombe]
16947	ENU00741	ANI61C4920: 1676..637	32-51	996-1029	EST	"h8e02a1.rl, h8e02a1.fl"		335	335	e-121			"(S83228) beta-isopropylmalate dehydrogenase [Aspergillus niger, strain A733, Peptide, 363 aa] [Aspergillus niger]; (U51130) beta-isopropylmalate dehydrogenase [Aspergillus niger]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvng	Description
16948	ENU00742	ANI61C8213: 915..1043	22-42	998-1022	EST	"y3h11a1.r1, y3h11a1.fl"		163	163	2E-39			"mitogen-activated protein kinase HOG1 (MAP kinase HOG1) (osmosensing protein HOG1) ; protein kinase HOG1 (EC 2.7.1.-), mitogen-activated - yeast (Saccharomyces cerevisiae) ; (X89514) mitogen-activated protein kinase [Saccharomyces cerevisiae] ; (Z73285) ORF YLR113w [Saccharomyces cerevisiae] "
16949	ENU00743	ANI61C3025: 40-60	1023-1042	1023-1042	EST	"m0h12a1.r1, m0h12a1.fl"		35	35	1			(D49835) DNA-binding protein [Homo sapiens]
16950	ENU00744	ANI61C7853: 22-54	22-54	994-1029	EST	"i7e03a1.r1, i7e03a1.fl"		32	32	8.9			(Z70755) weak similarity with xenopus XFIN protein (Swiss Prot accession number P08045) [Caenorhabditis elegans]
16951	ENU00745	ANI61C5148: 39-62	1025-1047	1025-1047	EST	"f0f11a1.r1, f0f11a1.fl"		271	271	5E-85			(AF088906) clock-controlled gene-9 protein [Neurospora crassa]
16952	ENU00746	ANI61C331:2 34-53	34-53	1022-1042	EST	"r5d11a1.r1, r5d11a1.fl"		36	36	0.46			(AC004138) unknown protein [Arabidopsis thaliana]
16953	ENU00747	ANI61C8247: 22-50	22-50	1010-1034	EST	"x7a08a1.r1, x7a08a1.fl"		36	36	0.6			(AC006528) putative mudra transposase protein [Arabidopsis thaliana]
16954	ENU00748	ANI61C2872: 42-62	42-62	1023-1056	EST	"j7c11a1.r1, j7c11a1.fl"		341	341	4E-93			"glycogen (starch) synthase, isoform 2 ; UDPglucose--starch glucosyltransferase (EC 2.4.1.11) 2 - yeast (Saccharomyces cerevisiae) ; (U17244) Gsy2p: Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae] "
16955	ENU00749	ANI61C7556: 22-51	22-51	1004-1039	EST	"r4b04a1.r1, r4b04a1.fl"		33	33	3			(AF038614) contains similarity to Lentinula edodes MFBA=234.5 kda mature fruiting body adhesion protein (GB:S75826) [Caenorhabditis elegans]
16956	ENU00750	ANI61C9370: 66-87	66-87	1058-1085	EST	"o8a11a1.r1, o8a11a1.fl"		136	136	5E-37			glutathione-dependent formaldehyde dehydrogenase (FDH) (FALDH) ; (L33464) alcohol dehydrogenase 3 [Methylobacter marinus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16957	ENU00751	ANI61C8056: 4476..3414	22-46	1007-1042	EST	"j0b08a1.r1, j0b08a1.fl"		108	108	2E-27			(AL031181) putative cell division involvement [Schizosaccharomyces pombe] ; (AL035064) septin interacting protein homolog [Schizosaccharomyces pombe] hypothetical 58.3 KD protein in PMT2-CCR4 intergenic region ; FUN26 protein - yeast (Saccharomyces cerevisiae) ; (L05146) Fun26p [Saccharomyces cerevisiae] ; (L05027) ORF YAL022 [Saccharomyces cerevisiae]
16958	ENU00752	ANI61C2678: 22-41 1085..2147	22-41	1011-1042	EST	"c7h03a1.r1, c7h03a1.fl"		95	95	6E-21			
16959	ENU00753	ANI61C9359: 40-59 1978..3041	40-59	1027-1061	EST	"l0g11a1.r1, l0g11a1.fl"		157	157	2E-37			(AJ001414) GTPase activating protein [Yarrowia lipolytica]
16960	ENU00754	ANI61C9824: 65-87 3270..4335	65-87	1060-1088	EST	"c8a03a1.r1, c8a03a1.fl"		123	123	2E-27			(Z47357) cDNA EST yk375c3.5 comes from this gene; cDNA EST yk375c3.3 comes from this gene [Caenorhabditis elegans]
16961	ENU00755	ANI61C6035: 29-52 97..2530	29-52	1023-1054	EST	"y4b09a1.r1, y4b09a1.fl"		34	34	1.4			(Z75539) predicted using Genefinder; cDNA EST EMBL:C13354 comes from this gene; cDNA EST EMBL:C11309 comes from this gene; cDNA EST yk477e3.3 comes from this gene; cDNA EST yk477e3.5 comes from this gene; cDNA EST yk462a1.3 comes...
16962	ENU00756	ANI61C2053: 25-60 1438..369	25-60	1027-1052	EST	"j9e12a1.r1, j9e12a1.fl"		319	319	2E-86			hypothetical 35.7 KD protein C26A3.1.1 in chromosome I ; (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]
16963	ENU00757	ANI61C9659: 37-58 1356..278	37-58	1048-1073	EST	"c6c09a1.r1, c6c09a1.fl"		32	32	5.4			(AC007087) unknown protein [Arabidopsis thaliana]
16964	ENU00758	ANI61C7277: 47-68 2375..1297	47-68	1064-1083	EST	"d1d08a1.r1, d1d08a1.fl"		139	139	3E-32			(X92868) NADP-dependent alcohol dehydrogenase [Bacillus subtilis] ; (Z99117) NADP-dependent alcohol dehydrogenase [Bacillus subtilis]
16965	ENU00759	ANI61C7087: 22-45 2146..1066	22-45	1025-1060	EST	"c4e01a1.r1, c4e01a1.fl"		128	128	8E-29			(AL023705) hypothetical protein [Schizosaccharomyces pombe]
16966	ENU00760	ANI61C4304: 54-73 1805..717	54-73	1065-1100	EST	"g6d09a1.r1, g6d09a1.fl"							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16967	ENU00761	ANI61C7147: 3274..4365	22-53	1041-1071	EST	"i3h06a1.r1, i3h06a1.fl"			492	e-138			calcium/calmodulin-dependent protein kinase (CMPK) ; Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans ; (M74120) calmodulin-dependent protein kinase [Emericella nidulans] ; (AF054580) calmodulin-dependent protein kinase [Emericella nidulans] ; thioredoxin H-type 2 (TRX-H2) ; thioredoxin h2 - common tobacco ; (Z11803) thioredoxin [Nicotiana tabacum] ; thioredoxin [Nicotiana tabacum]
16968	ENU00762	ANI61C8263: 1773..682	25-44	1054-1075	EST	"r1e01a1.r1, r1e01a1.fl"			34	2.4			(U95611) Cap1 [Candida albicans]
16969	ENU00763	ANI61C2172: 30..1130	51-72	1088-1109	EST	"y4e06a1.r1, y4e06a1.fl"			55	0.000000			(U28789) PACT [Mus musculus]
16970	ENU00764	ANI61C2654: 2689..1587	38-57	1078-1097	EST	"g3c02a1.r1, g3c02a1.fl"			38	0.12			ubiquitin-like protein 9 - Arabidopsis thaliana
16971	ENU00765	ANI61C3229: 820..1921	22-45	1054-1081	EST	"n8a02a1.r1, n8a02a1.fl"			117	6E-28			PRL1/PRL2-like protein ; (AB004535)
16972	ENU00766	ANI61C385:2 135..3237	22-47	1063-1082	EST	"i8d10a1.r1, i8d10a1.fl"			476	e-133			PRL1 [Schizosaccharomyces pombe]
16973	ENU00767	ANI61C1048 1:1932..3042	52-72	1086-1120	EST	"m7g04a1.r1, m7g04a1.fl"			33	3.2			(Z69368) unknown
16974	ENU00768	ANI61C3011: 3667..2551	64-83	1105-1139	EST	"w8e03a1.r1, w8e03a1.fl"			63	0.000000			[Schizosaccharomyces pombe]
										004			transcription factor
													[Schizosaccharomyces pombe] ; (Z97211) atf-creb-family transcription factor [Schizosaccharomyces pombe]
16975	ENU00769	ANI61C1136: 6747..7865	27-48	1068-1103	EST	"f0g07a1.r1, f0g07a1.fl"			142	2E-37			hypothetical protein YLR189c - yeast (Saccharomyces cerevisiae) ; (U17246)
16976	ENU00770	ANI61C6977: 1453..332	40-60	1091-1119	EST	"o8f01a1.r1, o8f01a1.fl"							Ylr189cp [Saccharomyces cerevisiae]
16977	ENU00771	ANI61C9177: 214..1342	22-52	1088-1108	EST	"d5h06a1.r1, d5h06a1.fl"			32	7.4			(X73888) cytochrome c [Escherichia coli]
16978	ENU00772	ANI61C2197: 3006..1873	71-89	1146-1165	EST	"k5h01a1.r1, k5h01a1.fl"			34	2.5			"(S82067) T-cell receptor beta chain variable region {C beta region} [human, melanoma-specific cytotoxic T-cell clone DT252 12-6C7, melanoma patient 252, Peptide Partial, 86 aa] [Homo sapiens] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
16979	ENU00773	ANI61C9855: 2951..4097	59-78	1143-1163	EST	"l3g07a1.r1, l3g07a1.fl"		81	130	1E-14			(AL031852) hypothetical protein [Schizosaccharomyces pombe]
16980	ENU00774	ANI61C632:5 76..1724	41-71	1120-1147	EST	"r8b07a1.r1, r8b07a1.fl"			131	2E-29			(U18061) CAP20 [Glomerella cingulata]
16981	ENU00775	ANI61C1086 5:3245..2093	43-64	1121-1152	EST	"q0e02a1.r1, q0e02a1.fl"			66	7E-30			(AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe]
16982	ENU00776	ANI61C9103: 57..1211	22-55	1113-1133	EST	"p0b11a1.r1, p0b11a1.fl"			275	7E-12			(AB011822) clathrin light chain [Schizosaccharomyces pombe]
16983	ENU00777	ANI61C9039: 3716..4873	72-92	1152-1187	EST	"o8g08a1.r1, o8g08a1.fl"				5E-73			"(Z98559) SPAC23C11.17; len:485aa, similar eg. to YPR125W, Q06493, chromosome xvi orf, (454aa), fasta scores, opt:1063, E():0, (43.5% identity in 418 aa overlap)
16984	ENU00778	ANI61C1093 0:691..1848	44-65	1132-1159	EST	"f2fl2a1.r1, f2fl2a1.fl"			217	9E-56			[Schizosaccharomyces pombe] "
16985	ENU00779	ANI61C1188: 2015..3173	22-51	1108-1138	EST	"g9h01a1.r1, g9h01a1.fl"			148	3E-48			"(D14846) endo alpha-1,4 polygalactosaminidase precursor [Pseudomonas sp.] "
16986	ENU00780	ANI61C1036 1:1081..2244	36-59	1133-1157	EST	"m5e02a1.r1, m5e02a1.fl"			222	5E-57			unknown ; (AF075599) ubiquitin conjugating enzyme 12 [Homo sapiens] ; (AB012191) Nedd8-conjugating enzyme hUbc12 [Homo sapiens]
16987	ENU00781	ANI61C6804: 3054..1885	22-49	1125-1149	EST	"j0f02a1.r1, j0f02a1.fl"			138	1E-31			(AB010900) YNL123w homolog [Schizosaccharomyces pombe]
16988	ENU00782	ANI61C6107: 2132..962	24-59	1126-1152	EST	"c8c02a1.r1, c8c02a1.fl"			112	9E-27			hypothetical 27.7 KD protein in PRP19-HSP104 intergenic region ; hypothetical protein YLL027w - yeast (Saccharomyces cerevisiae) ; (Z73132) ORF YLL027w [Saccharomyces cerevisiae]
16989	ENU00783	ANI61C3323: 3852..2682	67-85	1169-1195	EST	"x7b06a1.r1, x7b06a1.fl"			36	0.52			(AF094516) E1-like protein [Homo sapiens]
16990	ENU00784	ANI61C893:1 958..785	23-49	1125-1153	EST	"t2h07a1.r1, t2h07a1.fl"			34	0.0008			(AF104860) putative RNA-binding protein PRP-1 [Caenorhabditis elegans] "(AF045646) contains similarity to human cyclin A/CDK2-associated protein p19, an RNA polymerase II elongation factor-like protein (GB:U33760) [Caenorhabditis elegans] "
16991	ENU00785	ANI61C8934: 804..1977	31-50	1134-1162	EST	"x8c05a1.r1, x8c05a1.fl"			35	1.2			(AJ006350) polymerase [Duck hepatitis B virus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
16992	ENU00786	ANI61C1135	68-93	1176-1200	EST	"i7e08a1.r1, i7e08a1.fl"		53	0.000003			(AL034490) putative tyrosine kinase [Schizosaccharomyces pombe]
16993	ENU00787	ANI61C3480: 8:1793..2967 3144..1961	22-55	1140-1163	EST	"o8d09a1.r1, o8d09a1.fl"		33	4.6			(D43921) pre-acrosome localization protein [Mus musculus] ; (D88509) AZ-1 [Mus musculus]
16994	ENU00788	ANI61C9543: 2435..1249	45-64	1158-1189	EST	"w9a11a1.r1, w9a11a1.fl"		68	3E-23			(AF050672) ribosomal protein L13E [Candida albicans] ; (AL033497) ribosomal protein L13e [Candida albicans] ; (U80854) ribosomal protein L13 [Candida albicans]
16995	ENU00789	ANI61C1064 4:3051..4241	68-87	1184-1215	EST	"h4e03a1.r1, h4e03a1.fl"		41	0.021			(AF083325) phosphatidylcholine transferase [Homo sapiens]
16996	ENU00790	ANI61C3465: 1756..566	28-51	1142-1177	EST	"e0b10a1.r1, e0b10a1.fl"		43	0.004			"(AB000628) UDP-GlcNAc:alpha-1,3-D-mannoside b-1,4-N-Acetylglucosaminyltransferase IV [Bos taurus]"
16997	ENU00791	ANI61C9562: 520..1713	52-72	1182-1202	EST	"g5c09a1.r1, g5c09a1.fl"		189	3E-55			GTP-binding protein SARA ; (Z67742) sarA [Aspergillus niger]
16998	ENU00792	ANI61C6956: 339..1538	26-45	1161-1183	EST	"r2b05a1.r1, r2b05a1.fl"		157	2E-37			(X99853) oxoglutarate malate translocator [Solanum tuberosum]
16999	ENU00793	ANI61C2326: 1236..32	27-47	1168-1189	EST	"r5e09a1.r1, r5e09a1.fl"		45	0.001			(AL023634) hypothetical protein [Schizosaccharomyces pombe]
17000	ENU00794	ANI61C6814: 4189..2970	22-42	1169-1199	EST	"f0a12a1.r1, f0a12a1.fl"		122	5E-27			hypothetical 32.6 KD protein in VPS15-YMC2 intergenic region ; hypothetical protein YBR101c - yeast (Saccharomyces cerevisiae) ; (X78993) YBR0830 [Saccharomyces cerevisiae] ; (Z35970) ORF YBR101c [Saccharomyces cerevisiae]
17001	ENU00795	ANI61C7104: 2817..1597	22-56	1167-1200	EST	"n8e07a1.r1, n8e07a1.fl"		60	3E-18			"RNase Irp1=base non-specific acid ribonuclease [Irpex lacteus, Peptide, 250 aa]"
17002	ENU00796	ANI61C6919: 2563..1338	24-43	1172-1207	EST	"n0b06a1.r1, n0b06a1.fl"		322	5E-94			aminopeptidase Y (EC 3.4.11.-) precursor - yeast (Saccharomyces cerevisiae)
17003	ENU00797	ANI61C3368: 7084..8312	30-49	1186-1216	EST	"g3b06a1.r1, g3b06a1.fl"		437	e-122			(AL033385) transketolase [Schizosaccharomyces pombe]
17004	ENU00798	ANI61C4572: 3705..2471	53-72	1214-1244	EST	"m0d06a1.r1, m0d06a1.fl"						

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17005	ENU00799	ANI61C1536: 22-54 2827..4066	22-54	1200-1219	EST	"d5b01a1.r1, d5b01a1.fl"		36	0.72				inhibitory regulator protein IRA2 ; (M33779) IRA2 protein (IRA2) [Saccharomyces cerevisiae]
17006	ENU00800	ANI61C9250: 26-61 1679..440	26-61	1194-1223	EST	"d3f01a1.r1, d3f01a1.fl"		244	8E-64				probable NADP-dependent oxidoreductase P1 ; zeta-crystallin homolog - Arabidopsis thaliana ; (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
17007	ENU00801	ANI61C9202: 22-48 2072..3324	22-48	1213-1232	EST	"o8f12a1.r1, o8f12a1.fl"		226	e-118				ubiquitin--protein ligase RSP5 ; hypothetical protein YER125w - yeast (Saccharomyces cerevisiae) ; (U18916) Rsp5p [Saccharomyces cerevisiae]
17008	ENU00802	ANI61C1055 22-54 7:2994..4251	22-54	1204-1237	EST	"g9e09a1.r1, g9e09a1.fl"		125	2E-30				"NADH-cytochrome B5 reductase precursor (P34/P32) ; cytochrome-b5 reductase (EC 1.6.2.2), mitochondrial outer membrane form - yeast (Saccharomyces cerevisiae) ; (Z26877) unknown [Saccharomyces cerevisiae] ; (Z28150) ORF YKL150w [Saccharomyces cerevisiae] ; (X81474) NADH-cytochrome b5 reductase [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] "
17009	ENU00803	ANI61C6800: 31-51 2631..1372	31-51	1221-1248	EST	"g5d10a1.r1, g5d10a1.fl"		72	7E-12				nuclear protein SON1 (UB fusion degradation protein 5) ; nuclear protein SON1 - yeast (Saccharomyces cerevisiae) ; (L00928) nuclear protein [Saccharomyces cerevisiae] ; (Z48432) nuclear protein SON1 (L00928) [Saccharomyces cerevisiae] ; (Z74068) ORF YDL020c [Saccharomyces cerevisiae]
17010	ENU00804	ANI61C5194: 49-68 1603..335	49-68	1242-1275	EST	"dlh08a1.r1, dlh08a1.fl"		128	1E-58				40S ribosomal protein S4 (omnipotent suppressor protein SUP44) (RP12) (S2E) ; ribosomal protein S2.e - yeast (Saccharomyces cerevisiae) ; (M59375) ribosomal protein S4 [Saccharomyces cerevisiae] ; (Z72645) ORF YGL123w [Saccharomyces cerevisiae] ; (X94106) SUP44 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17011	ENU00805	ANI61C6105: 868..2147	38-57	1252-1275	EST	"d3a07a1.r1, d3a07a1.fl"			220	2E-56		"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe] "
17012	ENU00806	ANI61C1430: 5544..6828	22-51	1241-1264	EST	"d3b03a1.r1, d3b03a1.fl"			197	8E-74		(AL021730) hypothetical protein [Schizosaccharomyces pombe]
17013	ENU00807	ANI61C7432: 640..1925	22-43	1233-1265	EST	"t2d09a1.r1, t2d09a1.fl"			34	1.7		(Z94043) hypothetical protein [Bacillus subtilis]; (Z99121) alternate gene name: yzkA; similar to cell wall-binding protein [Bacillus subtilis]
17014	ENU00808	ANI61C1065 4:2016..726	50-71	1279-1298	EST	"k0h11a1.r1, k0h11a1.fl"			98	1E-19		probable glucose transporter RCO-3; (U54768) RCO3 [Neurospora crassa]
17015	ENU00809	ANI61C6107: 3106..4399	33-53	1259-1284	EST	"r7c07a1.r1, r7c07a1.fl"			108	1E-58		(AL022103) deoxycytidylate deaminase [Schizosaccharomyces pombe]
17016	ENU00810	ANI61C9185: 2399..1101	28-51	1254-1284	EST	"m5f03a1.r1, m5f03a1.fl"			94	7E-33		(U22463) T-2 toxin biosynthesis protein; tri7 [Fusarium sporotrichoides]
17017	ENU00811	ANI61C289:3 229..1930	22-50	1254-1279	EST	"r7f07a1.r1, r7f07a1.fl"			324	8E-88		"(S66039) NAD(+)-specific glutamate dehydrogenase, NAD-GDH {EC 1.4.1.2} [Neurospora crassa, Peptide, 1047 aa] [Neurospora crassa] ; Glu dehydrogenase [Neurospora crassa] "
17018	ENU00812	ANI61C7273: 3807..2486	35-55	1280-1314	EST	"k5g01a1.r1, k5g01a1.fl"			87	5E-20		"hypothetical 23.0 KD protein C3F10.12C in chromosome I; (Z69369) SPAC3F10.12c, unknown, 201, similar to transcription factors and SW:CBF1_YEAST P17106 centromere-binding protei n 1 (39.8% identity in 113 aa) overlap, contains PS00038 Myc-type, 'helix-loop-helix' dimerization dom..."
17019	ENU00813	ANI61C8229: 840..2170	63-84	1321-1351	EST	"i2b02a1.r1, i2b02a1.fl"			34	2.3		hypothetical 73.3 KD protein C6G9.14 in chromosome I; (Z81317) serine rich pumilio family rna binding domain protein [Schizosaccharomyces pombe]
17020	ENU00814	ANI61C8716: 4027..2695	22-50	1281-1312	EST	"z1c12a1.r1, z1c12a1.fl"			34	2.3		(U78551) mucin MUC5B [Homo sapiens]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17021	ENU00815	ANI50C1117 4_1:1679..307	22-49	1331- 1352	EST	"b0g03a1.r1, b0g03a1.fl"			102	2E-38			DNA-directed RNA polymerase II 19 KD polypeptide ; (D86554) RNA polymerase II subunit Rpb7 [Schizosaccharomyces pombe] ; (D89594) RNA polymerase II subunit Rpb7 [Schizosaccharomyces pombe] ; (AF027821) Rpb7 [Schizosaccharomyces pombe] ; (AF055916) RNA polymerase II subunit Rpb7 [Schizosaccharomyces pombe]
17022	ENU00816	ANI61C1037 4:1210..2584	37-59	1339- 1369	EST	"r1a02a1.r1, r1a02a1.fl"			199	e-113			"probable arginyl-TRNA synthetase, cytoplasmic (arginine--TRNA ligase) (ARGRS) ; probable arginine--tRNA ligase (EC 6.1.1.19) - yeast (Saccharomyces cerevisiae) ; (U51032) Ydr341cp [Saccharomyces cerevisiae] "
17023	ENU00817	ANI61C2914: 20..1402	41-61	1353- 1381	EST	"o0d06a1.r1, o0d06a1.fl"			741	0			(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus] HPBRII-7 protein - human ; (X67337) Human pre-mRNA cleavage factor I 68 kDa subunit [Homo sapiens] ; (X67336) HPBRII-7 [Homo sapiens] hypothetical protein YOR197w - yeast (Saccharomyces cerevisiae) ; (Z75105) ORF YOR197w [Saccharomyces cerevisiae]
17024	ENU00818	ANI61C3137: 161..1	28-49	1372- 1396	EST	"t2h11a1.r1, t2h11a1.fl"			43	0.007			Repressible alkaline phosphatase precursor ; alkaline phosphatase (EC 3.1.3.1) - yeast (Saccharomyces cerevisiae) ; (U33050) Pho8p: repressible alkaline phosphatase; CAI: 0.16 [Saccharomyces cerevisiae] (AL031743) putative protein transport protein [Schizosaccharomyces pombe]
17025	ENU00819	ANI61C8615: 539..1951	54-73	1400- 1424	EST	"e0g10a1.r1, e0g10a1.fl"			353	2E-96			
17026	ENU00820	ANI61C9379: 1868..447	40-59	1389- 1417	EST	"j0g12a1.r1, j0g12a1.fl"			233	3E-64			
17027	ENU00821	ANI61C3740: 88..1508	55-75	1411- 1434	EST	"j9c11a1.r1, j9c11a1.fl"			201	1E-50			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17028	ENU00822	ANI61C9283: 22-57 5828..4401		1372-1407	EST	"d3b06a1.r1, d3b06a1.fl"		87	87	3E-16			"mitochondrial acidic protein MAM33 precursor ; hypothetical protein YIL070c - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 266, CAI: 0.21 [Saccharomyces cerevisiae]"
17029	ENU00823	ANI61C9283: 24-43 5839..4401		1385-1420	EST	"p0e09a1.r1, p0e09a1.fl"		87	87	3E-16			"mitochondrial acidic protein MAM33 precursor ; hypothetical protein YIL070c - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 266, CAI: 0.21 [Saccharomyces cerevisiae]"
17030	ENU00824	ANI61C9283: 22-57 5828..4381		1394-1427	EST	"x9c12a1.r1, x9c12a1.fl"		87	87	3E-16			"mitochondrial acidic protein MAM33 precursor ; hypothetical protein YIL070c - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 266, CAI: 0.21 [Saccharomyces cerevisiae]"
17031	ENU00825	ANI61C5338: 23-50 743..567		1394-1429	EST	"p0c02a1.r1, p0c02a1.fl"		100	100	3E-23			(AL023518) hypothetical protein [Schizosaccharomyces pombe]
17032	ENU00826	ANI61C1649: 42-61 2395..941		1420-1454	EST	"g5c04a1.r1, g5c04a1.fl"		217	217	2E-55			probable serine/threonine-protein kinase C29A4.16 ; (Z97210) protein
17033	ENU00827	ANI61C8443: 22-46 4202..2748		1411-1434	EST	"d5a07a1.r1, d5a07a1.fl"		282	282	4E-77			kinase [Schizosaccharomyces pombe] type II proteins geranylgeranyltransferase beta subunit (type II protein geranyl-geranyltransferase beta subunit) (GGTase-II-beta) (PGGT) (YPT1/SEC4 proteins geranylgeranyltransferase beta subunit) ; probable protein prenyltransferase (EC 2.5.1.-) BET2 - yeast (Saccharomyces cerevisiae) ; (U25842) Protein Geranyl-geranyltransferase beta subunit (Swiss Prot. accession number P20133; P32433) [Saccharomyces cerevisiae]
17034	ENU00828	ANI61C7625: 40-59 1891..409		1443-1468	EST	"g6c08a1.r1, g6c08a1.fl"		51	51	0.00002			(Z46970) secreted acid phosphatase 2 (SAP2) [Leishmania mexicana]
17035	ENU00829	ANI61C7625: 40-59 1891..409		1443-1468	EST	"d3g05a1.r1, d3g05a1.fl"		51	51	0.00002			(Z46970) secreted acid phosphatase 2 (SAP2) [Leishmania mexicana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17036	ENU00830	ANI61C9270: 2951..1463	54-73	1465-1500	EST	"c7f12a1.r1, c7f12a1.fl"		70	3E-11				(AF039217) inv candidate homolog [Homo sapiens]
17037	ENU00831	ANI61C2972: 53-72 4977..3488	53-72	1466-1499	EST	"j4g02a1.r1, j4g02a1.fl"		236	e-102				"Succinic semialdehyde dehydrogenase ; (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens] ; (AL031230) dJ73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24)) [Homo sapiens] "
17038	ENU00832	ANI61C1086 6:1100..2594	22-45	1441-1474	EST	"o8g12a1.r1, o8g12a1.fl"		344	e-151				26S protease regulatory subunit 6A homolog (TAT-binding protein homolog 1) (TBP-1) ; (D88663) Tat binding protein 1 [Brassica rapa]
17039	ENU00833	ANI61C1649: 2416..896	54-73	1511-1532	EST	"g6g06a1.r1, g6g06a1.fl"		217	2E-55				probable serine/threonine-protein kinase C29A4.16 ; (Z97210) protein kinase [Schizosaccharomyces pombe]
17040	ENU00834	ANI61C2242: 29-48 4904..3363	29-48	1499-1527	EST	"w7b01a1.r1, w7b01a1.fl"		146	1E-95				arginine permease; arginine transport protein - yeast [Saccharomyces cerevisiae] ; (M11724) amino acid permease [Saccharomyces cerevisiae] ; (U18795) Can1p: arginine permease [Saccharomyces cerevisiae]
17041	ENU00835	ANI61C9231: 66-86 733..2284	66-86	1550-1575	EST	"d5c12a1.r1, d5c12a1.fl"		90	6E-29				(U77605) two-component histidine kinase CHK-1 [Glomerella cingulata] ; (U77606) two-component histidine kinase CHK-1 [Glomerella cingulata]
17042	ENU00836	ANI61C1103 67-88 3:4042..5596	67-88	1544-1579	EST	"w7h10a1.r1, w7h10a1.fl"		157	1E-37				(M16076) low temperature essential protein [Saccharomyces cerevisiae]
17043	ENU00837	ANI61C3573: 3114..1551	43-63	1540-1564	EST	"i0h03a1.r1, i0h03a1.fl"		195	3E-80				probable membrane protein YDR105c - yeast [Saccharomyces cerevisiae] ; (Z47746) unknown [Saccharomyces cerevisiae] ; (Z48758) unknown [Saccharomyces cerevisiae]
17044	ENU00838	ANI61C1048 55-78 2:1783..214	55-78	1562-1582	EST	"d3c06a1.r1, d3c06a1.fl"		159	5E-38				hypothetical protein YDR330w - yeast [Saccharomyces cerevisiae] ; (U32517) Ydr330wp [Saccharomyces cerevisiae]
17045	ENU00839	ANI61C9735: 65-84 2323..754	65-84	1557-1592	EST	"q0d11a1.r1, q0d11a1.fl"		411	e-158				3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase) ; (X94307) HMG-CoA-reductase [Gibberella fujikuroi]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17046	ENU00840	ANI61C1122 9:1380..2970	26-50	1539-1574	EST	"j0d08a1.r1, j0d08a1.fl"			151	1E-35		probable membrane protein YDL074c - yeast (Saccharomyces cerevisiae) ; (Z74122) ORF YDL074c [Saccharomyces cerevisiae] hypothetical 73.3 KD protein C6G9.14 in chromosome I ; (Z81317) serine rich pumilio family rna binding domain protein [Schizosaccharomyces pombe] "(D89173) similar to Saccharomyces cerevisiae hypothetical 36.4KD protein in SOD1-CPA2 intergenic region, SWISS-PROT Accession Number P47143 [Schizosaccharomyces pombe] ; (AL023781) adenosine kinase [Schizosaccharomyces pombe] " (AB004535) BEM46 protein [Schizosaccharomyces pombe] (AJ001836) fumarylacetoacetate hydrolase [Emericella nidulans] (AL035707) putative salicylate hydroxylase [Streptomyces coelicolor] (U43775) secreted aspartic proteinase precursor [Glomerella cingulata] (X00528) URF c-ras (sc-2) [Saccharomyces cerevisiae] PRL1/PRL2-like protein ; (AB004535) PRL1 [Schizosaccharomyces pombe] (AF009418) trichothecene biosynthesis transcription factor [Myrothecium roridum] (Y13700) MEAB protein [Emericella nidulans] (AL023290) putative ATP-dependent RNA helicase [Schizosaccharomyces pombe] (Z99759) hypothetical protein [Schizosaccharomyces pombe] retrovirus-related polypeptide - Arabidopsis thaliana retrotransposon Ta1-3 ; (X13291) polypeptide [Arabidopsis thaliana]
17047	ENU00841	ANI61C9431: 31-51 997..2601	31-51	1563-1593	EST	"c8a01a1.r1, c8a01a1.fl"			247	1E-64		
17048	ENU00842	ANI61C2435: 27-50 2495..888	27-50	1568-1592	EST	"y6e09a1.r1, y6e09a1.fl"			213	8E-64		
17049	ENU00843	ANI61C6294: 23-48 1092..2726	23-48	1581-1615	EST	"r2d07a1.r1, r2d07a1.fl"			58	0.000000		
17050	ENU00844	ANI61C3681: 56-75 2484..2906	56-75	1621-1648	EST	"d3e01a1.r1, d3e01a1.fl"			129	3E-40		
17051	ENU00845	ANI61C1021 42-61 3:146..1781	42-61	1606-1635	EST	"r6e06a1.r1, r6e06a1.fl"			62	0.000000		
17052	ENU00846	ANI61C4412: 22-49 8068..6409	22-49	1604-1639	EST	"k5g08a1.r1, k5g08a1.fl"			226	9E-76		
17053	ENU00847	ANI61C1073 23-42 5:82..1774	23-42	1639-1673	EST	"i3e07a1.r1, i3e07a1.fl"			87	4E-16		
17054	ENU00848	ANI61C385:3 27-49 855..2149	27-49	1663-1691	EST	"i8f02a1.r1, i8f02a1.fl"			516	e-145		
17055	ENU00849	ANI61C6251: 43-62 7770..9499	43-62	1704-1730	EST	"w4h05a1.r1, w4h05a1.fl"			38	0.16		
17056	ENU00850	ANI61C1115 22-44 9:5337..3601	22-44	1697-1716	EST	"k5b02a1.r1, k5b02a1.fl"			35	0.45		
17057	ENU00851	ANI61C9577: 27-46 1769..31	27-46	1703-1723	EST	"h1c03a1.r1, h1c03a1.fl"			153	8E-68		
17058	ENU00852	ANI61C8358: 25-47 2055..294	25-47	1709-1744	EST	"f0e12a1.r1, f0e12a1.fl"			46	6E-13		
17059	ENU00853	ANI61C3679: 22-52 5806..4045	22-52	1709-1741	EST	"g9e10a1.r1, g9e10a1.fl"			156	6E-40		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17060	ENU00854	ANI61C8625: 4677..2877	25-44	1748-1783	EST	"k5e01a1.rl, k5e01a1.fl"			520	0		"(AL035085) t-complex protein 1, alpha subunit homolog; chaperonin family [Schizosaccharomyces pombe]"
17061	ENU00855	ANI61C380:3 55-74	55-74	1860-1887	EST	"g3e05a1.rl, g3e05a1.fl"			64	0.000000		alpha subunit homolog; chaperonin family [Schizosaccharomyces pombe]"
17062	ENU00856	ANI61C9368: 49-68	49-68	1878-1900	EST	"c8g06a1.rl, c8g06a1.fl"			39	0.1		peptidase [Bacillus subtilis]
17063	ENU00857	ANI61C1007: 59-80	59-80	1892-1911	EST	"o0g06a1.rl, o0g06a1.fl"			217	2E-55		(AF1117876) malate dehydrogenase [Vibrio cholerae]
17064	ENU00858	ANI61C8161: 26-52	26-52	1878-1901	EST	"m5b10a1.rl, m5b10a1.fl"			243	3E-63		"Arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) ; (L23430) endo-1,5-alpha-L-arabinase [Aspergillus niger] ; endo-1,5-alpha-L-arabinase [Aspergillus niger]"
17065	ENU00859	ANI61C8056: 22-48	22-48	1913-1940	EST	"k5e03a1.rl, k5e03a1.fl"			153	1E-66		(U38191) protein phosphatase 2A0 B' regulatory subunit beta3 isoform [Oryctolagus cuniculus] ; protein phosphatase 2A:subunit=B'isotype=beta3 [Oryctolagus cuniculus]
17066	ENU00860	ANI61C9304: 43-70	43-70	1972-1995	EST	"w7f03a1.rl, w7f03a1.fl"			50	0.000000		"probable malate dehydrogenase, mitochondrial precursor ; (AF002197) Similar to malate dehydrogenase; coded for by C. elegans cDNA cm7d6; coded for by C. elegans cDNA yk167g11.5; coded for by C. elegans cDNA cm15d12; coded for by C. elegans cDNA yk139h4.5; coded for by C. elegans cDNA yk169h8.5; co..."
17067	ENU00861	ANI61C1065 25-49	25-49	1957-1988	EST	"i0c04a1.rl, i0c04a1.fl"			52	0.00001		probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae]
17068	ENU00862	ANI61C1094 35-54	35-54	2000-2023	EST	"p0h02a1.rl, p0h02a1.fl"			94	3E-18		(AF049236) unknown [Arabidopsis thaliana]
		4:106..2136										MAP-homologous protein 1 ; microtubule-interacting protein MHP1 - yeast (Saccharomyces cerevisiae) ; (Z49317) ORF YJL042w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17069	ENU00863	ANI61C9558: 19..2128	40-59	2085-2107	EST	"g8b01a1.rl, g8b01a1.fl"		64	0.000000	003		prostaglandin G/H synthase 2 precursor (cyclooxygenase -2) (COX-2)
17070	ENU00864	ANI61C5339: 27-54	27-54	2184-2207	EST	"w7h02a1.rl, w7h02a1.fl"		37	0.47			(prostaglandin-endoperoxide synthase 2) (prostaglandin H2 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II) ; (U97696) cyclooxygenase-2 [Oryctolagus cuniculus]
17071	ENU00865	ANI61C1097 4:6218..5884	22-54	2211-2236	EST	"r4c11a1.rl, r4c11a1.fl"		35	1.8			(M88172) ORF2 [Saccharomyces cerevisiae]
17072	ENU00866	ANI61C5266: 22-54	22-54	2268-2295	EST	"i3a02a1.rl, i3a02a1.fl"		674	0			(M16724) Ig H-chain V-region [Mus musculus]
17073	ENU00867	ANI61C4810: 35..2379	56-75	2323-2358	EST	"c8g07a1.rl, c8g07a1.fl"		478	e-134			phosphoenolpyruvate carboxykinase [ATP] ; (U88575)
17074	ENU00868	ANI61C2582: 2273..4664	47-67	2362-2395	EST	"i7b04a1.rl, i7b04a1.fl"		869	0			phosphoenolpyruvate carboxykinase [Kluveromyces fragilis]
17075	ENU00869	ANI61C2959: 38-55	38-55	2464-2485	EST	"f2f10a1.rl, f2f10a1.fl"		94	5E-18			PHO85 protein - yeast (Saccharomyces cerevisiae) ; (U43503) L-ph16p [Saccharomyces cerevisiae]
17076	ENU00870	ANI61C2609: 45-64	45-64	2647-2677	EST	"y4h10a1.rl, y4h10a1.fl"		39	0.11			probable ATP-dependent transporter YER036C ; hypothetical protein YER036c - yeast (Saccharomyces cerevisiae) ; (U18796) Yer036cp [Saccharomyces cerevisiae]
17077	ENU00871	ANI61C8923: 31-55	31-55	2778-2813	EST	"v7h12a1.rl, v7h12a1.fl"		95	2E-18			"ribosome receptor, 180k - dog ; (X87224) ribosome receptor [Canis familiaris]"
17078	ENU00872	ANI61C5853: 22-45	22-45	153-180	EST	"c9g08a1.rl, c9g08a1.fl"		749	36	0.06		zinc finger protein MSN2 (multicopy suppressor of SNF1 protein 2) ; finger protein MSN2 - yeast (Saccharomyces cerevisiae) ; (L08838) zinc finger protein [Saccharomyces cerevisiae] ; (Z48502) Msn2p [Saccharomyces cerevisiae]
17079	ENU00873	ANI61C4443: 22-43	22-43	749-771	EST	"h4e12a1.rl, h4e12a1.fl"		1069				(Y09899) hypothetical protein [Calothrix viguieri]
		1..1009										(X60288) medium chains of clathrin associated protein complex [Saccharomyces cerevisiae]

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17080	ENU00874	ANI61C2796: 112-131 1099..555	112-131	477-496	EST	"m8c12a1.rl, m8e12a1.fl"		1371	60	0.000000 01			Molybdopterin biosynthesis MOEA protein; (X99625) moeA [Synecococcus sp.]
17081	ENU00875	ANI61C9928: 22-47 968..780	22-47	173-198	EST	"e9c10a1.rl, e9c10a1.fl"		694	56	0.000000 07			(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
17082	ENU00876	ANI61C7486: 3341..3090			EST	"b0f07a1.rl, b0f07a1.fl"		902	148	2E-35			cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR); L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala); (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala]
17083	ENU00877	ANI61C5317: 3198..2946			EST	"g7a10a1.rl, g7a10a1.fl"		1140	39	0.008			"(AF106583) contains similarity to electron transfer flavoprotein beta (pfam: PF01012, Score=278.7, E=7.6e-80, N=1) [Caenorhabditis elegans]"
17084	ENU00878	ANI61C4978: 4589..3141	22-47	808-829	EST	"o0b05a1.rl, o0b05a1.fl"		2014	33	3.1			(AE001428) predicted integral membrane protein [Plasmodium falciparum]
17085	ENU00879	ANI61C4126: 24-43 1849..3657	24-43	801-828	EST	"n3f03a1.rl, n3f03a1.fl"		2230	284	5E-76			Plasma membrane ATPase (proton pump); (L07305) ATPase [Ajeilomyces capsulatus]; H ATPase [Ajeilomyces capsulatus]
17086	ENU00880	ANI61C6585: 187..1301	22-48	802-829	EST	"y6c06a1.rl, y6c06a1.fl"		2321	213	1E-62			40S ribosomal protein SA homolog (ribosome-associated protein 1); (U36470) putative ribosome-associated protein [Neurospora crassa]
17087	ENU00881	ANI61C2344: 2313..1554	30-49	716-739	EST	"r5d10a1.rl, r5d10a1.fl"		5376	42	0.004			(AL023706) small nuclear ribonucleoprotein [Schizosaccharomyces pombe]
17088	ENU00882	ANI61C7644: 671..1661	22-45	716-740	EST	"g4a08a1.rl, g4a08a1.fl"		2375	34	1			(AF053614) dorsal B [Drosophila melanogaster]
17089	ENU00883	ANI61C7757: 875..1999	33-54	631-658	EST	"i0e12a1.rl, i0e12a1.fl"		3986	55	0.000000 5			(Z98269) EG:87B1.6 [Drosophila melanogaster]
17090	ENU00884	ANI61C3006: 472..132	31-48	459-479	EST	"t2h02a1.rl, t2h02a1.fl"		1218	36	0.23			(L16975) alpha-acetolactate synthase [Lactococcus lactis]
17091	ENU00885	ANI61C8082: 968..2224	29-50	807-829	EST	"w4h08a1.rl, w4h08a1.fl"		2888	89	5E-17			(AJ001726) complex I intermediate associated protein CIA35 [Neurospora crassa]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17092	ENU00886	ANI61C9138: 1.403	192-215	355-382	EST	"z5g05al.rl, z5g05al.fl"		1434	31	3.3		TANKYRase; (AF082556) TRF1-interacting ankyrin-related ADP-ribose polymerase [Homo sapiens]
17093	ENU00887	ANI61C1062	46-66	779-803	EST	"g6c02al.rl, g6c02al.fl"		1671				genome polyprotein [contains: coat proteins VP1 TO VP4; core proteins P2A TO P2C; probable proteins P3A TO P3C; RNA-directed RNA polymerase P3D]; genome polyprotein - simian hepatitis A virus (strain AGM-27) ; (D00924)
17094	ENU00888	ANI61C5632: 5336..5794	22-44	366-385	EST	"t2a07al.rl, t2a07al.fl"		1840	34	0.9		polyprotein [Simian hepatitis A virus] hypothetical protein UL42 ; hypothetical protein UL42 - human cytomegalovirus (strain AD169) ; (X17403) HCMVUL42 [human herpesvirus 5]
17095	ENU00889	ANI61C1047 4:1681..1526			EST	"x7c05al.rl, x7c05al.fl"		622	30	2.7		(AB011182) KIAA0610 protein [Homo sapiens]
17096	ENU00890	ANI61C4449: 55-73 795..153	55-73	595-622	EST	"j4e03al.rl, j4e03al.fl"		1476	36	0.19		(L35053) homolog of retroviral gag genes; putative [Magnaporthe grisea]
17097	ENU00891	ANI61C1232: 12838..7822	26-45	803-823	EST	"y3fl1al.rl, y3fl1al.fl"		1921	47	0.0002		"mucin 2 precursor, intestinal - human (fragments) "
17098	ENU00892	ANI61C9271: 750..2417	27-48	778-805	EST	"v7al1al.rl, v7al1al.fl"		1510	36	0.35		"leucyl-TRNA synthetase, cytoplasmic (leucine--TRNA ligase) (LEURS) ; leucine--tRNA ligase (EC 6.1.1.4), cytosolic - Neurospora crassa ; (M30473) leucyl-tRNA synthetase [Neurospora crassa] "
17099	ENU00893	ANI61C9708: 2350..2833	22-49	453-479	EST	"o6a04al.rl, o6a04al.fl"		3942	32	2.7		(U30905) mod2.2 [Drosophila melanogaster]
17100	ENU00894	ANI61C1372: 2240..2084	63-82	379-406	EST	"f0h08al.rl, f0h08al.fl"		586	31	7.8		(AB010636) SADH [Candida parapsilosis]
17101	ENU00895	ANI61C440:1 404..1883	28-55	458-479	EST	"y6a07al.rl, y6a07al.fl"		1697	31	4.6		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvtg	Description
17102	ENU00896	ANI61C7521: 1..266	42-61	184-203	EST	"o8e01a1.r1, o8e01a1.fl"		947	32	0.89			cytochrome C oxidase polypeptide VI precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain VI precursor - yeast (Saccharomyces cerevisiae) ; (M10138) cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] ; (U00062) Cox6p: cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] beta-hexosaminidase precursor (N-acetyl-beta-glucosaminidase) (beta-GLCNACase) (beta-N-acetylhexosaminidase) hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
17103	ENU00897	ANI61C7493: 839..1	25-44	793-818	EST	"o9a11a1.r1, o9a11a1.fl"		1362	273	1E-72			histone H1 ; histone H1 - yeast (Saccharomyces cerevisiae) ; (U43703) Lpi17p [Saccharomyces cerevisiae] "isopenicillin N synthetase (IPNS) ; isopenicillin N synthase (EC 1.-.-.-) - Emericella nidulans ; Chain A, Isopenicillin N Synthase From Aspergillus Nidulans (Manganese Complex) ; Isopenicillin N Synthase From Aspergillus Nidulans (Acv-Fe-Complex) ; Isopenicillin N Synthase From Aspergillus Nidulans (Acv-Fe-Complex) ; (M21882) isopenicillin N synthetase [Emericella nidulans] ; (M18111) isopenicillin N synthetase [Emericella nidulans] ; isopenicillin N synthetase [Emericella nidulans]"
17104	ENU00898	ANI61C1683: 1577..347	22-48	789-816	EST	"l3e10a1.r1, l3e10a1.fl"		1667	123	1E-27			
17105	ENU00899	ANI61C4586: 1161..1	22-46	726-753	EST	"x7d08a1.r1, x7d08a1.fl"		4544	46	0.0002			
17106	ENU00900	ANI61C291:2 918..3081	22-49	434-461	EST	"q0c04a1.r1, q0c04a1.fl"		602	240	4E-63			
17107	ENU00901	ANI61C3610: 1..106			EST	"k0e09a1.r1, k0e09a1.fl"		388					

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17108	ENU00902	ANI61C7523: 2791..2602	22-48	454-478	EST	"a0g08a1.r1, a0g08a1.fl"		718	59	0.000000			(U40945) coded for by C. elegans cDNA yk74b9.3; coded for by C. elegans cDNA yk74b9.5; similar to repeat of calcium channel alpha subunits; similar to tetracycline resistance protein; similar to hypothetical protein in HSP30-PMP1 region (SP... (Z68115) F19H6.3 [Caenorhabditis elegans]
17109	ENU00903	ANI61C297:7 304..8452	28-55	772-798	EST	"m5c12a1.r1, m5c12a1.fl"		1268	34	1.4			Versicolorin reductase ; (U34740) putative ketoreductase [Emericella nidulans]
17110	ENU00904	ANI61C1233: 938..1276	71-95	421-448	EST	"g8d01a1.r1, g8d01a1.fl"		1164					Diphthine synthase (diphthamide biosynthesis methyltransferase) ; methyltransferase DPH5 - yeast (Saccharomyces cerevisiae) ; (M83375) DPH5 [Saccharomyces cerevisiae] ; (U17246) Dph5p: diphthine synthase [Saccharomyces cerevisiae] (U80437) coded for by C. elegans cDNA yk126f11.5 [Caenorhabditis elegans]
17111	ENU00905	ANI61S1679: 1..674	106-127	438-464	EST	"z4b06a1.r1, z4b06a1.fl"		3725	273	1E-72			kinesin-like protein KLPA ; kinesin-related protein KLPA - Emericella nidulans ; (X64603) KLPA [Emericella nidulans]
17112	ENU00906	ANI61C6471: 5890..4840	28-55	786-813	EST	"s9d11a1.r1, s9d11a1.fl"		2414	284	7E-76			(AL023706) apoptosis specific protein homologue [Schizosaccharomyces pombe]
17113	ENU00907	ANI61C4735: 701..1976	24-43	771-790	EST	"t2a06a1.r1, t2a06a1.fl"		2094	32	5.3			(AL049522) coiled coil protein [Schizosaccharomyces pombe]
17114	ENU00908	ANI61C5578: 1582..1058	32-51	482-504	EST	"q0b12a1.r1, q0b12a1.fl"		1506	116	8E-26			putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
17115	ENU00909	ANI61C8897: 1..171			EST	"y6c03a1.r1, y6c03a1.fl"		508					(AJ010262) MT5-MMP protein [Mus musculus]
17116	ENU00910	ANI61C7525: 8274..8659	48-67	452-479	EST	"z7c06a1.r1, z7c06a1.fl"		918	42	0.003			
17117	ENU00911	ANI61C1106 7:1012..1146	22-45	431-458	EST	"j4a04a1.r1, j4a04a1.fl"		536	33	1.6			
17118	ENU00912	ANI61C4849: 611..413	38-57	436-461	EST	"g0f03a1.r1, g0f03a1.fl"		754	57	0.000000			
17119	ENU00913	ANI61C7771: 4777..3187	26-47	787-814	EST	"g4e02a1.r1, g4e02a1.fl"		2308	37	0.21			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17120	ENU00914	ANI61C1042 9:2617..3123	22-42	455-474	EST	"w7h05a1.r1, w7h05a1.fl"		3172	32	2.7			hydroxyproline-rich glycoprotein - maize; (X63134) hydroxyproline-rich glycoprotein [Zea mays]; Hyp-rich glycoprotein [Zea mays]
17121	ENU00915	ANI61C2120: 1531..1896	78-101	454-479	EST	"r4e04a1.r1, r4e04a1.fl"		1204	41	0.004			hypothetical protein YDR514c - yeast (Saccharomyces cerevisiae); (U33057) Ydr514cp [Saccharomyces cerevisiae]; (U33057) No definition line found [Saccharomyces cerevisiae]
17122	ENU00916	ANI61C3320: 5548..4259	44-63	767-786	EST	"w7g10a1.r1, w7g10a1.fl"		1162	32	4			"alpha-1D adrenergic receptor (alpha 1D-adrenoceptor) (alpha-1A adrenergic receptor); (S80044) alpha 1d-adrenergic receptor [mice, brain, Peptide, 562 aa] [Mus sp.]"
17123	ENU00917	ANI61C8010: 1..1664	22-46	804-827	EST	"a0e06a1.r1, a0e06a1.fl"		764	56	0.000000 4			hypothetical protein YLR019w - yeast (Saccharomyces cerevisiae); (Z73191) ORF YLR019w [Saccharomyces cerevisiae]
17124	ENU00918	ANI61C9711: 1514..259			EST	"g2c02a1.r1, g2c02a1.fl"		2428	143	1E-33			(AF080599) Medusa [Emericella nidulans]
17125	ENU00919	ANI61C2577: 1..976	23-42	802-829	EST	"n0f06a1.r1, n0f06a1.fl"		1614	102	2E-35			proteasome component C1 (macropain subunit C1) (proteinase YSCC subunit 1) (multicatalytic endopeptidase complex subunit C1); multicatalytic endopeptidase complex (EC 3.4.99.46) chain YC1 - yeast (Saccharomyces cerevisiae); (M55436) yeast proteasome subunit YC1 [Saccharomyces cerevisiae]; (Z75270) ORF YOR362c [Saccharomyces cerevisiae]
17126	ENU00920	ANI61C8013: 1140..1	117-136	712-730	EST	"m7a01a1.r1, m7a01a1.fl"		2952	34	1.8			"malate oxidoreductase (NAD), mitochondrial 65 KD isoform precursor (malic enzyme) (ME) (NAD-dependent malic enzyme) (NAD-ME); malate dehydrogenase (decarboxylating) (EC 1.1.1.39) precursor, mitochondrial - prince's feather; (U01162) C4 photosynthetic NAD-dependent malic enzyme subunit alpha precursor [Amaranthus hypochondriacus]"

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17127	ENU00921	ANI61C8963: 5134..4659	22-46	339-362	EST	"m8a06a1.r1, m8a06a1.fl"		1751	34	0.89			Centromere protein C (CENP-C) (centromere autoantigen C); centromere protein C - human; (M95724) centromere autoantigen C [Homo sapiens]
17128	ENU00922	ANI61C7935: 2554..2136	60-87	452-479	EST	"z1c07a1.r1, z1c07a1.fl"		2524	121	3E-27			(U75874) sconCp [Emericella nidulans]
17129	ENU00923	ANI61C2272: 1615..1	43-66	715-742	EST	"t2f05a1.r1, t2f05a1.fl"		1880	116	1E-25			Ribose-phosphate pyrophosphokinase (phosphoribosyl pyrophosphate synthetase 1); ribose-phosphate pyrophosphokinase (EC 2.7.6.1) PRPS1 - yeast (Saccharomyces cerevisiae); (X70069) ribose-phosphate pyrophosphokinase [Saccharomyces cerevisiae]; (L04130) phosphoribosylpyrophosphate synthetase [Saccharomyces cerevisiae]; (X74151) orf11; homologous to human ribose-phosphate PP-kinase [Saccharomyces cerevisiae]; (Z28181) ORF YKL181w [Saccharomyces cerevisiae]
17130	ENU00924	ANI61C7364: 1423..2469	71-90	806-827	EST	"w7g01a1.r1, w7g01a1.fl"		1444	52	0.000006			(AC004697) unknown protein [Arabidopsis thaliana]
17131	ENU00925	ANI61C9397: 1765..1376	22-41	452-479	EST	"k0g08a1.r1, k0g08a1.fl"		746	31	7.8			(AF093543) transforming acidic coiled-coil containing protein 3 [Homo sapiens]
17132	ENU00926	ANI61C192:1 574..1	34-53	803-822	EST	"i8f03a1.r1, i8f03a1.fl"		985	51	0.00001			(Z98944) beta transducin [Schizosaccharomyces pombe]
17133	ENU00927	ANI61C1107 3:5748..4158	22-42	810-829	EST	"m2b12a1.r1, m2b12a1.fl"		2682	41	0.011			(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
17134	ENU00928	ANI61C1017 9:179..713	26-45	490-508	EST	"x7g07a1.r1, x7g07a1.fl"		1800	52	0.000002			hypothetical 63.5 KD protein ZK353.1 in chromosome III; ZK353.1 protein - Caenorhabditis elegans; (L15313) putative [Caenorhabditis elegans] (D00570) open reading frame (251 AA) [Mus musculus]
17135	ENU00929	ANI61C1048 4:6220..6375	37-56	457-479	EST	"w6d02a1.r1, w6d02a1.fl"		584	35	0.4			(AB011003) UDP-N-acetylglucosamine pyrophosphorylase [Candida albicans]
17136	ENU00930	ANI61C7526: 585..823	61-80	454-479	EST	"c9f03a1.r1, c9f03a1.fl"		960	100	1E-20			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17137	ENU00931	ANI61C1132: 7881..8283			EST	"e9f09a1.rl, e9f09a1.fl"		1286	35	0.31			Immediate-early protein IE180 ; (X15120) immediate-early protein (AA 1-1460) [Pseudorabies virus]
17138	ENU00932	ANI61C1059 2:3950..4954	23-42	809-829	EST	"c5g03a1.rl, c5g03a1.fl"		1326	52	0.000006			CDC2+/CDC28-related protein kinase R2 ; protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog - rice ; (X58194) cdc2+/CDC28-related protein kinase [Oryza sativa]
17139	ENU00933	ANI61C6527: 1..736	22-41	809-828	EST	"h1h05a1.rl, h1h05a1.fl"		1667	128	4E-29			(AJ001259) NIPSNAP2 protein [Homo sapiens]
17140	ENU00934	ANI61C7672: 34-53 4030..5198	34-53	807-829	EST	"m8b06a1.rl, m8b06a1.fl"		1514	76	3E-13			(AL024499) cDNA EST EMBL:C08541 comes from this gene; cDNA EST EMBL:C07241 comes from this gene [Caenorhabditis elegans]
17141	ENU00935	ANI61C2286: 1..736	31-50	685-712	EST	"c4a07a1.rl, c4a07a1.fl"		779	57	1E-11			SNF2 protein homolog YBR245c - yeast (Saccharomyces cerevisiae) (D14072) Homoserine kinase [Methylobacillus glycogenes]
17142	ENU00936	ANI61C1137 2:314..1056	22-41	658-682	EST	"s8a02a1.rl, s8a02a1.fl"		2469	32	3.4			(AF016419) contains similarity to the class II chitinases [Caenorhabditis elegans]
17143	ENU00937	ANI61C1140 4:3102..1439	34-56	805-829	EST	"r5a03a1.rl, r5a03a1.fl"		2678	39	0.031			
17144	ENU00938	ANI61C7672: 5304..5172			EST	"z4h12a1.rl, z4h12a1.fl"		478					"glyceraldehyde 3-phosphate dehydrogenase (GAPDH) ; glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - yeast (Zygosaccharomyces rouxii) ; (D00134) glyceraldehyde-3-phosphate dehydrogenase [Zygosaccharomyces rouxii] ; dehydrogenase, glyceraldehydephosphate [Zygosaccharomyces rouxii]"
17145	ENU00939	ANI61C1140 64-83 4:4368..3759	64-83	562-589	EST	"c5d10a1.rl, c5d10a1.fl"		2348	127	8E-29			(AC002387) putative reverse transcriptase [Arabidopsis thaliana] probable membrane protein YLR251w - yeast (Saccharomyces cerevisiae) ; (U20865) Ylr251wp [Saccharomyces cerevisiae]
17146	ENU00940	ANI61C7366: 1228..778	29-56	448-475	EST	"t2g04a1.rl, t2g04a1.fl"		1578	34	0.69			
17147	ENU00941	ANI61C528:2 305..3935	59-78	788-807	EST	"s8c04a1.rl, s8c04a1.fl"		2977	37	0.21			

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17148	ENU00942	ANI61C1140 4:499..1235	43-62	672-699	EST	"g2a10a1.r1, g2a10a1.fl"		1080	44	0.000000			Response regulator MCS4 (mitotic catastrophe suppressor 4); (Y111927) Mcs4 protein [Schizosaccharomyces pombe]; (AF004694) Mcs4 [Schizosaccharomyces pombe]; (AL033388) response regulator mcs4 [Schizosaccharomyces pombe] Amidophosphoribosyltransferase (glutamine phosphoribosylpyrophosphate amidotransferase) (ATase); (U32992) glutamine phosphoribosylpyrophosphate amidotransferase [Saccharomyces kluyveri]
17149	ENU00943	ANI61C8832: 1..2242	30-49	805-829	EST	"r5c10a1.r1, r5c10a1.fl"		1177	136	6E-51			"high molecular mass early light-inducible protein precursor (ELIP) (clone HV58); early light-induced protein, high molecular weight, precursor (clone HV58) - barley chloroplast; (X15693) precursor peptide (AA -31 to 200) [Hordeum vulgare]"
17150	ENU00944	ANI61C2967: 2113..2695	22-48	459-485	EST	"z1g08a1.r1, z1g08a1.fl"		2132	36	0.22			phosphoribosylaminoimidazolecarboxamide formyltransferase 2 (aicar transformylase) / IMP cyclohydrolase (inosinase) (IMP synthetase) (ATIC); hypothetical protein YMR120c - yeast (Saccharomyces cerevisiae); (Z49273) unknown [Saccharomyces cerevisiae]
17151	ENU00945	ANI61C1049 5:2235..2509	30-49	456-479	EST	"t2g09a1.r1, t2g09a1.fl"		634	67	3E-24			Fibrillarlin (nucleolar protein 1); nucleolar protein NOP1 - yeast (Saccharomyces cerevisiae); (J05230) fibrillarlin [Saccharomyces cerevisiae]; (Z48432) nucleolar protein NOP1 (J05230) [Saccharomyces cerevisiae]; (Z74062) ORF YDL014w [Saccharomyces cerevisiae]
17152	ENU00946	ANI61C6247: 1430..2985	50-69	803-829	EST	"g6e01a1.r1, g6e01a1.fl"		1061	279	2E-74			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17153	ENU00947	ANI61C4858: 2982..1883	24-44	799-826	EST	"d5b09a1.r1, d5b09a1.fl"		2712	60	7E-13			3-oxoacyl-[acyl-carrier protein] reductase (3-ketoacyl-acyl carrier protein reductase); (Z99112) 3-ketoacyl-acyl carrier protein reductase [Bacillus subtilis]
17154	ENU00948	ANI61C2136: 102-127 1..538	102-127	455-482	EST	"13b08a1.r1, 13b08a1.fl"		1258	31	5			(Y14446) thylacine 1 [Xenopus laevis]
17155	ENU00949	ANI61C465:7 090..7491	33-51	425-452	EST	"q0b02a1.r1, q0b02a1.fl"		1258	120	5E-27			probable succinyl-CoA:3-ketoacid-coenzyme A transferase precursor (3-oxoacid CoA-transferase); (Z48178) similar to 3-oxoacid CoA-transferase; cDNA EST EMBL:Z14816 comes from this gene; cDNA EST EMBL:Z14946 comes from this gene; cDNA EST EMBL:Z14946 comes from this gene; cDNA EST EMBL:D69746 comes from this gene; cDNA EST yk219b6.3 comes from this gene; cDNA EST y... (X06830) uracil permease (AA 1-633) [Saccharomyces cerevisiae] (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] (L16844) yps-3 [Histoplasma capsulatum] (AL022121) hypothetical protein Rv3677c [Mycobacterium tuberculosis] immediate-early protein pip92 - mouse; (M59821) growth factor-inducible protein [Mus musculus]; (L26490) growth factor inducible immediate early protein [Mus musculus] 3-isopropylmalate dehydrogenase (beta-IPM dehydrogenase) (IMDH) (3-IPM-DH); probable 3-isopropylmalate dehydrogenase (EC 1.1.1.85) - Lactococcus lactis subsp. lactis; (U92974) LeuB [Lactococcus lactis] (L42348) HOL1 [Saccharomyces cerevisiae]
17156	ENU00950	ANI61C3864: 1..297			EST	"t2f07a1.r1, t2f07a1.fl"		1146	29	7.5			
17157	ENU00951	ANI61C4216: 362..635	22-48	440-467	EST	"c1f08a1.r1, c1f08a1.fl"		1018	33	1.2			
17158	ENU00952	ANI61C919:2 555..1951	43-70	562-584	EST	"i8h09a1.r1, i8h09a1.fl"		1074	146	2E-34			
17159	ENU00953	ANI61C1708: 3798..3145	204-223	590-609	EST	"k0e02a1.r1, k0e02a1.fl"		960	45	0.0004			
17160	ENU00954	ANI61C8676: 1123..1195	67-91	452-479	EST	"q0h01a1.r1, q0h01a1.fl"		232	32	3.5			
17161	ENU00955	ANI61C1709: 2473..1562	51-70	806-829	EST	"i7g01a1.r1, i7g01a1.fl"		1540	31	9.1			
17162	ENU00956	ANI61C1311: 836..566			EST	"q0a06a1.r1, q0a06a1.fl"		894	39	0.005			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17163	ENU00957	ANI61C6704: 2767..2307	22-44	444-469	EST	"c6a05a1.rl, c6a05a1.fl"		1200	57	0.000000			"STE50 protein ; STE50 protein - yeast (Saccharomyces cerevisiae) ; (Z111116) STE50 protein [Saccharomyces cerevisiae] ; (X59720) YCL032w, len:346 [Saccharomyces cerevisiae] " (AL031350) putative secreted protein [Streptomyces coelicolor] (U34998) Rad9 [Coprinus cinereus]
17164	ENU00958	ANI61C1419: 713..267	23-46	455-478	EST	"d5e02a1.rl, d5e02a1.fl"		787	34	0.69			troponin:isotype=T [Oryctolagus cuniculus] (Z96072) hypothetical protein Rv2704 [Mycobacterium tuberculosis] (AL049485) probable acetyl coA acetyltransferase (thiolase) [Streptomyces coelicolor] (AC005314) dnaJ-like protein [Arabidopsis thaliana] hypothetical 27.9 KD protein in TRER-ACO intergenic region ; (D83967) YfjR [Bacillus subtilis] ; (Z99108) similar to 3-hydroxyisobutyrate dehydrogenase [Bacillus subtilis] ; (D78509) YfjR [Bacillus subtilis]
17165	ENU00959	ANI61C1099: 3348..2260			EST	"w7a08a1.rl, w7a08a1.fl"		1161	78	6E-14			
17166	ENU00960	ANI61C4365: 8..835	91-108	705-727	EST	"m8d07a1.rl, m8d07a1.fl"		1108	34	1.7			
17167	ENU00961	ANI61C9733: 998..2932	27-46	774-798	EST	"m8h06a1.rl, m8h06a1.fl"		2491	54	0.000001			
17168	ENU00962	ANI61C1141 0:1441..2506			EST	"t2e06a1.rl, t2e06a1.fl"		2520	32	4			
17169	ENU00963	ANI61C7677: 1..1476			EST	"i2f01a1.rl, i2f01a1.fl"		2444	36	0.35			
17170	ENU00964	ANI61C3972: 3664..2542	33-50	809-829	EST	"e4a03a1.rl, e4a03a1.fl"		2818	76	3E-13			
17171	ENU00965	ANI61C7377: 774..693			EST	"c5b04a1.rl, c5b04a1.fl"		314					
17172	ENU00966	ANI61C1253: 2367..2856	22-45	443-462	EST	"n3d08a1.rl, n3d08a1.fl"		1312	95	3E-19			(AF000381) non-functional folate binding protein [Homo sapiens] (AB007867) KIAA0407 [Homo sapiens]
17173	ENU00967	ANI61C1253: 3473..4542	27-46	789-806	EST	"y6f01a1.rl, y6f01a1.fl"		1530	33	2.3			Folate receptor beta precursor (FR-beta) (folate receptor 2) (folate-binding protein 2) ; folate-binding protein 2 precursor - mouse ; (M64817) folate-binding protein 2 [Mus musculus] (AE001585) Polymorphic Outer Membrane Protein G Family [Chlamydia pneumoniae] (U90722) iron superoxide dismutase A [Trypanosoma cruzi]
17174	ENU00968	ANI61C1065 7:2436..4372	22-49	800-819	EST	"g5g02a1.rl, g5g02a1.fl"		1414	34	1.8			
17175	ENU00969	ANI61C2979: 1..128			EST	"f0g10a1.rl, f0g10a1.fl"		508	29	4.8			
17176	ENU00970	ANI61C8041: 1..2081	22-45	809-829	EST	"o8h08a1.rl, o8h08a1.fl"		2584	32	6.9			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17177	ENU00971	ANI61C754;1 714..2949	32-51	789-809	EST	"w8e12a1.rl, w8e12a1.fl"		1788	216	1E-55		(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana] chorion protein B11 [Bombyx mori]
17178	ENU00972	ANI61C7686; 376..186			EST	"w6g12a1.rl, w6g12a1.fl"		722	37	0.1		(D87071) similar to C.elegans protein encoded in cosmid T20D3 (Z68220). [Homo sapiens]
17179	ENU00973	ANI61C1253; 44-63 1736..2028	44-63	439-458	EST	"c4d11a1.rl, c4d11a1.fl"		900	32	2		probable membrane protein YLR409c - yeast (Saccharomyces cerevisiae); (U19729) Ylr409cp [Saccharomyces cerevisiae]
17180	ENU00974	ANI61C9961; 22-42 3208..1496	22-42	805-829	EST	"o8e11a1.rl, o8e11a1.fl"		1770	93	3E-41		(AP000003) 323aa long hypothetical oligopeptide transport ATP-binding protein APPF [Pyrococcus horikoshii]
17181	ENU00975	ANI61C538;5 861..4655	50-72	802-829	EST	"j7e12a1.rl, j7e12a1.fl"		1070	31	9.1		PHO85 protein - yeast (Saccharomyces cerevisiae); (U43503) Lph16p [Saccharomyces cerevisiae]
17182	ENU00976	ANI61C8580; 22-40 10160..10494	22-40	456-475	EST	"t2e04a1.rl, t2e04a1.fl"		1244	45	0.0005		[AJ132944] G protein alpha subunit [Sclerotinia sclerotiorum]
17183	ENU00977	ANI61C3642; 333..2055			EST	"x7h06a1.rl, x7h06a1.fl"		2534	64	3E-22		"iron(III) dicitrate transport protein fecB precursor, periplasmic - Escherichia coli; (M26397) fecB [Escherichia coli]"
17184	ENU00978	ANI61C1253; 22-48 4323..4874	22-48	493-512	EST	"r8a05a1.rl, r8a05a1.fl"		799	32	3		(U42580) a197R [Paramecium bursaria Chlorella virus 1]
17185	ENU00979	ANI61C1044 39-66 5:2744..2913	39-66	446-472	EST	"g9g07a1.rl, g9g07a1.fl"		556	32	2		melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium; (D83643) polyketide synthase [Colletotrichum lagenarium] (Z98209) hypothetical protein Rv2735c [Mycobacterium tuberculosis]
17186	ENU00980	ANI61C4924; 36-63 2118..1286	36-63	791-812	EST	"g7e09a1.rl, g7e09a1.fl"		988	136	3E-31		(X94355) D17L [Cowpox virus]; (Y11842) C17L [Cowpox virus] (AF000381) non-functional folate binding protein [Homo sapiens]
17187	ENU00981	ANI61C7851; 23-41 2891..347	23-41	785-804	EST	"h0g09a1.rl, h0g09a1.fl"		1996	34	1.4		
17188	ENU00982	ANI61C5337; 22-49 2750..1911	22-49	745-770	EST	"j7b07a1.rl, j7b07a1.fl"		1386	31	8.9		
17189	ENU00983	ANI61C1253; 54-75 2871..3085	54-75	414-433	EST	"w9b12a1.rl, w9b12a1.fl"		828	122	2E-27		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17190	ENU00984	ANI61C7436: 3010..3766	22-47	662-689	EST	"n0a07a1.r1, n0a07a1.fl"		2622	39	0.027			mitochondrial import receptor subunit TOM40 (MOM38 protein) (transLOC of outer membrane 40 KD subunit) ; mitochondrial import receptor MOM38 - Neurospora crassa ; (X56883) outer membrane protein [Neurospora crassa] ; outer membrane protein MOM38 [Neurospora crassa] "Potassium transport protein, high-affinity ; potassium transport protein TRK1, high-affinity - yeast (Saccharomyces cerevisiae) ; (M21328) potassium transporter (put.) ; putative [Saccharomyces cerevisiae] ; (Z49404) ORF YJL129c [Saccharomyces cerevisiae]"
17191	ENU00985	ANI61C3176: 767..1801	22-46	805-829	EST	"x9g10a1.r1, x9g10a1.fl"		1644	35	0.61			probable peroxisomal membrane protein PMP20 (allergen ASP F 3) ; (U58050) peroxisomal-like protein [Aspergillus fumigatus] hypothetical 21.6 KD protein CY251.07 ; (Z74410) hypothetical protein Rv0089 [Mycobacterium tuberculosis] (AF006829) slow myosin heavy chain 2 [Coturnix coturnix]
17192	ENU00986	ANI61C5927: 398..139	51-71	417-443	EST	"o0h05a1.r1, o0h05a1.fl"		998	51	0.000006			(U19615) LET 858 [Caenorhabditis elegans] ; (Z81525) cDNA EST yk282b7.5 comes from this gene; cDNA EST EMBL:D28011 comes from this gene; cDNA EST EMBL:D28010 comes from this gene; cDNA EST EMBL:D33543 comes from this gene; cDNA EST EMBL:D36381 comes from this gene; cDNA ... glutamine synthetase (glutamate-- ammonia ligase) ; (L78067) glutamine synthetase [Glomerella cingulata]
17193	ENU00987	ANI61C2449: 514..335	22-48	416-443	EST	"z1c10a1.r1, z1c10a1.fl"		666	41	0.005			
17194	ENU00988	ANI61C1019 22-48	176-196	EST	"m5e01a1.r1, m5e01a1.fl"		1000	29	5.3				
17195	ENU00989	ANI61C5024: 0:1..252		EST	"o0b12a1.r1, o0b12a1.fl"		348						
17196	ENU00990	ANI61C1021 1..88 7:1032..1784	22-46	705-732	EST	"d5h11a1.r1, d5h11a1.fl"		1270	39	0.046			
17197	ENU00991	ANI61C1005: 351..885	23-42	420-444	EST	"l3c09a1.r1, l3c09a1.fl"		1536	130	6E-30			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17198	ENU00992	ANI61C2206: 2704..3989	22-48	729-749	EST	"y8c08a1.r1, y8c08a1.fl"		2464	146	1E-34			putative nicotinate-nucleotide pyrophosphorylase (carboxylating) (quinolinate phosphoribosyltransferase (decarboxylating)) (QAPRTase) ; hypothetical protein YFR047c - yeast (Saccharomyces cerevisiae) ; (D50617) YFR047C [Saccharomyces cerevisiae] ; (D44597) unknown [Saccharomyces cerevisiae]
17199	ENU00993	ANI61C3359: 404..571	109-131	459-479	EST	"j0a12a1.r1, j0a12a1.fl"		626	31	4.6			(U60315) MC157R [Molluscum contagiosum virus subtype 1]
17200	ENU00994	ANI61C7960: 6227..6123			EST	"w9g10a1.r1, w9g10a1.fl"		378					
17201	ENU00995	ANI61C7447: 4468..4870	22-49	446-467	EST	"j9e03a1.r1, j9e03a1.fl"		1296	31	4.6			Envelope polypeptide GP160 precursor (contains: GP120 and GP41) ; (M29975) env polypeptide [Simian immunodeficiency virus]
17202	ENU00996	ANI61C1044 6:195..405	142-166	343-370	EST	"g2b12a1.r1, g2b12a1.fl"		768	123	4E-28			pyruvate decarboxylase ; (U73194) pyruvate decarboxylase [Emmericella nidulans]
17203	ENU00997	ANI61C1650: 389..165			EST	"k0g02a1.r1, k0g02a1.fl"		858					
17204	ENU00998	ANI61C4762: 1571..931	55-74	597-620	EST	"g3b05a1.r1, g3b05a1.fl"		1282					
17205	ENU00999	ANI61C379:3 906..5711	22-48	763-790	EST	"g5a12a1.r1, g5a12a1.fl"		2452	41	0.011			PQ-rich protein - human ; (Z50194) PQ-rich protein [Homo sapiens]
17206	ENU01000	ANI61C1160: 9772..7996	22-45	807-829	EST	"m2e11a1.r1, m2e11a1.fl"		3110					
17207	ENU01001	ANI61C8118: 1281..1515	23-43	454-479	EST	"o8g10a1.r1, o8g10a1.fl"		898	32	3.5			hypothetical 52.0 KD protein in RPL17A-BOB1 intergenic region ; hypothetical protein YBL086c - yeast (Saccharomyces cerevisiae) ; (X79489) D-466 protein [Saccharomyces cerevisiae] ; (Z35847) ORF YBL086c [Saccharomyces cerevisiae]
17208	ENU01002	ANI61C4702: 988..662	37-56	453-479	EST	"q0b06a1.r1, q0b06a1.fl"		1112					

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17209	ENU01003	ANI61C9802: 3344..2176	67-86	799-826	EST	"w6b07a1.r1, w6b07a1.fl"		1844	115	4E-25			hypothetical 62.4 KD protein in GLS1-hypothetical intergenic region precursor; KAP95 intergenic region precursor; probable membrane protein YLR343w - yeast (Saccharomyces cerevisiae); (U19028) Ylr343wp [Saccharomyces cerevisiae]
17210	ENU01004	ANI61C8507: 22-45	22-45	805-829	EST	"y8a02a1.r1, y8a02a1.fl"		2922	36	0.35			(AF038388) actin-filament binding protein Frabin [Rattus norvegicus]
17211	ENU01005	ANI61C1110 2551..504	22-47	747-774	EST	"c9g10a1.r1, c9g10a1.fl"		1110	108	2E-28			(AB017627) acetyltransferase [Candida albicans]
17212	ENU01006	ANI61C1110 9:1779..969	57-76	522-549	EST	"d5d04a1.r1, d5d04a1.fl"		1892	51	0.000007			"40S ribosomal protein S30; ribosomal protein S30.e, cytosolic - yeast (Saccharomyces cerevisiae); (U48699) Rps30ap [Saccharomyces cerevisiae]; (U48700) yrpS30 [Saccharomyces cerevisiae]; (U17243) L8003.23 gene product [Saccharomyces cerevisiae]; (Z75090) ORF YOR182c [Saccharomyces cerevisiae]; (U83406) Rps30bp [Saccharomyces cerevisiae]; (U83407) Rps30bp [Saccharomyces cerevisiae]"
17213	ENU01007	ANI61C5934: 26..419	115-133	376-398	EST	"c7d03a1.r1, c7d03a1.fl"		1473	33	1.2			Sodium/hydrogen exchanger 4 (NA(+)/H(+) exchanger 4) (NHE-4); Na+/H+-exchanging protein 4 - rat; (M85301) sodium-hydrogen exchange protein-isoform 4 [Rattus norvegicus]
17214	ENU01008	ANI61C2384: 1274..2113	22-47	792-819	EST	"j7d01a1.r1, j7d01a1.fl"		1128					(AB010442) PMR1 [Penicillium digitatum]
17215	ENU01009	ANI61C9175: 2292..4912	22-42	798-825	EST	"q0g01a1.r1, q0g01a1.fl"		1669	254	6E-88			"Insulin-like growth factor binding protein 2 precursor (IGFBP-2) (IBP-2) (IGF-binding protein 2); insulin-like growth factor-binding protein-2 - sheep; (S44612) insulin-like growth factor-binding protein-2, IGFBP-2 [sheep, Peptide, 317 aa] [Ovis aries]"
17216	ENU01010	ANI61C8913: 2865..2634	22-47	434-457	EST	"r4b02a1.r1, r4b02a1.fl"		912	31	6			(M19113) env polypeptide [Rous-associated virus type 1]
17217	ENU01011	ANI61C1052 7:620..1	44-67	500-519	EST	"r1a07a1.r1, r1a07a1.fl"		1744	32	2.7			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17218	ENU01012	ANI61C8273: 5678..6704	38-57	785-812	EST	"g4c02a1.r1, g4c02a1.fl"		2766	234	7E-61			"mitochondrial 60S ribosomal protein L9 precursor (YML9) ; ribosomal protein L3 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X87941) ORF 269 [Saccharomyces cerevisiae] ; (Z73004) ORF YGR220c [Saccharomyces cerevisiae] "
17219	ENU01013	ANI61C2166: 1988..875	24-47	762-785	EST	"m0h08a1.r1, m0h08a1.fl"		1984	164	4E-51			"peptide transporter PTR2-A ; (U01171) similar to S. cerevisiae PTR2 gene, GenBank Accession Number L11994 [Arabidopsis thaliana] "
17220	ENU01014	ANI61C7324: 1345..1	22-47	772-792	EST	"s8h02a1.r1, s8h02a1.fl"		1576					(AB008791) Phosphoinositide 3-Kinase-C2gamma [Mus musculus]
17221	ENU01015	ANI61C4383: 1070..1715	22-45	587-614	EST	"x9f09a1.r1, x9f09a1.fl"		1518					TTP1 protein ; TTP1 protein - yeast (Saccharomyces cerevisiae) ; (Z35884) ORF YBR015c [Saccharomyces cerevisiae]
17222	ENU01016	ANI61C4007: 126..2015	29-48	802-829	EST	"g7a12a1.r1, g7a12a1.fl"		1528	32	6.9			
17223	ENU01017	ANI61C9760: 44-63 5294..4181	44-63	807-829	EST	"c5a08a1.r1, c5a08a1.fl"		1588	81	9E-15			
17224	ENU01018	ANI61C4167: 1081..1	22-45	719-746	EST	"f2f09a1.r1, f2f09a1.fl"		3198					(AE001093) A. fulgidus predicted coding region AF0189 [Archaeoglobus fulgidus]
17225	ENU01019	ANI61C1178: 975..1	22-41	730-749	EST	"g4h05a1.r1, g4h05a1.fl"		1580	34	1.4			hypothetical 42.0 KD protein in thi12-RPD3 intergenic region ; probable arylalcohol dehydrogenase YNL331c - yeast (Saccharomyces cerevisiae) ; (X83226) homologous to arylalcohol dehydrogenase of P.chrysosporium [Saccharomyces cerevisiae] ; (Z71607) ORF YNL331c [Saccharomyces cerevisiae]
17226	ENU01020	ANI61C5675: 3316..1999	22-48	799-826	EST	"m5a07a1.r1, m5a07a1.fl"		1486	288	3E-77			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17227	ENU01021	ANI61C4093: 441..92	47-66	456-478	EST	"o8h05a1.r1, o8h05a1.fl"		1380	49	0.00002			"acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kD subunit); NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 12K chain precursor - Neurospora crassa; (X59258) NADH dehydrogenase (ubiquinone) 12 kD subunit [Neurospora crassa]; (X83578) mitochondrial acyl carrier protein [Neurospora crassa]"
17228	ENU01022	ANI61C5291: 1953..703	22-46	805-829	EST	"j7g12a1.r1, j7g12a1.fl"		2592	80	2E-14			(Z99113) similar to alcohol dehydrogenase [Bacillus subtilis]; (Z99114) similar to alcohol dehydrogenase [Bacillus subtilis]
17229	ENU01023	ANI61C6729: 1961..1860			EST	"cle09a1.r1, cle09a1.fl"		564					Nitrogen assimilation transcription factor NIRA; nitrate assimilation regulatory protein nirA - Emericella nidulans; (M68900) NIRA protein [Emericella nidulans]
17230	ENU01024	ANI61C1024 24-43 4:5995..6792	24-43	741-768	EST	"c9h08a1.r1, c9h08a1.fl"		1782	68	1E-10			Pentafunctional arom polypeptide [contains: 3-dehydroquinase synthase; 3-dehydroquinase dehydratase (3-dehydroquinase); shikimate 5-dehydrogenase; shikimate kinase; EPSP synthase]; ARO1 protein - yeast (Saccharomyces cerevisiae); (X06077)
17231	ENU01025	ANI61C1045 59-78 2:2704..3893	59-78	800-827	EST	"flg10a1.r1, flg10a1.fl"		1146	71	1E-11			arom multifunctional enzyme (AA 1-1588) [Saccharomyces cerevisiae]; (Z48179) Aro1p [Saccharomyces cerevisiae]
17232	ENU01026	ANI61C9977: 30-49 1302..3160	30-49	805-829	EST	"b0b05a1.r1, b0b05a1.fl"		1338	33	2.3			possible regulatory function (alternatively spliced) protein p30 II - Human T-cell leukemia virus type I (U83323) major surface glycoprotein [Pneumocystis carinii]
17233	ENU01027	ANI61C1052 44-63 7:3506..3746	44-63	458-479	EST	"t2g10a1.r1, t2g10a1.fl"		688	32	2.7			(U13672) beta-glucosidase [Candida wickerhamii]; beta-glucosidase [Candida wickerhamii]
17234	ENU01028	ANI61C1052 9:7316..6486			EST	"t2h09a1.r1, t2h09a1.fl"		1505	182	1E-52			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17235	ENU01029	ANI61C6022: 1666..938	50-77	681-708	EST	"y8g05al.r1, y8g05al.fl"		1439	221	7E-59			(AB010442) PMR1 [Penicillium digitatum]
17236	ENU01030	ANI61C5297: 1379..1534	22-41	443-470	EST	"m0c08al.r1, m0c08al.fl"		566	31	6			(X85135) alpha-51D-immobilization antigen [Paramecium tetraurelia]
17237	ENU01031	ANI61C7000: 1714..888	40-59	786-806	EST	"w8cl1al.r1, w8cl1al.fl"		745	34	1.3			(AE001617) Phopholipase D Superfamily [Chlamydia pneumoniae]
17238	ENU01032	ANI61C9509: 1..698	22-46	646-673	EST	"z3a08al.r1, z3a08al.fl"		1114	106	1E-23			"kynureninase (EC 3.7.1.3) - rat; kynureninase, L-kynurenine hydrolase {EC 3.7.1.3} [rats, liver cytosol, Peptide, 464 aa]"
17239	ENU01033	ANI61C2073: 1786..656	22-41	805-829	EST	"z3el1al.r1, z3el1al.fl"		1196					"ATP synthase beta chain, mitochondrial precursor; H+-transporting ATP synthase (EC 3.6.1.34) beta chain - Neurospora crassa; (X53720) F(1)-ATPase beta-subunit precursor (519 AA) [Neurospora crassa]; (M84192) mitochondrial ATPase beta-subunit [Neurospora crassa]"
17240	ENU01034	ANI61C896:1 140..2239	55-74	806-829	EST	"y8h10al.r1, y8h10al.fl"		1346	287	6E-77			"(AE001140) glu-tRNA amidotransferase, subunit B (gatB) [Borrelia burgdorferi]"
17241	ENU01035	ANI61C818:5 2..2394	60-79	780-799	EST	"d3e03al.r1, d3e03al.fl"		1482	31	9.1			(X64795) fatty-acid synthase [Corynebacterium ammoniagenes]
17242	ENU01036	ANI61C499:2 29..5	104-129	386-413	EST	"y6f12al.r1, y6f12al.fl"		853	32	2			RCC1-like G exchanging factor RLG; (AF060219) RCC1-like G exchanging factor RLG [Homo sapiens]
17243	ENU01037	ANI61C4773: 529..38	156-175	458-478	EST	"y6g08al.r1, y6g08al.fl"		1443	34	0.9			hypothetical 83.0 KD protein in ATP1-ROX3 intergenic region; hypothetical protein YBL097w - yeast (Saccharomyces cerevisiae); (X79489) C-728 protein [Saccharomyces cerevisiae]; (Z35858) ORF YBL097w [Saccharomyces cerevisiae]
17244	ENU01038	ANI61C412:5 479..3114	51-70	802-829	EST	"j0a03al.r1, j0a03al.fl"		1680	74	1E-12			(Z83866) hypothetical protein Rv3058c [Mycobacterium tuberculosis]
17245	ENU01039	ANI61C4395: 1..731	121-140	662-689	EST	"j0d06al.r1, j0d06al.fl"		1972	31	7.6			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17246	ENU01040	ANI61C317:4 271..5538	22-43	743-762	EST	"i2c04a1.rl, i2c04a1.fl"		1924	35	0.61		"glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana ; (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] ; Gln synthetase [Arabidopsis thaliana]"
17247	ENU01041	ANI61C1070 2:2736..506	22-40	805-829	EST	"j9g11a1.rl, j9g11a1.fl"		2058	32	5.3		(U42580) a197R [Paramecium bursaria Chlorella virus 1]
17248	ENU01042	ANI61C9348: 1052..1165			EST	"y6f02a1.rl, y6f02a1.fl"		406	36	0.23		(AF081803) non-receptor protein tyrosine kinase laloo [Xenopus laevis] (AL031174) t-complex protein 1 gamma subunit homolog
17249	ENU01043	ANI61C7287: 411..698	35-54	456-479	EST	"p0a05a1.rl, p0a05a1.fl"		1740	138	5E-35		[Schizosaccharomyces pombe] (Z98598) putative transcriptional regulator [Schizosaccharomyces pombe]
17250	ENU01044	ANI61C9662: 1428..3521	22-45	806-829	EST	"n8d02a1.rl, n8d02a1.fl"		3596	161	7E-42		"78 kda apamin binding protein [cattle, brain synaptosomes, Peptide, 438 aa]"
17251	ENU01045	ANI61C9112: 5158..6271	25-48	800-827	EST	"j0h04a1.rl, j0h04a1.fl"		1162	31	9.1		(AE000776) molybdopterin converting factor subunit 2 [Aquifex aeolicus]
17252	ENU01046	ANI61C1038 1:1514..1070	27-54	452-479	EST	"c5e06a1.rl, c5e06a1.fl"		1022	76	2E-13		Replication factor-A protein 1 (single-stranded DNA-binding protein P68 subunit) ; (U59385) single-stranded DNA binding protein p68 subunit
17253	ENU01047	ANI61C8620: 2890..1835	46-65	803-829	EST	"d5e10a1.rl, d5e10a1.fl"		2544	180	1E-44		[Schizosaccharomyces pombe] ; (U75446) Rpa1 [Schizosaccharomyces pombe] ; (AL034563) replication factor-a protein 1
17254	ENU01048	ANI61C1030 2:4028..5287	22-49	765-792	EST	"r2h07a1.rl, r2h07a1.fl"		2484	39	0.054		[Schizosaccharomyces pombe] mucin (clone PGM-2A) - pig ; gastric mucin - pig (fragment) ; (U10281) gastric mucin [Sus scrofa]
17255	ENU01049	ANI61C1204: 906..1459	46-73	500-527	EST	"e0h10a1.rl, e0h10a1.fl"		1344	32	2.3		maturase-related protein - maize (fragment) ; (U09987) maturase-related protein [Zea mays]
17256	ENU01050	ANI61C6602: 3140..3042			EST	"m0e08a1.rl, m0e08a1.fl"		362				
17257	ENU01051	ANI61C1046 2:3354..41	22-44	769-788	EST	"z4h03a1.rl, z4h03a1.fl"		4624	31	9.1		(U96487) V-A TPase proteolipid [Desulfurococcus sp. SY]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
17258	ENU01052	ANI61C8867: 271..1			EST	"w6f07a1.rl", w6f07a1.fl"		646	42	0.000000		07	hypothetical oxidoreductase in KGD1-SIM1 intergenic region ; probable membrane protein YIL124w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae] (Y17554) ornithine carbamoyltransferase [Bacillus licheniformis] (AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus] Defender against cell death 1 (DAD-1) ; (D86562) DAD1 protein [Sus scrofa] (AB001488) similar to ORF14 of <i>enterococcus faecalis</i> transposon TN916. [Bacillus subtilis] ; (Z99106) similar to transposon protein [Bacillus subtilis] hypothetical protein 1 - Porphyromonas gingivalis ; transposase [Porphyromonas gingivalis]
17259	ENU01053	ANI61C8772: 66-85 1349..1162		454-479	EST	"g3a06a1.rl", g3a06a1.fl"		706	31	4.6			(AF026977) microsomal glutathione S-transferase 3 [Homo sapiens] (Z49806) adenylyl cyclase type VII [Bos taurus] (Y00318) heavy chain of factor I [Homo sapiens]
17260	ENU01054	ANI61C1071 40-60 3:1384..3265		802-829	EST	"g2f07a1.rl", g2f07a1.fl"		1135	33	2.3			B-lymphocyte antigen CD19 precursor - mouse ; (M62542) CD19 [Mus musculus] (Z98979) tat binding homolog [Schizosaccharomyces pombe] methionyl aminopeptidase (EC 3.4.11.18) 2 - rat ; (L10652) initiation factor 2 associated 67 kDa protein [Rattus rattus]
17261	ENU01055	ANI61C4672: 22-49 798..1		711-738	EST	"v7d01a1.rl", v7d01a1.fl"		3663	70	2E-11			
17262	ENU01056	ANI61C7906: 58-85 1632..963		623-646	EST	"d4a06a1.rl", d4a06a1.fl"		1202	33	2.3			
17263	ENU01057	ANI61C6993: 29-48 1951..2151		442-461	EST	"d2h03a1.rl", d2h03a1.fl"		562	32	2.7			
17264	ENU01058	ANI61C2402: 38-57 2788..1770		802-829	EST	"m0d10a1.rl", m0d10a1.fl"		1676					
17265	ENU01059	ANI61C6033: 49-76 836..1		735-762	EST	"r5g05a1.rl", r5g05a1.fl"		4528	47	0.0002			
17266	ENU01060	ANI61C1113 22-49 0:5863..5477		442-469	EST	"r2d04a1.rl", r2d04a1.fl"		1365	33	1.2			
17267	ENU01061	ANI61C1113 25-45 0:6242..7566		802-829	EST	"g6h02a1.rl", g6h02a1.fl"		1386	32	5.3			
17268	ENU01062	ANI61S4418: 48-74 263..437		392-416	EST	"p0f02a1.rl", p0f02a1.fl"		474					
17269	ENU01063	ANI61C710:9 53-72 84..892		406-433	EST	"z4a06a1.rl", z4a06a1.fl"		316	31	7.8			
17270	ENU01064	ANI61C4270: 22-41 2290..3972		792-819	EST	"i3g06a1.rl", i3g06a1.fl"		1208	46	0.0004			
17271	ENU01065	ANI61C7744: 49-68 2557..2444		444-466	EST	"i0c09a1.rl", i0c09a1.fl"		402	64	2E-19			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvtg	Description
17272	ENU01066	ANI61C1765: 2877..1842	22-45	802-829	EST	"h1a09a1.rl, h1a09a1.fl"		1438	148	6E-40			hypothetical 27.4 KD protein in MER2-BNA1 intergenic region ; hypothetical protein YJR024c - yeast (Saccharomyces cerevisiae) ; (Z49524)
17273	ENU01067	ANI61C1768: 2263..1583	106-125	636-660	EST	"p0f03a1.rl, p0f03a1.fl"		3281	33	1.8			ORF YJR024c [Saccharomyces cerevisiae] ; (X87297) J1545 [Saccharomyces cerevisiae] (AF003136) F28B3.6 [Caenorhabditis elegans]
17274	ENU01068	ANI61C1144 35-53 6:1583..803	35-53	724-743	EST	"i7e07a1.rl, i7e07a1.fl"		1538	141	5E-33			homoserine O-acetyltransferase (homoserine O-trans-acetylase) ; homoserine O-acetyltransferase (EC 2.3.1.31) - fungus (Ascobolus immersus) ; (M26662) met2 [Ascobolus immersus]
17275	ENU01069	ANI61C4601: 34-53 1044..2517	34-53	801-820	EST	"g9h06a1.rl, g9h06a1.fl"		1910	66	4E-10			probable sucrose utilization protein SUC1
17276	ENU01070	ANI61C8638: 22-47 1299..208	22-47	802-821	EST	"i8b01a1.rl, i8b01a1.fl"		822	37	0.21			transcription factor XLFB1a - African clawed frog
17277	ENU01071	ANI61C1999: 22-48 284..176	22-48	341-368	EST	"c1d12a1.rl, c1d12a1.fl"		360	32	2.5			(AF109904) type IV-A pilus assembly protein PilC [Vibrio cholerae]
17278	ENU01072	ANI61C1190: 43-63 9336..7397	43-63	804-829	EST	"j0g08a1.rl, j0g08a1.fl"		1287	85	5E-16			Insulin-degrading enzyme (insulysin) (insulinase) (insulin protease) ; (M21188) insulin-degrading enzyme [Homo sapiens]
17279	ENU01073	ANI61C1496: 692..1			EST	"j4d05a1.rl, j4d05a1.fl"		1035	45	0.0006			"unknown ; (U97670) eukaryotic translation initiation factor eIF3, p35 subunit [Homo sapiens] "
17280	ENU01074	ANI61C7238: 30-56 1608..3544	30-56	767-794	EST	"l3c11a1.rl, l3c11a1.fl"		1462	101	7E-21			hypothetical 69.5 KD protein C22G7.05 in chromosome I ; hypothetical protein SPAC22G7.05 - fission yeast (Schizosaccharomyces pombe) ; (Z54328) hypothetical protein [Schizosaccharomyces pombe] (Z83860) hypothetical protein Rv2337c [Mycobacterium tuberculosis]
17281	ENU01075	ANI61C6857: 23-46 2312..1825	23-46	451-472	EST	"c5f05a1.rl, c5f05a1.fl"		1376	31	4.6			PQ-rich protein - human ; (Z50194) PQ-rich protein [Homo sapiens]
17282	ENU01076	ANI61C8941: 55-82 446..1359	55-82	806-829	EST	"j7b09a1.rl, j7b09a1.fl"		1136	41	0.011			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17283	ENU01077	ANI61C1056: 1179..950	31-49	345-372	EST	"o8a03a1.rl, o8a03a1.fl"		858	30	7.8		(AL032621) similar to Acyl-CoA dehydrogenase; cDNA EST EMBL:D75425 comes from this gene; cDNA EST EMBL:M89392 comes from this gene; cDNA EST EMBL:M89303 comes from this gene; cDNA EST EMBL:D27766 comes from this gene; cDNA EST ... (AL023290) putative serine-rich zinc-finger protein [Schizosaccharomyces pombe]
17284	ENU01078	ANI61C1191: 24-46 5322..4443	24-46	804-823	EST	"z7d04a1.rl, z7d04a1.fl"		1274	64	0.000000		
17285	ENU01079	ANI61C6579: 39-58 990..22	39-58	740-761	EST	"c5d09a1.rl, c5d09a1.fl"		2024	37	0.21		(Z72496) mucin MUC5B [Homo sapiens]
17286	ENU01080	ANI61C3388: 22-49 1847..1622	22-49	457-477	EST	"y3c11a1.rl, y3c11a1.fl"		807	34	0.9		transPOSase ; (L49438) transposase [Chelatobacter heintzii]
17287	ENU01081	ANI61C7193: 22-46 2856..1594	22-46	757-784	EST	"g5e11a1.rl, g5e11a1.fl"		1572	32	5.3		(AF051344) latent transforming growth factor-beta binding protein 4S [Homo sapiens]
17288	ENU01082	ANI61C433:1 45-72 027..1492	45-72	425-452	EST	"c0f09a1.rl, c0f09a1.fl"		2400	38	0.061		LDL receptor 2 precursor - African clawed frog
17289	ENU01083	ANI61C7805: 51-70 1604..1117	51-70	449-476	EST	"z3e12a1.rl, z3e12a1.fl"		1132	86	1E-27		pyruvate kinase (PK) ; pyruvate kinase (EC 2.7.1.40) - Emericella nidulans ; (M36918) pyruvate kinase [Emericella nidulans]
17290	ENU01084	ANI61C7912: 37-56 647..2376	37-56	802-829	EST	"d3g06a1.rl, d3g06a1.fl"		1350	32	5.3		(Z92771) rmlA2 [Mycobacterium tuberculosis]
17291	ENU01085	ANI61C7016: 22-48 5055..5615	22-48	511-538	EST	"g3a07a1.rl, g3a07a1.fl"		3050	32	4.1		(AL032647) predicted using Genefinder [Caenorhabditis elegans]
17292	ENU01086	ANI61C9830: 22-41 5230..4032	22-41	783-802	EST	"r6g04a1.rl, r6g04a1.fl"		1709	34	1.4		(AF057557) anti-Fas-induced apoptosis [Homo sapiens]
17293	ENU01087	ANI61C8362: 22-49 1533..741	22-49	738-765	EST	"w6e06a1.rl, w6e06a1.fl"		2643	36	0.43		(AF088906) clock-controlled gene-9 protein [Neurospora crassa]
17294	ENU01088	ANI61C9371: 22-42 1572..223	22-42	794-821	EST	"y4f11a1.rl, y4f11a1.fl"		2612	51	0.000009		(U76621) short-chain alcohol dehydrogenase [Aspergillus parasiticus]
17295	ENU01089	ANI61S420:4 47-68 5..458	47-68	391-418	TPEST							(AL032684) ER lumen protein retaining receptor protein [Schizosaccharomyces pombe]
17296	ENU01090	ANI61C5867: 69-88 916..1310	69-88	402-421	TPEST				32	1.9		

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17297	ENU01091	ANI61C1970: 22-47 85..504	22-47	382-399	TPEST								(AE001270) DNA helicase II (uvrD) [Treponema pallidum]
17298	ENU01092	ANI61C2877: 39-58 761..329	39-58	410-429	TPEST			32	32	2.1			(AE001556) putative [Helicobacter pylori 199]
17299	ENU01093	ANI61C9950: 31-50 1693..1253	31-50	410-429	TPEST			31	31	4.9			3-hydroxyisobutyrate dehydrogenase precursor (HIBADH) ; 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) precursor - rat (fragment) ; (J04628) 3-hydroxyisobutyrate dehydrogenase [Rattus norvegicus]
17300	ENU01094	ANI61C6837: 22-44 2183..2659	22-44	437-456	TPEST			90	90	8E-18			(AL031004) putative protein [Arabidopsis thaliana]
17301	ENU01095	ANI50C1_24 3:387..875	72-91	496-518	TPEST			31	31	7.6			(AC003952) hypothetical protein [Arabidopsis thaliana] ; (AC006201) hypothetical protein [Arabidopsis thaliana]
17302	ENU01096	ANI61C878:1 184..1678	38-60	469-490	TPEST			30	30	6.3			(U95045) velvet A [Emericella nidulans]
17303	ENU01097	ANI61C7544: 47-66 771..1304	47-66	521-538	TPEST			62	62	0.000000			(AF007101) PKS module 2 [Streptomyces hygroscopicus]
17304	ENU01098	ANI61C5207: 62-80 566..931	62-80	366-385	TPEST			30	30	9.7			Choriongonadotropic hormone-like receptor (CGH-R) ; chorionic gonadotropin receptor - Xanthomonas maltophilia (fragment) ; (X68371) chorionic gonadotropin receptor homologue [Stenotrophomonas maltophilia]
17305	ENU01099	ANI61C8333: 22-51 1221..1614	22-51	350-374	TPEST			30	30	0.85			"surface antigen 51A - Paramecium tetraurelia (SGC5) (fragments) ; protein 51A,surface [Paramecium tetraurelia] "
17306	ENU01100	ANI61C3918: 31-55 2719..2318	31-55	371-390	TPEST			33	33	0.85			"(X80835) len: 676, CAI: 0.13 [Saccharomyces cerevisiae] "
17307	ENU01101	ANI61C9642: 22-51 1261..1663	22-51	356-382	TPEST			30	30	7.7			
17308	ENU01102	ANI50C9535 _1:677..1088	72-91	406-441	TPEST			30	30	7.7			
17309	ENU01103	ANI61C7666: 56-81 510..99	56-81	405-425	TPEST			31	31	3.5			
17310	ENU01104	ANI61C6789: 59-78 2590..3012	59-78	419-439	TPEST			31	31	3.5			

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17317	ENU01111	ANI61C8828: 1150..1606	22-46	413-436	TPEST				94	5E-19			phosphoribosyl pyrophosphate synthetase I ; ribose-phosphate pyrophosphokinase I (phosphoribosyl pyrophosphate synthetase I) (PPRIBP) (PRS-I) ; ribose-phosphate pyrophosphokinase (EC 2.7.6.1) catalytic chain I - human ; ribose-phosphate pyrophosphokinase (EC 2.7.6.1) catalytic chain I - rat ; (X15331)
													phosphoribosylpyrophosphate synthetase (AA 1-319) [Homo sapiens] ; (X16554) ribose-phosphate pyrophosphokinase subunit I (AA 1-318) [Rattus norvegicus] ; (M31084) phosphoribosylpyrophosphate synthetase [Rattus norvegicus] ; (M29392)
													phosphoribosylpyrophosphate synthetase (PRPS1) precursor [Rattus norvegicus] ; (M17258) phosphoribosyl pyrophosphate synthetase I [Rattus norvegicus] ; (D00860) phosphoribosyl pyrophosphate synthetase subunit I [Homo sapiens]
17318	ENU01112	ANI61C201:2 02..135	23-58	415-438	TPEST				31	4			Retrovirus-related pol polyprotein from transposon TNT 1-94 [contains: protease ; reverse transcriptase ; endonuclease] ; hypothetical protein - common tobacco ; (X13777) ORF [Nicotiana tabacum]
17319	ENU01113	ANI61C8982: 6933..7395	22-52	423-442	TPEST								
17320	ENU01114	ANI61C1131 65-89	65-89	465-490	TPEST				41	0.004			probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae) ; (Z48758) unknown [Saccharomyces cerevisiae]
17321	ENU01115	ANI61C5275: 515..41	43-65	454-475	TPEST								(AB023216) KIAA0999 protein [Homo sapiens]
17322	ENU01116	ANI61C562:7 984..7507	44-63	460-479	TPEST				33	1.1			

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17323	ENU01117	ANI61C1758: 22-47 7700..8181	22-47	433-461	TPEST				42	0.003			(AL034433) hypothetical protein [Schizosaccharomyces pombe]
17324	ENU01118	ANI61C5576: 25-45 2156..1673	25-45	446-466	TPEST				33	1.5			hypothetical 69.0 KD protein in SIR1 3'region ; hypothetical protein YCL070C homolog YKR106w - yeast (Saccharomyces cerevisiae) ; (Z28202) ORF YKR106w [Saccharomyces cerevisiae]
17325	ENU01119	ANI61C9263: 28-49 671..841	28-49	459-479	TPEST				33	1.2			(AB013161) NADH dehydrogenase subunit 5 [Pteris rapae]
17326	ENU01120	ANI61C1516: 25-54 224..720	25-54	450-479	TPEST				37	0.11			(Z94043) hypothetical protein [Bacillus subtilis] ; (Z99121) similar to reticuline oxidase [Bacillus subtilis]
17327	ENU01121	ANI61C6698: 54-76 1303..782	54-76	498-533	TPEST				152	9E-41			"(AB018078) oligo-1,4 - 1,4-glucantransferase / amylo-1,6-glucosidase [Saccharomyces cerevisiae]"
17328	ENU01122	ANI61C5920: 37-56 821..289	37-56	492-527	TPEST				32	3.9			"(Y15197) microtubule-associated protein, MAP-115 [Mus musculus]"
17329	ENU01123	ANI61C151:1 29-63 01..638	29-63	505-524	TPEST				103	1E-30			"ATP synthase subunit 4, mitochondrial precursor ; (AF019222) F1Fo-ATP synthase subunit 4 [Kluyveromyces lactis]"
17330	ENU01124	ANI61C6008: 39-60 111..694	39-60	546-580	TPEST				29	9.9			nucleic acid-binding protein E5.1 - human ; (L37368) RNA-binding protein [Homo sapiens]
17331	ENU01125	ANI61C9308: 51-70 1214..866	51-70	338-357	TPEST				30	6.5			(AE000839) conserved protein [Methanobacterium thermoautotrophicum]
17332	ENU01126	ANI61C5797: 25-44 2461..2832	25-44	335-354	TPEST								

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17333	ENU01127	ANI61C5908: 49-68 1378..971	49-68	395-414	TPEST			208	208	1E-53		methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (methionine synthase, vitamin-B12 independent isozyme) (cobalamin-independent methionine synthase) (delta-P8 protein) ; 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - yeast (Saccharomyces cerevisiae) ; (U18839) Met6p: 5-methyltetrahydropteroyl triglutamate--homocysteine methyltransferase [Saccharomyces cerevisiae] ; (U32508) N5-methyltetrahydrofolate homocysteine methyltransferase [Saccharomyces cerevisiae] "
17334	ENU01128	ANI61C9488: 56-75 164..583	56-75	412-433	TPEST			62	62	0.000000		[AF032443] ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]
17335	ENU01129	ANI61C4718: 43-62 1049..1697	43-62	406-423	TPEST			44	44	0.0005		ubiquitin - Mediterranean fruit fly ; ubiquitin [Homo sapiens] ; ubiquitin [Homo sapiens] ; ubiquitin [Scombridae gen. sp.] ; ubiquitin [Thunnus sp.]
17336	ENU01130	ANI61C1041 9:958..1395	49-73	426-444	TPEST			33	33	1.3		ribonucleoprotein - Arabidopsis thaliana ; (M98340) ribonucleoprotein [Arabidopsis thaliana] ; Ser/Arg-rich protein [Arabidopsis thaliana]
17337	ENU01131	ANI61C8459: 43-70 2225..2664	43-70	421-440	TPEST			87	87	8E-17		"isoleucyl-TRNA synthetase, cytoplasmic (isoleucine--TRNA ligase) (ILERS) ; (AB004538) isoleucyl-TRNA synthetase, cytoplasmic [Schizosaccharomyces pombe] "
17338	ENU01132	ANI61C3284: 66-85 1298..1739	66-85	446-465	TPEST			31	31	3.8		(U41624) contains EGF-like repeats; similar to C. elegans protein D1044.3 [Caenorhabditis elegans]
17339	ENU01133	ANI61C3633: 64-83 1231..1672	64-83	444-463	TPEST			32	32	2.2		(Y16104) replicase protein [Physalis mottle tymovirus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17340	ENU01134	ANI61C146:3 353..3798	44-63	428-447	TPEST						31	3.9	(X95665) cDNA6 [Brugia pahangi]
17341	ENU01135	ANI61C1097 71-90		458-477	TPEST						31	5.2	(U31364) envelope glycoprotein gp120 [Human immunodeficiency virus type 1]
17342	ENU01136	ANI61C4927: 67-86 2707..2253		451-479	TPEST								
17343	ENU01137	ANI61C9105: 41-60 324..780		436-455	TPEST			54	0.000000	5			mitochondrial inheritance component MDM12; (U64674) mitochondrial inheritance component Mdm12p [Schizosaccharomyces pombe]
17344	ENU01138	ANI61C1096 26-48 4:2276..2732		421-440	TPEST			34	0.61				(Z94121) hypothetical protein Rv3903c [Mycobacterium tuberculosis]
17345	ENU01139	ANI61C1439: 23-42 1444..1654		421-440	TPEST			31	4.1				"Sex-determining transformer protein 2 precursor; cell communication-mediating membrane protein pTra2A - Caenorhabditis elegans; (S42187) pTra2A=membrane protein mediating cell communication [Caenorhabditis elegans, Peptide, 1475 aa]
17346	ENU01140	ANI61C6152: 49-71 3576..4040		439-471	TPEST								[Caenorhabditis elegans]; (M91371) membrane protein [Caenorhabditis elegans] "
17347	ENU01141	ANI61C6102: 46-66 276..740		449-468	TPEST			32	1.8				hypothetical protein MJ0416; hypothetical protein MJ0416 - Methanococcus jannaschii; (U67493) M. jannaschii predicted coding region MJ0416 [Methanococcus jannaschii] (AE001284) hypothetical protein [Chlamydia trachomatis]
17348	ENU01142	ANI61C15:15 38-58 66..1100		441-462	TPEST			31	4.1				(AF044209) nuclear receptor co-repressor N-CoR [Homo sapiens] (AL022268) putative kinase/phosphohydrolase [Streptomyces coelicolor]
17349	ENU01143	ANI61C1146 39-61 1:2569..3036		445-464	TPEST			34	0.82				(U97194) weak similarity to the triple-helical domain of collagens [Caenorhabditis elegans]
17350	ENU01144	ANI61C1043 56-75 5:6035..6502		462-481	TPEST			31	4.1				
17351	ENU01145	ANI61C3709: 49-68 2945..3415		459-478	TPEST			32	2.4				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17352	ENU01146	ANI61C6857: 25-44 1391..1501	48-67	434-455	TPEST			34	66	0.48			(U70378) envelope polyprotein [Feline leukemia virus]
17353	ENU01147	ANI61C6835: 48-67 2443..2915	459-478	434-453	TPEST			32	66	1E-10			(Z99168) 40s ribosomal protein [Schizosaccharomyces pombe]
17354	ENU01148	ANI61C6874: 22-48 636..1109	444-463	454-473	TPEST			30	32	3.3			GATA binding factor-1A (transcription factor XGATA-1A) ; transcription factor GATA-1A - African clawed frog ; (M76566) GATA binding factor-1 [Xenopus laevis]
17356	ENU01150	ANI61C8642: 27-46 742..1226	450-469	446-465	TPEST			31	39	5.7			(AF036486) replication protein [Plasmid pNZ4000]
17357	ENU01151	ANI61C8646: 22-48 1626..2111	454-473	454-473	TPEST			30	30	10			DNA-directed RNA polymerase II largest subunit (RPB1) (Z46935) weak similarity to conglutin (PIR accession number A33090); cDNA EST EMBL:T01355 comes from this gene; cDNA EST yk383f3.3 comes from this gene [Caenorhabditis elegans]
17358	ENU01152	ANI61C1065 25-44 9:1045..1535	504-527	504-527	TPEST			67	67	1E-10			(AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]
17359	ENU01153	ANI61C8133: 72-91 993..496	504-523	541-561	TPEST			32	32	3.8			(AC004146) Hypothetical protein [Arabidopsis thaliana]
17360	ENU01154	ANI61C1904: 31-50 126..660	535-557	597-625	TPEST			76	56	3.9			(AB001347) brain beta 3 spectrin [Rattus norvegicus]
17361	ENU01155	ANI61C7675: 63-82 5031..4491	597-625	1001-1020	TPEST			56	112	3E-28			"dismutase,Mn superoxide [Saccharomyces cerevisiae]" (AF047694) glutaredoxin [Vernicia fordii]
17362	ENU01156	ANI61C8356: 35-54 3042..2478	60-79	1001-1020	TPEST			56	112	3E-15			"ribosomal protein L31.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (U19729) Ylr406cp: member of L31E ribosomal protein family [Saccharomyces cerevisiae]"
17363	ENU01157	ANI61C3552: 53-72 812..198								5E-24			
17364	ENU01158	ANI61C1713: 60-79 194..1196											

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17365	ENU01159	ANI61C5740: 26-54 325..666	26-54	303-325	TPEST			32	32	1.9			hypothetical zinc finger protein ZK112.2 in chromosome III ; ZK112.2 protein - Caenorhabditis elegans ; (L14324) homology with xnf7 gene product of Xenopus laevis; putative [Caenorhabditis elegans] ; (AF047027) B box zinc finger protein Ncl-1 [Caenorhabditis elegans] homocitrate dehydratase ; LYS7 protein - yeast (Saccharomyces cerevisiae) ; (U17378) Lys7p [Saccharomyces cerevisiae] ; (Z48502) unknown [Saccharomyces cerevisiae] ; LYS7 gene [Saccharomyces cerevisiae] (U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus] "Aldehyde dehydrogenase (ALDDH) ; aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans ; (M16197) aldehyde dehydrogenase [Emerticella nidulans] ; dehydrogenase, aldehyde [Emerticella nidulans] " "glycine cleavage system H protein ; glycine cleavage system protein H - Escherichia coli ; (M57690) H-protein [Escherichia coli] ; (X73958) H protein [Escherichia coli] ; (U28377) ORF_f129 [Escherichia coli] ; (AE000374) in glycine cleavage complex, carrier of aminomethyl moiety via covalently bound lipoyl cofactor [Escherichia coli] "
17366	ENU01160	ANI61C4514: 64-85 123..474	64-85	352-373	TPEST			58	58	0.000000 03			
17367	ENU01161	ANI61C1020 53-74 7:3388..3022	53-74	358-377	TPEST			218	218	1E-56			
17368	ENU01162	ANI61C4777: 41-60 602..972	41-60	350-369	TPEST			65	65	2E-10			
17369	ENU01163	ANI61C8131: 22-48 716..1093	22-48	338-357	TPEST			38	38	0.023			
17370	ENU01164	ANI61C3265: 28-47 855..1246	28-47	358-377	TPEST								
17371	ENU01165	ANI50C9281 22-46 1:81..484	22-46	364-383	TPEST								
17372	ENU01166	ANI61C5234: 35-54 1329..926	35-54	372-396	TPEST			31	31	3.3			bride of sevenless precursor - fruit fly (Drosophila melanogaster)

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17373	ENU01167	ANI61C1395: 22-57 2335..2745	22-57	371-390	TPEST			32	32	1.5			"(Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA..."
17374	ENU01168	ANI50C392_1:327..740	22-41	373-393	TPEST			31	31	4.5			(L34120) maturase [Chrysosplenium lowense]
17375	ENU01169	ANI61C8729: 71-90 1331..1741	71-90	424-443	TPEST			34	34	0.63			(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
17376	ENU01170	ANI61C1146 25-44 2:3984..4400	25-44	380-399	TPEST			32	32	2.7			(Z99125) hypothetical protein MLCL536.10 [Mycobacterium leprae]
17377	ENU01171	ANI61C8297: 70-89 459..553	70-89	435-454	TPEST			33	33	0.96			(AE001455) APOLIPOprotein N-acyltransferase [Helicobacter pylori j99]
17378	ENU01172	ANI61C6475: 22-46 1146..711	22-46	389-415	TPEST			34	34	0.75			(AF039043) contains a short region of similarity to troponin T cardiac isoform [Caenorhabditis elegans]
17379	ENU01173	ANI61C9506: 72-91 1442..1881	72-91	449-469	TPEST			31	31	6.5			glucose inhibited division protein B ; (U97573) gidB homolog [Treponema pallidum] ; (AE001263) glucose-inhibited division protein B (gidB) [Treponema pallidum]
17380	ENU01174	ANI61C1078 33-52 7:1158..1597	33-52	411-430	TPEST			96	96	2E-19			(AL033388) hypothetical integral membrane protein
17381	ENU01175	ANI61C8580: 33-52 7426..6986	33-52	410-431	TPEST			31	31	3.8			[Schizosaccharomyces pombe]
17382	ENU01176	ANI61C4227: 34-54 548..989	34-54	410-433	TPEST			38	38	0.051			(X90569) elastic titin [Homo sapiens]
17383	ENU01177	ANI61C8167: 23-42 688..1130	23-42	403-423	TPEST			36	36	0.15			proline-rich protein - tomato ; (X57076) proline rich protein [Lycopersicon esculentum]
17384	ENU01178	ANI61C2132: 35-54 6703..6260	35-54	417-436	TPEST								(Z98763) probable vacuolar sorting protein [Schizosaccharomyces pombe]
17385	ENU01179	ANI50C1_19 49-80 04:109..552	49-80	431-450	TPEST								

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17386	ENU01180	ANI61C1878: 814..1258	42-61	424-444	TPEST			43	0.001				DNA-directed RNA polymerase III 36 KD polypeptide (C34) ; DNA-directed RNA polymerase (EC 2.7.7.6) III chain C34 - yeast (Saccharomyces cerevisiae) ; (X63746) DNA dependent RNA polymerase c(III) subunit c34 [Saccharomyces cerevisiae] ; (X77395) RNA polymerase III [Saccharomyces cerevisiae] ; (Z71618) ORF YNR003c [Saccharomyces cerevisiae]
17387	ENU01181	ANI61C1093 0:756..891	58-78	443-462	TPEST			30	8.6				OP protein - Kennedy yellow mosaic virus ; (D00637) ORF for overlapping protein [Kennedy yellow mosaic virus]
17388	ENU01182	ANI61C1062 6:825..1273	66-85	445-472	TPEST			62	2E-21				JSN1 protein ; hypothetical protein YJR091c - yeast (Saccharomyces cerevisiae) ; (L43493) Jsn1 gene product [Saccharomyces cerevisiae] ; (Z49591) ORF YJR091c [Saccharomyces cerevisiae]
17389	ENU01183	ANI61C1029 5:1420..1870	26-45	414-433	TPEST			33	1.3				hypothetical protein - Neurospora crassa
17390	ENU01184	ANI61C4085: 2934..3384	22-57	410-430	TPEST			31	3.9				lipase modulator precursor (LIPase helper protein) ; (D50588) lipase modulator protein [Pseudomonas aeruginosa] ; (AB008452) proposal modulator or activator protein for lipase [Pseudomonas aeruginosa]
17391	ENU01185	ANI61C8185: 1518..1068	28-36	416-436	TPEST			81	4E-15				"hypothetical 36.8 KD protein C26A3.16 in chromosome I ; (Z69240) yeast dsk2 homolog, ubiquitin-like protein [Schizosaccharomyces pombe]
17392	ENU01186	ANI61C7357: 805..355	59-78	447-467	TPEST								
17393	ENU01187	ANI61C3768: 171..621	22-55	409-430	TPEST								

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17394	ENU01188	ANI61C7771: 3089..2638	22-47	409-431	TPEST			229	229	1E-59		probable sterigmatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emericella nidulans] (AF087280) (N-acetylneuraminyl)-galactosylglucosylceramide N-acetylglactosaminyl transferase [Chlamydia trachomatis] (AF035619) pyridoxine biosynthesis protein [Cercospora nicotianae] (AL023780) putative mra stability protein [Schizosaccharomyces pombe] Cutinase precursor (L1) ; (D38311) Cutinase [Aspergillus oryzae] (AC006413) hypothetical protein [Arabidopsis thaliana] (U08029) NADH:nitrate reductase [Spinacia oleracea] (D45163) embryonic muscle myosin heavy chain [Halocynthia roretzi] (AL049485) putative squalene-hopene cyclase [Streptomyces coelicolor] amidase (EC 3.5.1.4) - Aspergillus oryzae ; (D10492) acetamidase [Aspergillus oryzae] (U12978) BS-84 [Homo sapiens]
17395	ENU01189	ANI61C4061: 1295..1746	22-41	412-431	TPEST			31	31	6.7		
17396	ENU01190	ANI61C9579: 2756..2651	25-47	416-435	TPEST			132	132	1E-30		
17397	ENU01191	ANI61C7353: 5766..6218	41-62	431-451	TPEST			50	50	0.00001		
17398	ENU01192	ANI61C3827: 108..560	39-61	427-449	TPEST			49	49	0.00002		
17399	ENU01193	ANI61C7142: 44-63	44-63	436-455	TPEST			31	31	6.7		
17400	ENU01194	ANI61C1079: 462..915	40-59	431-452	TPEST			30	30	8.9		
17401	ENU01195	ANI61C873: 77..1231	40-60	430-452	TPEST			31	31	4		
17402	ENU01196	ANI61C7089: 391..845	22-48	415-434	TPEST			32	32	3		
17403	ENU01197	ANI61C7024: 307..762	66-85	447-479	TPEST			35	35	0.35		
17404	ENU01198	ANI61C5486: 363..819	49-68	440-463	TPEST			31	31	5.2		
17405	ENU01199	ANI61C6338: 1079..1535	38-58	433-452	TPEST			32	32	1.8		putative aspartate aminotransferase 1 (transaminase A) (ASPA T) ; aspartate transaminase (EC 2.6.1.1) - Methanococcus jannaschii ; (U67459) aspartate aminotransferase (aspB1) [Methanococcus jannaschii] (AF033210) major surface glycoprotein [Pneumocystis carinii f. sp. hominis] (AF015193) NADH dehydrogenase subunit 4 [Onchocerca volvulus] (Y14157) Toucan protein [Drosophila melanogaster]
17406	ENU01200	ANI61C7622: 1109..653	60-79	454-474	TPEST			30	30	8.9		
17407	ENU01201	ANI61C623: 84..641	40-61	433-455	TPEST			31	31	6.9		
17408	ENU01202	ANI61C1042: 7:1510..1053	22-47	418-437	TPEST			37	37	0.07		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17409	ENU01203	ANI61C9327: 2055..2512	22-48	413-437	TPEST			31	31	4		(AF078788) similar to Batten disease-related protein CLN3 [Caenorhabditis elegans]
17410	ENU01204	ANI61C1083: 560..1017	22-52	418-437	TPEST			31	31	6.9		COI intron 10 protein - Podospora anserina mitochondrion (SGC3) ; (X55026) Dod COI i10 grp IB protein [Podospora anserina]
17411	ENU01205	ANI61C7776: 3365..3823	22-53	419-438	TPEST			32	32	2.4		Ig heavy chain V region (129) - mouse
17412	ENU01206	ANI61C5075: 59-76	59-76	450-476	TPEST			31	31	6.9		acidic protein - Caenorhabditis elegans (fragment) ; (M77697) acid-rich protein [Caenorhabditis elegans]
17413	ENU01207	ANI61C1119: 563..1022	27-46	423-445	TPEST			31	31	6.9		"(AF004668) Sia alpha2,3Galbeta1,4GlcNAcalpha 2,8-sialyltransferase [Homo sapiens] "
17414	ENU01208	ANI50C1088 848..730	22-41	422-441	TPEST			110	110	5E-24		"Dihydrolipoamide dehydrogenase precursor ; dihydrolipoamide dehydrogenase (EC 1.8.1.4) precursor - yeast (Saccharomyces cerevisiae) ; (J03645) dihydrolipoamide dehydrogenase [Saccharomyces cerevisiae] ; (M20880) lipoamide dehydrogenase [Saccharomyces cerevisiae] ; (Z46255) lpd1, dhlp1, len: 499. CAl: 0.26, DLDH_YEAST P09624 dihydrolipoamide dehydrogenase precursor [Saccharomyces cerevisiae] ; (D50617) dihydrolipoamide dehydrogenase precursor [Saccharomyces cerevisiae] ; (D44596) lipoamide dehydrogenase [Saccharomyces cerevisiae] "
17415	ENU01209	ANI61C8837: 2185..2647	22-47	423-442	TPEST			31	31	6.9		Neural-cadherin 2 precursor (N-cadherin 2) ; N-cadherin 2 precursor - African clawed frog ; (X57675) N-cadherin [Xenopus laevis]
17416	ENU01210	ANI61C6002: 1181..1644	22-43	424-443	TPEST			31	31	5.4		
17417	ENU01211	ANI61C1140 7:2457..2920	56-75	458-477	TPEST			31	31	5.4		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17418	ENU01212	ANI61C7170: 34-53 2840..3304	34-53	437-456	TPEST				109	8E-24		40S ribosomal protein S9 (S7) ; (X96613) cytoplasmic ribosomal protein S7 [Podospira anserina]
17419	ENU01213	ANI61C8617: 22-49 384..850	22-49	426-445	TPEST				139	8E-33		"probable 3-hydroxybutyryl-CoA dehydrogenase (beta-hydroxybutyryl-CoA dehydrogenase) (BHBD) ; (U29084) similar to Clostridium acetobutylicum NAD-dependent beta-hydroxybutyryl-CoA dehydrogenase, PIR Accession Number A43723 [Bacillus subtilis] "
17420	ENU01214	ANI61C6250: 23-42 562..1029	23-42	429-448	TPEST				31	5.4		"(AL031866) ORF8, len: 255 aa, hutC, highly similar to histidine utilization repressor from P22773 Pseudomonas putida, 63.2% identity in 242 aa overlap, Fasta scores opt: 1022, E():0. [Yersinia pestis] "
17421	ENU01215	ANI61C6358: 22-52 283..750	22-52	428-447	TPEST				33	1.1		complement C3d/Epstein-Barr virus receptor precursor - human
17422	ENU01216	ANI50C3036 38-57 9.2:215..682	38-57	443-463	TPEST				34	0.48		(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]
17423	ENU01217	ANI61C1071 38-57 9:530..998	38-57	445-464	TPEST				34	0.62		(Z82256) cDNA EST yk251g7.3 comes from this gene; cDNA EST yk251g7.5 comes from this gene; cDNA EST comes from this gene; cDNA EST EMBL:D68223 comes from this gene; cDNA EST EMBL:C12737 comes from this gene; cDNA EST yk389c8.5 comes from this gene; cDNA EST ...
17424	ENU01218	ANI61C1011: 53-73 1883..2351	53-73	453-479	TPEST				98	3E-20		het-c2 protein - Podospira anserina ; (U05236) HET-C2 [Podospira anserina]
17425	ENU01219	ANI61C1189: 22-56 5906..6375	22-56	430-449	TPEST							Aflatoxin biosynthesis polyketide synthase (PKS) ; (L42765) polyketide synthase [Aspergillus parasiticus] ;
17426	ENU01220	ANI61C3019: 52-72 744..1213	52-72	449-479	TPEST				33	1.4		(L42766) polyketide synthase [Aspergillus parasiticus] ; polyketide synthase [Aspergillus parasiticus]
17427	ENU01221	ANI61C5910: 48-67 913..1384	48-67	453-477	TPEST							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
17428	ENU01222	ANI61C8200: 22-53 2736..3208	22-53	433-452	TPEST						31	7.2	"probable 3',5'-cyclic phosphodiesterase R08D7.6 ; (Z12017) predicted using Genefinder; similar to cyclic GMP phosphodiesterases; cDNA EST EMBL:D32815 comes from this gene; cDNA EST EMBL:D33365 comes from this gene; cDNA EST EMBL:D36169 comes from this gene; cDNA EST EMBL:D3369..."
17429	ENU01223	ANI61C6431: 22-45 39..511	22-45	420-452	TPEST						32	1.9	(AL021711) putative protein [Arabidopsis thaliana]
17430	ENU01224	ANI61C4316: 39-62 323..796	39-62	449-470	TPEST						31	5.5	"(Z98551) predicted using hexExon; MAL3P6.11 (PFC0760c), Hypothetical protein, len: 3395 aa [Plasmodium falciparum] "
17433	ENU01227	ANI61C1804: 46-66 223..698	46-66	449-479	TPEST						30	9.5	(AE000829) unknown [Methanobacterium thermoautotrophicum]
17434	ENU01228	ANI61C6494: 46-68 5210..5685	46-68	452-479	TPEST						30	9.5	ATP-dependent RNA helicase DBP7 ; probable purine nucleotide-binding protein YKR024c - yeast (Saccharomyces cerevisiae) ; (Z28249) ORF YKR024c [Saccharomyces cerevisiae]
17435	ENU01229	ANI50C3665 27-46 0_1.99..574	27-46	441-460	TPEST						77	8E-14	ribosomal protein S27 (metallopanstimulin 1) ; 40S ribosomal protein S27 (metallopan-stimulin 1) (MPS-1) ; growth factor-inducible zinc finger protein MPS-1 - human ; (L19739) metallopanstimulin [Homo sapiens] ; (U57847) ribosomal protein S27 [Homo sapiens]
17436	ENU01230	ANI61C3327: 28-48 630..154	28-48	443-462	TPEST						32	3.2	(X66593) apocytochrome B [Pichia pijperi]
17437	ENU01231	ANI61C1110 51-78 7:6219..6695	51-78	465-485	TPEST						32	3.2	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
17438	ENU01232	ANI61C8963: 43-71 1519..1043	43-71	453-477	TPEST				33	1.4		Focal adhesion kinase 1 (FADK 1) (PP125FAK) ; (AF020777) focal adhesion kinase; pp125FAK [Rattus norvegicus]
17439	ENU01233	ANI61C3345: 27-49 5280..5497	27-49	439-462	TPEST				34	0.49		(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
17440	ENU01234	ANI61C1113: 39-59 1:4458..4936	39-59	454-475	TPEST				31	5.6		(Z34814) voltage-dependent L-type Ca channel alpha 1 subunit [Homo sapiens]
17441	ENU01235	ANI61C9369: 22-51 891..1370	22-51	439-459	TPEST				31	4.3		(AL049558) putative phosphatidylinositol-kinase [Schizosaccharomyces pombe]
17442	ENU01236	ANI61C8497: 23-58 2125..2254	23-58	438-461	TPEST				43	0.001		ubiquitinone biosynthesis monooxygenase COQ6 ; hypothetical protein YGR255c - yeast (Saccharomyces cerevisiae) ; (Z73040) ORF YGR255c [Saccharomyces cerevisiae] ; (X99228) G9165 [Saccharomyces cerevisiae] ; (AF003698) COQ6 monooxygenase [Saccharomyces cerevisiae]
17443	ENU01237	ANI61C7016: 36-59 2389..2869	36-59	455-474	TPEST				34	0.65		(AF070999) tetracycline resistance protein [IncQ plasmid pLE1120]
17444	ENU01238	ANI61C4368: 23-51 1614..2095	23-51	443-462	TPEST				32	1.9		(L15365) stage specific activator protein; SSAP [Strongylocentrotus purpuratus]
17445	ENU01239	ANI61C9514: 39-58 474..956	39-58	453-479	TPEST							
17446	ENU01240	ANI61C5951: 24-57 3827..4310	24-57	443-464	TPEST							
17447	ENU01241	ANI61C1810: 22-41 108..591	22-41	443-463	TPEST							
17448	ENU01242	ANI61C9348: 52-71 1059..575	52-71	467-494	TPEST							

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17449	ENU01243	ANI61C5968: 25-44 413..899	448-469	448-469	TPEST			41	0.007				S-adenosylmethionine synthetase (methionine adenosyltransferase) (ADOMET synthetase); methionine adenosyltransferase (EC 2.5.1.6) - Neurospora crassa; (U21547) S-adenosylmethionine synthetase [Neurospora crassa]; Met(S-adenosyl) synthetase [Neurospora crassa] probable membrane protein YPL134c - yeast (Saccharomyces cerevisiae); (U43703) Lp11p [Saccharomyces cerevisiae]
17450	ENU01244	ANI50C6889 _1:811..1300	57-76	484-504	TPEST			112	1E-24				(AL022103) histidyl-tRNA synthetase [Schizosaccharomyces pombe]
17451	ENU01245	ANI61C2652: 22-45 538..1028	450-470	450-470	TPEST			72	3E-12				"acid phosphatase (EC 3.1.3.2) AcpH-1 precursor, lysosomal - fruit fly (Drosophila melanogaster) "
17452	ENU01246	ANI61C8330: 22-54 422..912	451-470	451-470	TPEST			31	5.8				(AF012656) putative potassium transporter AtKT1p [Arabidopsis thaliana]
17453	ENU01247	ANI61C6392: 22-52 1606..1115	452-471	452-471	TPEST			31	5.8				(Y08257) orf c04030 [Sulfolobus solfataricus]
17454	ENU01248	ANI61C1118 25-49 5:9614..10105	455-474	455-474	TPEST			32	3.4				(Z81095) cDNA EST yk421g8.3 comes from this gene; cDNA EST yk421g8.5 comes from this gene; cDNA EST yk449e1.5 comes from this gene [Caenorhabditis elegans]
17455	ENU01249	ANI61C8898: 28-50 487..979	455-478	455-478	TPEST			31	4.4				
17456	ENU01250	ANI61C2666: 29-48 673..1165	458-479	458-479	TPEST			31	4.4				
17457	ENU01251	ANI61C9112: 22-48 3526..4018	453-472	453-472	TPEST			31	4.4				
17458	ENU01252	ANI61C1116 22-52 3:2713..3206	452-473	452-473	TPEST			32	3.4				
17459	ENU01253	ANI61C8609: 28-63 70..563	449-479	449-479	TPEST			32	3.4				(U66846) orf5 [Streptococcus pneumoniae]
17460	ENU01254	ANI61C1754: 23-58 1628..2122	456-475	456-475	TPEST			102	5E-25				probable chorismate mutase (CM); (Z98529) putative chorismate mutase [Schizosaccharomyces pombe]
17461	ENU01255	ANI61C8431: 28-49 367..861	458-480	458-480	TPEST			102	5E-25				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	%	Description
17462	ENU01256	ANI61C9659: 26-45 4760..5255	26-45	458-479	TPEST				83	1E-15				chitin synthase (EC 2.4.1.16) chsB - Emericella nidulans ; (D21269) chitin synthase [Emericella nidulans] ; (D83216) chitin synthase B [Emericella nidulans] ; chitin synthetase [Emericella nidulans]
17463	ENU01257	ANI61C1188: 25-46 1760..1264	25-46	450-479	TPEST				32	3.5				(AE001593) L11 Ribosomal Protein [Chlamydia pneumoniae]
17464	ENU01258	ANI61C5136: 22-50 876..380	22-50	457-476	TPEST				32	2.6				kinesin-like protein KIF4 ; microtubule-associated motor KIF4 - mouse ; (D12646) KIF4 [Mus musculus]
17465	ENU01259	ANI61C5180: 22-54 3039..3535	22-54	443-476	TPEST				42	0.003				"112.3 KD protein in PYK1-SNC1 intergenic region ; FUN12 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Fun12p: 97kDa protein, function unknown [Saccharomyces cerevisiae] "
17466	ENU01260	ANI61C8540: 22-52 1966..2462	22-52	457-476	TPEST				39	0.027				(U53180) coded for by C. elegans cDNA CEMSE31F; Similar to alpha-SNAP protein [Caenorhabditis elegans] (L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]
17467	ENU01261	ANI61C4234: 22-50 1980..2477	22-50	458-477	TPEST				31	7.8				Alcohol dehydrogenase II
17468	ENU01262	ANI61C5359: 22-48 628..1125	22-48	451-477	TPEST				34	0.52				(AF139463) early growth response 2 protein [Homo sapiens]
17469	ENU01263	ANI61C8971: 22-48 325..823	22-48	453-478	TPEST				31	4.6				(AB011141) KIAA0569 protein [Homo sapiens]
17470	ENU01264	ANI61C1025 8:2368..2866	23-49	458-479	TPEST									
17471	ENU01265	ANI61C5977: 22-54 393..891	22-54	449-478	TPEST									
17472	ENU01266	ANI61C3031: 22-55 1532..1034	22-55	458-478	TPEST									
17473	ENU01267	ANI61C1094 9:515..1013	48-67	485-504	TPEST									
17474	ENU01268	ANI61C1139 3:663..427	22-48	462-479	TPEST									

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17475	ENU01269	ANI61C5317: 22-50 2883..2384	22-50	448-479	TPEST			81	81	4E-15			PSI protein ; DNAJ-like protein homolog - fission yeast (Schizosaccharomyces pombe) ; (L37753) Psi protein [Schizosaccharomyces pombe] ; DnaJ-like protein [Schizosaccharomyces pombe]
17476	ENU01270	ANI61C3239: 22-56 275..774	22-56	449-479	TPEST			31	31	6			transforming growth factor-beta type III receptor - chicken ; (L01121) transforming growth factor-beta type III receptor [Gallus gallus] (X57581) coat protein [Bamboo mosaic virus] ; (D26017) ORF5=25k; encodes the coat protein [Bamboo mosaic virus]
17477	ENU01271	ANI61C404:4 22-51 052..3553	22-51	449-479	TPEST			32	32	3.5			hypothetical protein YOR281c - yeast (Saccharomyces cerevisiae) ; (X89633) hypothetical protein [Saccharomyces cerevisiae] ; (Z75189) ORF YOR281c [Saccharomyces cerevisiae]
17478	ENU01272	ANI61C1089 22-52 8:650..1149	22-52	457-479	TPEST			38	38	0.035			potential proteasome component C5 (multicatalytic endopeptidase complex subunit C5) ; multicatalytic endopeptidase complex (EC 3.4.99.46) chain PRS3 - yeast (Saccharomyces cerevisiae) ; (M34777) proteasome subunit [Saccharomyces cerevisiae] ; (D00845) proteasome subunit [Saccharomyces cerevisiae] ; (X78214) PRS3 [Saccharomyces cerevisiae] ; (Z35802) ORF YBL041w [Saccharomyces cerevisiae]
17479	ENU01273	ANI61C1084: 22-54 1095..1594	22-54	447-479	TPEST			169	169	8E-42			(D64056) LMP7 of nurse shark [Ginglymostoma cirratum] RIBOnuclease E (RNase E)
17480	ENU01274	ANI61C3960: 22-54 108..607	22-54	449-479	TPEST			32	32	2.7			(Z95398) unknown [Mycobacterium leprae]
17481	ENU01275	ANI61C4862: 22-44 1434..1933	22-44	449-479	TPEST			32	32	2			
17482	ENU01276	ANI61C9745: 22-49 3851..4350	22-49	460-479	TPEST			31	31	6			
17483	ENU01277	ANI61C9978: 26-45 2987..2487	26-45	458-484	TPEST								

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17484	ENU01278	ANI61C9255: 66-85 394..898	66-85	509-528	TPEST			64	64	5E-10			hypothetical 27.7 KD protein in UME3-HDA1 intergenic region; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae); (Z71300) ORF YNL024c [Saccharomyces cerevisiae]
17485	ENU01279	ANI61C319:3 24-56 472..2960	24-56	472-494	TPEST			53	53	2E-15			putative carboxymethylglutaminyl hydrolase (DH) ; hypothetical protein YDL086w - yeast (Saccharomyces cerevisiae); (Z74134) ORF YDL086w [Saccharomyces cerevisiae]
17486	ENU01280	ANI61C8494: 59-78 1258..1770	59-78	507-529	TPEST			102	102	2E-38			hypothetical 16.9 KD protein in ALD6-PDR12 intergenic region; hypothetical protein YPL059w - yeast (Saccharomyces cerevisiae); (U39205) Lpe13p [Saccharomyces cerevisiae]
17487	ENU01281	ANI61C7555: 49-69 3253..3767	49-69	486-521	TPEST			32	32	2.2			(X92761) VP1 RNA polymerase [Infectious bursal disease virus]
17488	ENU01282	ANI61C1123 62-97 2:3621..4141	62-97	513-540	TPEST			38	38	0.000000 4			hypothetical 71.3 KD protein in SCM4-MUP1 intergenic region; hypothetical protein YGR054w - yeast (Saccharomyces cerevisiae); (Z72839) ORF YGR054w [Saccharomyces cerevisiae]
17489	ENU01283	ANI61C1024 30-49 7:3693..3172	30-49	490-509	TPEST			38	38	0.000000 4			hypothetical 64.5 KD protein in COX4-GTS1 intergenic region; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae); (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae]; (Z72708) ORF YGL186c [Saccharomyces cerevisiae]
17490	ENU01284	ANI61C134:4 23-50 274..4798	23-50	485-504	TPEST			31	31	4.9			(Z78542) predicted using Genefinder; similar to cuticlin [Caenorhabditis elegans]
17491	ENU01285	ANI61C7388: 63-82 4097..4622	63-82	518-546	TPEST			31	31	4.9			
17492	ENU01286	ANI61C3381: 50-69 634..1161	50-69	500-535	TPEST			31	31	4.9			

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17493	ENU01287	ANI61C9600: 4057..4585	27-47	494-513	TPEST				151	4E-36			hypothetical oxidoreductase in APRE-COMK intergenic region (ORFX) ; (Y14084) hypothetical protein [Bacillus subtilis] ; (Z99109) similar to alcohol dehydrogenase [Bacillus subtilis]
17494	ENU01288	ANI61C9874: 23-43	489-510	TPEST				31	8.5				(U93416) RXR [Anemonia sulcata]
17495	ENU01289	ANI61C4254: 32-52	501-520	TPEST				32	2.2				(AF055368) heat shock protein DnaJ homolog [Vibrio harveyi]
17496	ENU01290	ANI61C4296: 22-54	491-511	TPEST				31	8.5				(AF080235) glycosyl transferase homolog [Streptomyces cyanogenus]
17497	ENU01291	ANI61C8256: 23-52	497-517	TPEST				105	3E-22				(U40843) ORFS8; Method: conceptual translation supplied by author. [Saccharomyces cerevisiae]
17498	ENU01292	ANI61C6581: 38-57	509-537	TPEST				58	0.000000	05			heterogeneous nuclear ribonucleoprotein K ; transformation upregulated nuclear protein - human ; (X72727) transformation upregulated nuclear protein [Homo sapiens]
17499	ENU01293	ANI61C9637: 61-80	548-567	TPEST				173	8E-43				Pepidyl-prolyl cis-trans isomerase (PPIase) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
17500	ENU01294	ANI61C8828: 42-62	529-552	TPEST				37	0.0007				(U43281) Lpg18p [Saccharomyces cerevisiae]
17501	ENU01295	ANI61C8803: 27-46	515-539	TPEST				34	0.79				(Z81523) similar to Myb DNA-binding proteins (2 domains); cDNA EST yk300c3.5 comes from this gene [Caenorhabditis elegans]
17502	ENU01296	ANI61C7538: 25-44	525-544	TPEST				55	0.000000	4			(AF021797) peroxisomal receptor for PTS2-containing proteins Pex7p [Pichia pastoris]

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17503	ENU01297	ANI61C7165: 1783..1218	25-44	522-548	TPEST				34	0.62			hypothetical 9.1 KD protein C23C11.12 in chromosome I; (Z98559) very hypothetical protein [Schizosaccharomyces pombe]
17504	ENU01298	ANI61C953:1 812..1243	22-47	522-549	TPEST			71		5E-12			"ATP synthase alpha chain, mitochondrial precursor; H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - Neurospora crassa; (M84191) mitochondrial ATPase alpha-subunit [Neurospora crassa]"
17505	ENU01299	ANI61C3229: 22-51 1354..1925	22-51	520-551	TPEST			106		2E-22			"ubiquitin / ribosomal protein CEP52 - yeast (Saccharomyces cerevisiae); (X05728) ubiquitin [Saccharomyces cerevisiae]; (X05729) ubiquitin [Saccharomyces cerevisiae]; (X73541) UBI2 [Saccharomyces cerevisiae]; (Z28319) ORF YKR094c [Saccharomyces cerevisiae]; (Z38059) ubi1, len: 128, CAI: 0.74, spliced, S34428 S34428 ubiquitin-52 amino acid fusion protein [Saccharomyces cerevisiae]"
17506	ENU01300	ANI61C2576: 46-74 492..1065	46-74	545-577	TPEST			76		1E-16			ubiquitin-like protein SMT3; SMT3 protein - yeast (Saccharomyces cerevisiae); (U27233) Smt3p [Saccharomyces cerevisiae]; (U33057) suppressor of MIF2 mutations; CAI: 0.31 [Saccharomyces cerevisiae]
17507	ENU01301	ANI61C2666: 24-43 3325..3907	24-43	544-564	TPEST			32		2.5			light repressible receptor protein kinase - Arabidopsis thaliana; (X97774) light repressible receptor protein kinase [Arabidopsis thaliana]
17508	ENU01302	ANI61C2751: 26-50 280..881	26-50	564-585	TPEST			32		3.5			(AB007769) polygalacturonase B [Aspergillus oryzae]
17509	ENU01303	ANI61C1001 29-48 9:3435..4045	29-48	566-597	TPEST			35		0.4			(AF037260) non-receptor protein tyrosine kinase Ack [Mus musculus]
17510	ENU01304	ANI61C5388: 31-50 1023..1634	31-50	569-600	TPEST								

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17511	ENU01305	ANI61C8549: 3074..3690	22-41	569-596	TPEST			34	34	1.2			hypothetical 15.6 KD protein in CSN-ADHB intergenic region ; (U93875) Yra1 [Bacillus subtilis] ; (X92868) unknown [Bacillus subtilis] ; (Z99117) similar to hypothetical proteins from B. subtilis [Bacillus subtilis] ubiquitin-conjugating enzyme E2-23 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) ; 23K ubiquitin carrier protein E2 - wheat ; (M28059) ubiquitin carrier protein [Triticum vulgare]
17512	ENU01306	ANI61C5686: 104..729	22-42	578-605	TPEST			34	34	0.091			hypothetical 8.2 KD protein C26A3.14C in chromosome I ; (Z69240) very hypothetical protein [Schizosaccharomyces pombe] (AF032382) metalloprotease-disintegrin [Xenopus laevis] ARP2/3 complex 21 KD subunit (P21-ARC) ; hypothetical protein YLR370c - yeast (Saccharomyces cerevisiae) ; (U19103) Ylr370cp [Saccharomyces cerevisiae] (AF097832) malonyl-CoA decarboxylase precursor [Homo sapiens]
17513	ENU01307	ANI61C7805: 59-78 4634..5266	59-78	629-649	TPEST			40	40	0.016			(AF084484) putative outer membrane protein [Helicobacter pylori]
17514	ENU01308	ANI61C3240: 62-82 4092..4852	62-82	752-780	TPEST			32	32	4.6			(M17199) Fus1 fusion peptide [Saccharomyces cerevisiae] ; (M16717) FUS1 protein [Saccharomyces cerevisiae] (AB006188) acidic class III chitinase OsChib3a [Oryza sativa]
17515	ENU01309	ANI61C1058 9:6896..6386	23-47	248-275	TPEST	cluster1512_1		29	29	0.052	99		
17516	ENU01310	ANI61C9440: 30-49 741..53	30-49	204-226	TPEST	cluster1544_1		30	30	2.9	99		
17517	ENU01311	ANI61C4443: 444..1			TPEST	cluster296_1		29	29	5.9	99		
17518	ENU01312	ANI61C6466: 104-130 1857..1207	104-130	274-293	TPEST	cluster1763_1					100		
17519	ENU01313	ANI61C8621: 27-48 542..310	27-48	358-385	TPEST	cluster2087_1		32	32	2.5	99		
17520	ENU01314	ANI61C8638: 24-51 205..371	24-51	361-388	TPEST	cluster4468_1		31	31	3.4	98		
17521	ENU01315	ANI61C915:7 72..1054			TPEST	cluster3413_2					100		
17522	ENU01316	ANI61C6923: 1927..1021			TPEST	cluster1947_1					99		

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17523	ENU01317	ANI61C1031			TPEST	cluster1615_1					99		
17524	ENU01318	ANI61C3480: 3:2651..2160			TPEST	cluster1734_1					100		
17525	ENU01319	ANI61C246:1 1923..2208	30-51	501-528	TPEST	cluster145_1		44	0.0007		97		A-agglutinin attachment subunit precursor ; a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae) ; (M60590) a-agglutinin core subunit [Saccharomyces cerevisiae] ; (Z71659) ORF YNR044w [Saccharomyces cerevisiae]
17526	ENU01320	ANI61C1253: 513..1			TPEST	cluster197_1					99		
17527	ENU01321	ANI61C353:3 704..3055			TPEST	cluster95_1		32	0.66		100		(U02970) unknown [Prototheca wickerhamii]
17528	ENU01322	ANI61C2481: 110..1			TPEST	cluster2573_1		29	5.7		100		(Z54284) D2085.2 [Caenorhabditis elegans]
17529	ENU01323	ANI61C3543: 57-76 672..475		302-329	TPEST	cluster3142_1		66	1E-10		97		(AJ001732) rAsp f 4 [Aspergillus fumigatus]
17530	ENU01324	ANI61C1120: 478..280			TPEST	cluster3142_1		57	0.000000	05	97		60S ribosomal protein L27A (L29) (CRP1) ; ribosomal protein L27a.e - Neurospora crassa ; (X06320) put. ribosomal protein [Neurospora crassa] ; (X13254) put. ribosomal protein (AA 1-149) [Neurospora crassa]
17531	ENU01325	ANI61C1064 9:387..1121			TPEST	cluster1086_1					100		
17532	ENU01326	ANI61C1035 6:2570..2951			TPEST	cluster202_1					98		
17533	ENU01327	ANI61C3610: 22-40 106..1	22-40	162-182	TPEST	cluster5177_1		31	1.1		96		"(Z34799) predicted using Genefinder; contains a proline-rich domain, and partial similarity to RD protein; cDNA EST EMBL:M89085 comes from this gene; cDNA EST EMBL:C10105 comes from this gene; cDNA EST yk480b4.5 comes from this.. "
17534	ENU01328	ANI61C5231: 22-48 281..729	22-48	430-457	TPEST	cluster1916_1		35	0.37		98		(U00066) weakly similar to notch protein in and just upstream of the poly-Gln region [Caenorhabditis elegans]

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17535	ENU01329	ANI61C7657: 702..1535	22-48	200-219	TPEST	cluster1739_1					99	
17536	ENU01330	ANI61C6509: 24-43	24-43	275-297	TPEST	cluster82_1		33	0.49		100	(U41293) unknown [Saccharomyces cerevisiae]
17537	ENU01331	ANI61C5234: 746..203			TPEST	cluster5_1					98	
17538	ENU01332	ANI61C6237: 1171..663			TPEST	cluster9200_1					99	
17539	ENU01333	ANI61C1073: 1..581			TPEST	cluster1562_1					100	
17540	ENU01334	ANI61C6247: 0:121..1			TPEST	cluster2835_1					100	
17541	ENU01335	ANI61C465:7 2985..2539			TPEST	cluster7959_1					99	
17542	ENU01336	ANI61C8418: 491..7090	22-43	524-551	TPEST	cluster102_1					96	
17543	ENU01337	ANI61C7015: 1248..2036			TPEST	cluster834_1					99	
17544	ENU01338	ANI61C6602: 6784..7046	102-123	473-498	TPEST	cluster5791_1		59	0.000000	003	99	(AL031541) putative dehydrogenase [Streptomyces coelicolor]
17545	ENU01339	ANI61C5686: 28-48	28-48	377-404	TPEST	cluster5752_1		31	5.3		100	(L20476) nicein [Mus musculus]
17546	ENU01340	ANI61C7016: 1..729	22-41	228-247	TPEST	cluster2753_1		32	1.3		98	"Chain C, Klebsiella Aerogenes Urease, H134a Variant "
17547	ENU01341	ANI61C5697: 5055..5615	27-47	173-198	TPEST	cluster8536_1		29	7		100	(Z81576) predicted using Genefinder [Caenorhabditis elegans]
17548	ENU01342	ANI61C1968: 1..322			TPEST	cluster6504_1					98	
17549	ENU01343	ANI61C7388: 306..654			TPEST	cluster1642_1					97	
17550	ENU01344	ANI61C1970: 5123..5205			TPEST	cluster1431_1					99	
17551	ENU01345	ANI61C7027: 110..592	71-98	245-272	TPEST	cluster2734_1		30	4.3		96	(Z81513) F26D2.13 [Caenorhabditis elegans]
17552	ENU01346	ANI61C8431: 1..485			TPEST	cluster6091_1					100	
17553	ENU01347	ANI61C8772: 26-44	26-44	810-829	TPEST	cluster2751_1		32	5.3		99	(AC004493) KIAA0324 [Homo sapiens]
17554	ENU01348	ANI61C1003 1162..1349			TPEST	cluster5455_1					97	
		ANI61C1003 6:462..766										

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17555	ENU01349	ANI61C1129 4:174..657	31-53	169-188	TPEST	cluster3593_1		41	0.0001		100		ADP/ATP carrier protein (AF085429) [Candida parapsilosis]
17556	ENU01350	ANI61C1041 9:931..1432	22-42	218-240	TPEST	cluster1735_1		30	4.4		100		nikD protein - Escherichia coli; (U00039) nikD [Escherichia coli]; (AE000423) ATP-binding protein of nickel transport system [Escherichia coli]
17557	ENU01351	ANI61C1473: 3644..4570			TPEST	cluster3819_1		33	0.3		99		ISL2 protein - Lactobacillus helveticus; (X77332) mobile genetic element [Lactobacillus helveticus]
17558	ENU01352	ANI61C4167: 1..315	44-63	575-596	TPEST	cluster554_1		33	1.6		97		(AF010227) receptor-associated coactivator 3 [Homo sapiens]
17559	ENU01353	ANI61C1042 9:2617..3123			TPEST	cluster10082_1		32	0.75		98		(AL035521) putative protein [Arabidopsis thaliana]
17560	ENU01354	ANI61C1513: 1..189	26-45	227-246	TPEST	cluster9499_1		32	2.4		99		Ig kappa chain V-J region (T24-9) - human (fragment); (Z27174) IG light chain variable region (VJ) [Homo sapiens]
17561	ENU01355	ANI61C1044 4:166..472	39-59	421-448	TPEST	cluster2130_1		55	1E-11		99		Prephenate dehydrogenase (NADP+) (PRDH); prephenate dehydrogenase (NADP+) (EC 1.3.1.13) - yeast (Saccharomyces cerevisiae); (Z36035) ORF YBR166c [Saccharomyces cerevisiae]
17562	ENU01356	ANI61C630:1 ..853	102-127	314-341	TPEST	cluster199_1		32	1.6		100		(AC005309) unknown protein [Arabidopsis thaliana]
17563	ENU01357	ANI61C7751: 919..339			TPEST	cluster8165_1		30	7		99		"Pre-RRNA processing protein SRD1; SRD1 protein - yeast (Saccharomyces cerevisiae); (X06322) open reading frame (AA 1 - 225) [Saccharomyces cerevisiae]; (X59720) YCR018c, len:225 [Saccharomyces cerevisiae]"
17564	ENU01358	ANI61C9283: 4849..4381	26-45	160-184	TPEST	cluster1651_1		36	0.22		99		(AC000348) T7N9.12 [Arabidopsis thaliana]
17565	ENU01359	ANI61C8934: 1977..1618	61-78	341-366	TPEST	cluster3049_1							
17566	ENU01360	ANI61C1559: 2194..1598			TPEST	cluster3480_1							
17567	ENU01361	ANI61C584:3 47..1244	102-125	537-564	TPEST	cluster385_1							

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17568	ENU01362	ANI61C8479: 161..1	45-64	316-335	TPEST	cluster4886_1		32	32	2.4	96	(AF041382) microtubule binding protein D-CLIP-190 [Drosophila melanogaster]
17569	ENU01363	ANI61C8138: 1614..1813	49-68	410-437	TPEST	cluster7184_1		33	33	1.5	99	(D64015) T-cluster binding protein [Homo sapiens]
17570	ENU01364	ANI61C6322: 110..558			TPEST	cluster2601_1					97	
17571	ENU01365	ANI61C9327: 2106..2554			TPEST	cluster8203_1		30	30	1.9	100	(U87460) putative endothelin receptor type B-like protein [Homo sapiens]
17572	ENU01366	ANI61C7768: 303..797	66-93	391-418	TPEST	cluster1794_1		32	32	1.8	100	Invected protein ; homeotic protein Invected - fruit fly (Drosophila melanogaster) ; (X05273) invected gene product (AA 1-576) [Drosophila melanogaster]
17573	ENU01367	ANI61C2166: 788..1243			TPEST	cluster5837_1					99	
17574	ENU01368	ANI61C1141: 0-2511..2083	22-44	457-484	TPEST	cluster227_1					99	
17575	ENU01369	ANI61C2172: 1225..767			TPEST	cluster1042_1					98	
17576	ENU01370	ANI61C4811: 684..363	43-64	491-518	TPEST	cluster9335_1		32	32	4.3	100	(Z70309) R102.7 [Caenorhabditis elegans]
17577	ENU01371	ANI61C2786: 94..411			TPEST	cluster10895_1					98	
17578	ENU01372	ANI61C7142: 521..939			TPEST	cluster1887_1		32	32	4.7	99	(AF067216) No definition line found [Caenorhabditis elegans]
17579	ENU01373	ANI61C1045: 9-1520..936	50-74	528-547	TPEST	cluster4943_1					99	
17580	ENU01374	ANI61C1092: 8-2247..897			TPEST	cluster1312_2		29	29	4.5	100	(Z81560) K02E2.5 [Caenorhabditis elegans]
17581	ENU01375	ANI61C1024: 1690..1009			TPEST	cluster548_1		29	29	5.8	99	hypothetical 180.2 KD protein in FAA4-HOR7 intergenic region ; probable membrane protein YMR247c - yeast (Saccharomyces cerevisiae)
17582	ENU01376	ANI61C1626: 1305..426			TPEST	cluster4702_1					99	
17583	ENU01377	ANI61C2195: 708..1			TPEST	cluster1093_1		29	29	4.8	98	Shufflon-specific DNA recombinase ; probable integrase - Escherichia coli ; (X12577) rci protein (AA 1-384) [Escherichia coli]

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17584	ENU01378	ANI61C289:2 882..1832			TPEST	cluster445_2					99		
17585	ENU01379	ANI61C1024 2:1738..1095	68-87	297-316	TPEST	cluster46_1		31	4.6		100		(AF064823) NADH dehydrogenase subunit 2 [Sarcophyton glaucum]
17586	ENU01380	ANI61C8193: 1014..1490	53-72	391-418	TPEST	cluster9706_1		31	3.7		99		FIXR protein ; fixR protein - Bradyrhizobium japonicum ; (X06167) fixR gene product (AA 1 - 278) [Bradyrhizobium japonicum]
17587	ENU01381	ANI61C8986: 4600..3743			TPEST	cluster1342_1					100		
17588	ENU01382	ANI61C6339: 2309..1292			TPEST	cluster259_1		60	0.000000	003	99		(AF039038) Similar to acyl-coA dehydrogenase; coded for by C. elegans cDNA yk335a7.3; coded for by C. elegans cDNA yk335a7.5 [Caenorhabditis elegans]
17589	ENU01383	ANI61C1146 7:1156..660			TPEST	cluster1179_1					99		
17590	ENU01384	ANI61C7165: 1807..1218			TPEST	cluster4098_1		28	7.5		100		(AF080235) NDP-hexose synthetase homolog [Streptomyces cyanogenus]
17591	ENU01385	ANI61C39:40 6..865	24-45	171-198	TPEST	cluster523_1		31	1.9		99		(U22016) retinoid X receptor interacting protein [Mus musculus]
17592	ENU01386	ANI61C7486: 3090..3341	22-44	321-348	TPEST	cluster268_1					97		
17593	ENU01387	ANI61C2935: 231..571	58-85	299-318	TPEST	cluster9762_1		76	4E-15		100		(AL033388) putative 50s ribosomal protein 114 [Schizosaccharomyces pombe]
17594	ENU01388	ANI61C3288: 3409..2600	56-75	245-264	TPEST	cluster5614_1		35	0.12		100		guanine nucleotide-binding protein beta subunit-like protein (cross-pathway control WD-repeat protein CPC-2) ; CPC2 protein - Neurospora crassa ; (X81875) CPC2 protein [Neurospora crassa]
17595	ENU01389	ANI61C7805: 1055..1604			TPEST	cluster4513_1					99		
17596	ENU01390	ANI61C435:3 206..3889			TPEST	cluster344_1					98		
17597	ENU01391	ANI61C9395: 6602..5856			TPEST	cluster1755_1					99		
17598	ENU01392	ANI61C6804: 2458..1883			TPEST	cluster4647_1					100		

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17599	ENU01393	ANI61C9397: 1369..1905			TPEST	cluster762_1					98		
17600	ENU01394	ANI61C9409: 48-67 2370..2856		191-209	TPEST	cluster275_1		47		0.00007	99		hypothetical 52.5 KD protein ZK945.1 in chromosome II ; (Z48544) similar to esterase; cDNA EST EMBL:T02204 comes from this gene; cDNA EST EMBL:D68873 comes from this gene; cDNA EST yk206h6.3 comes from this gene; cDNA EST yk206h6.5 comes from this gene; cDNA EST yk299e8.3 comes from...
17601	ENU01395	ANI61C941:1 117..602			TPEST	cluster19_1		48		0.00001	100		(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]
17602	ENU01396	ANI61C9418: 1..948	22-43	167-194	TPEST	cluster7260_1					98		
17603	ENU01397	ANI61C9422: 1802..1418	23-42	338-358	TPEST	cluster8272_1		31		3.6	99		(L40459) latent transforming growth factor-beta binding protein [Mus musculus]
17604	ENU01398	ANI61C2251: 1305..817			TPEST	cluster3259_1					100		
17605	ENU01399	ANI61C3368: 7485..8422	102-124	612-631	TPEST	cluster2767_1		64		7E-10	100		hypothetical 25.3 KD protein in PEX17-MER1 intergenic region ; hypothetical protein YNL213c - yeast (Saccharomyces cerevisiae) ; (X78898) N1323 [Saccharomyces cerevisiae] ; (Z71489) ORF YNL213c [Saccharomyces cerevisiae]
17606	ENU01400	ANI61C1026 8:597..1			TPEST	cluster658_1					99		
17607	ENU01401	ANI61C1194: 219..694			TPEST	cluster1975_1					99		
17608	ENU01402	ANI61C2364: 1747..1387			TPEST	cluster2952_1					98		
17609	ENU01403	ANI61C1111 6:1..415			TPEST	cluster902_1					96		
17610	ENU01404	ANI61C7935: 22-49 2554..2136		308-327	TPEST	cluster11415_1					99		

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17611	ENU01405	ANI61C6091: 25-45 994..593	592-612	592-612	TPEST	cluster9842_1		130	130	1E-29	99		(U62929) multidrug resistance protein 1 [Filobasidiella neoformans]; (U62930) multidrug resistance protein 1 [Filobasidiella neoformans] (AJ223999) PCZA363.3 [Amycolatopsis orientalis] (AF045014) translation release factor eRF3 [Podospora anserina]
17612	ENU01406	ANI61C9064: 102-125 347..1079	362-389	362-389	TPEST	cluster5610_1		31	31	6	99		
17613	ENU01407	ANI61C6422: 1679..2422			TPEST	cluster557_1		33	33	0.43	99		
17614	ENU01408	ANI61C6105: 1727..2188			TPEST	cluster1636_1					100		
17615	ENU01409	ANI61C2978: 22-49 237..71	188-215	188-215	TPEST	cluster4733_1		30	30	4	98		hypothetical 98.1 KD protein in ROM1-UPF3 intergenic region; hypothetical protein YGR071c - yeast (Saccharomyces cerevisiae); (Z72856) ORF YGR071c [Saccharomyces cerevisiae]
17616	ENU01410	ANI61C6431: 232..511			TPEST	cluster515_1					100		
17617	ENU01411	ANI61C2449: 22-49 335..514	505-524	505-524	TPEST	cluster11421_1					99		
17618	ENU01412	"ANI61C7284 22-47 :721..486, ANI61C1056 5:749..344"	360-379	360-379	MCEST	"j9h03a1.r1, j9h03a1.fl"		31	31	4.4			ANI61CM23046
17619	ENU01413	"ANI61C4704 :422..899, ANI61C356:2 934..3239"			MCEST	"x8e05a1.r1, x8e05a1.fl"		39	39	0.012			ANI61CM12685
17620	ENU01414	"ANI61C1141 2:902..395, ANI61C6395: 515..28"			MCEST	"z5c08a1.r1, z5c08a1.fl"		34	34	0.66			(AL030978) putative protein [Arabidopsis thaliana]
17621	ENU01415	"ANI61C4586 24-51 :1161..216, ANI61S160:3 09..1"	241-266	241-266	MCEST	"x7d08a1.r1, x7d08a1.fl"		33	33	0.54			(Z81586) predicted using Genefinder [Caenorhabditis elegans]
17622	ENU01416	"ANI61C1556 62-89 :1871..2127, ANI61C6675: 1..370"	322-348	322-348	MCEST	"i3a04a1.r1, i3a04a1.fl"		42	42	0.002			(AB018284) KIAA0741 protein [Homo sapiens]

Seq num	Seq.id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17623	ENU01417	"ANI61C8655 :121..57, ANI61C3164: 444..1"	22-45	379-405	MCEST	"o0c11a1.r1, o0c11a1.fl"		50	50	0.000009			nuclear transport factor 2 (NTF-2) (nuclear transport factor P10) ; hypothetical protein YER009w - yeast (Saccharomyces cerevisiae) ; (U18778) Ntf2p: Nuclear Transport Factor 2 [Saccharomyces cerevisiae] "elongation factor 2 (EF-2) ; (AE000876) translation elongation factor, EF-2 [Methanobacterium thermoautotrophicum]" [Schizosaccharomyces pombe]
17624	ENU01418	"ANI61C4903 :2045..1437, ANI61C9734: 1268..873"			MCEST	"m6a10a1.r1, m6a10a1.fl"		30	30	7.2			
17625	ENU01419	"ANI61C9301 :796..1232, ANI61C7484: 1126..1653"	26-46	478-505	MCEST	"z3a11a1.r1, z3a11a1.fl"		99	99	1E-25			
17626	ENU01420	"ANI61C1051 :7:1421..1334, ANI61C9111: 1393..948"	22-44	397-424	MCEST	"n3e04a1.r1, n3e04a1.fl"		35	35	0.26			(AF129887) ORF1 protein [TT virus]
17627	ENU01421	"ANI61C6610 :965..1484, ANI61C3639: 1..432"			MCEST	"u4g08a1.r1, u4g08a1.fl"		32	32	2.8			(Z66565) cDNA EST EMBL:D70617 comes from this gene; cDNA EST EMBL:C10400 comes from this gene; cDNA EST EMBL:C10605 comes from this gene; cDNA EST EMBL:C12377 comes from this gene; cDNA EST EMBL:C13473 comes from this gene; cDN...
17628	ENU01422	"ANI61C5489 :579..491, ANI61C9734: 1237..873"	22-48	284-303	MCEST	"flh08a1.r1, flh08a1.fl"		30	30	6.2			ANI61CM30058
17629	ENU01423	"ANI61C8742 :1061..419, ANI61C1138 6:661..194"	22-47	404-427	MCEST	"r5h03a1.r1, r5h03a1.fl"		36	36	0.16			(AL035064) protein kinase skp1p [Schizosaccharomyces pombe]
17630	ENU01424	"ANI61C2524 :253..465, ANI61C2973: 1974..2387"	23-42	287-306	MCEST	"k0a08a1.r1, k0a08a1.fl"		119	119	8E-27			ANI61CMS2644

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17631	ENU01425	"ANI61C9187 :100..1, ANI61C1037 2:1443..1134"	53-80	262-288	MCEST	"k5d05a1.r1, k5d05a1.fl"		59	59	0.000000			ANI61CM33423
17632	ENU01426	"ANI61C6862 :705..1032, ANI61C8239: 2125..2608"	22-47	242-264	MCEST	"m0d07a1.r1, m0d07a1.fl"		31	31	5.7			ANI61CM29073
17633	ENU01427	"ANI61C8256 :1722..2265, ANI61C126:2 58..636"			MCEST	"r3h08a1.r1, r3h08a1.fl"		44	44	0.0005			30 KD heat shock protein ; heat-shock protein 30 - Emericella nidulans ; (D32070) heat-shock protein 30 (HSP30) [Emericella nidulans] ; heat shock protein 30 [Emericella nidulans] ANI61CM44025
17634	ENU01428	"ANI61C1102 :9:1199..1584, ANI61C6494: 5368..5685"	23-47	269-296	MCEST	"m0h07a1.r1, m0h07a1.fl"		30	30	5			
17635	ENU01429	"ANI61C2451 :1000..1120, ANI61C5287: 2067..2417"			MCEST	"h0d12a1.r1, h0d12a1.fl"		32	32	1.2			ANI61CM28276
17636	ENU01430	"ANI61C8789 :1..645, ANI61C3400: 303..742"	22-42	398-417	MCEST	"i3f01a1.r1, i3f01a1.fl"		36	36	0.15			clathrin assembly protein AP180 short form - rat ; (X68877) assembly protein 180 (AP180) [Rattus norvegicus]
17637	ENU01431	"ANI61C7182 :227..700, ANI61C6591: 142..750"	41-65	563-587	MCEST	"n8a06a1.r1, n8a06a1.fl"		35	35	0.003			ANI61CM45211
17638	ENU01432	"ANI61C7673 :235..1652, ANI61C4595: 81..446"	22-46	321-344	MCEST	"y8h08a1.r1, y8h08a1.fl"		30	30	6.3			(L29246) UL103 homologue [Murine cytomegalovirus]
17639	ENU01433	"ANI61C9872 :1314..1216, ANI61C7232: 351..13"	23-42	219-238	MCEST	"n3c07a1.r1, n3c07a1.fl"		31	31	3.2			ANI61CM28370

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17640	ENU01434	"ANI61C1980 :217..579, ANI61C4162: 3806..4244"	65-91	390-417	MCEST	"n8b03a1.r1, n8b03a1.fl"			157	5E-38			"alpha-L-arabinofuranosidase precursor (arabinoxylan arabinofuranohydrolase) ; (Z78011) (1,4)-beta-D-arabinoxylan arabinofuranohydrolase [Aspergillus niger] "
17641	ENU01435	"ANI61C1899 :1460..1781, ANI61C5951: 259..563"	26-49	248-267	MCEST	"w5b10a1.r1, w5b10a1.fl"		30	30	5.9			(AL022244) hypothetical protein [Schizosaccharomyces pombe]
17642	ENU01436	"ANI61C7770 :1..323, ANI61C1069 5:105..432"	33-60	279-306	MCEST	"n3b02a1.r1, n3b02a1.fl"		52	52	0.000001			ANI61CM40121
17643	ENU01437	"ANI61C2219 :588..9, ANI61C426:3 52..1"	22-41	223-250	MCEST	"m6g01a1.r1, m6g01a1.fl"		116	116	4E-26			"1,4-alpha-glucan branching enzyme (glycogen branching enzyme) ; 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - yeast (Saccharomyces cerevisiae) ; (U18530) 1,4-alpha-glucan branching enzyme [Saccharomyces cerevisiae] "
17644	ENU01438	"ANI61C9501 :454..838, ANI61C8893: 4427..4742"	22-43	249-268	MCEST	"t2c07a1.r1, t2c07a1.fl"							ANI61CM4461
17645	ENU01439	"ANI61C6862 :94..483, ANI61C8239: 2117..2507"	22-49	250-272	MCEST	"b0h07a1.r1, b0h07a1.fl"		31	31	4.1			ANI61CM29073
17646	ENU01440	"ANI61C3773 :1028..754, ANI61C944:6 86..292"			MCEST	"c6c11a1.r1, c6c11a1.fl"		30	30	7.1			ANI61CM36375
17647	ENU01441	"ANI61C2967 :2121..2532, ANI61C4167: 1..395"	108-127	293-312	MCEST	"m7e11a1.r1, m7e11a1.fl"		31	31	5.5			(Y14459) polyprotein [porcine enterovirus 9]
17648	ENU01442	"ANI61C3279 :1318..868, ANI61C879:1 331..961"	22-49	320-339	MCEST	"w5g07a1.r1, w5g07a1.fl"		31	31	2.9			(AF054826) VAMP5 [Rattus norvegicus]

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17649	ENU01443	"ANI61C2870 :571..965, ANI61C4864: 2044..2382"	22-43	203-220	MCEST	"y4d10a1.r1, y4d10a1.fl"		30	30	5.5			74 KD serum albumin precursor ; 74K albumin precursor - African clawed frog
17650	ENU01444	"ANI61C8821 :2544..2217, ANI61C7328: 7157..6846"	22-47	225-244	MCEST	"w5b11a1.r1, w5b11a1.fl"		32	32	1.2			"(Z97348) predicted using hexExon; MAL3P1.12 (PFC0150w), Human hypothetical protein KIAA0249-related protein len: 1160 aa; Similarity to 2 human and an yeast hypothetical gene. Human hypothetical protein KIAA0249 (SW:Y249_HUMA..." ANI61CM50706
17651	ENU01445	"ANI61C1113 :5:3232..2655, ANI61C2269: 1156..671"	60-79	420-447	MCEST	"g6e03a1.r1, g6e03a1.fl"		32	32	3.3			
17652	ENU01446	"ANI61C2394 :1035..773, ANI61C1739: 3030..2657"	24-48	307-326	MCEST	"d4h03a1.r1, d4h03a1.fl"		82	82	1E-15			"Glucoamylase, Granular Starch-Binding Domain, Nmr, Minimized Average Structure ; Glucoamylase, Granular Starch-Binding Domain, Nmr, 5 Structures ; Glucoamylase, Granular Starch-Binding Domain Complex With Cyclodextrin, Nmr, Minimized Average Structure ; Glucoamylase, Granular Starch-Binding Domain Complex With Cyclodextrin, Nmr, 5 Structures "
17653	ENU01447	"ANI61C7652 :1075..880, ANI61C3745: 566..169"	62-89	349-371	MCEST	"w6h06a1.r1, w6h06a1.fl"		36	36	0.096			(AC006283) hypothetical protein [Arabidopsis thaliana]
17654	ENU01448	"ANI61C1041 :3:279..1, ANI61C1174: 1038..617"			MCEST	"r7g11a1.r1, r7g11a1.fl"		35	35	0.31			(AE001393) phospholipase A2-like a/b fold hydrolase [Plasmodium falciparum]
17655	ENU01449	"ANI61C2737 :738..813, ANI61C1194: 348..683"	61-80	216-239	MCEST	"r1d10a1.r1, r1d10a1.fl"		33	33	0.63			(Z99162) hypothetical protein [Schizosaccharomyces pombe]

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17656	ENU01450	"ANI61C7853 :2165..2592, ANI61C9581: 693..1308"	35-54	571-594	MCEST	"c9h06a1.rl, c9h06a1.fl"		50	50	0.00001		urea amidolyase [Pichia jadinii]
17657	ENU01451	"ANI61C3856 :5281..5547, ANI61C4618: 226..571"	29-48	304-324	MCEST	"c4c12a1.rl, c4c12a1.fl"		31	31	2.5		nucleolar protein p120 - mouse (fragment)
17658	ENU01452	"ANI61C9663 :2495..2828, ANI61C8533: 570..1025"	22-45	408-429	MCEST	"r3a11a1.rl, r3a11a1.fl"		31	31	5.2		soluble vascular endothelial cell growth factor receptor - human ; (U01134)
17659	ENU01453	"ANI61C1007 :7..345..54, ANI61C6856: 1302..921"	65-84	340-360	MCEST	"v3f04a1.rl, v3f04a1.fl"		30	30	6.8		soluble vascular endothelial cell growth factor receptor [Homo sapiens] (X70339) exon 2 [Saccharomyces cerevisiae]
17660	ENU01454	"ANI61C2394 :2893..3227, ANI61C6325: 3137..3527"	57-84	346-367	MCEST	"c9f01a1.rl, c9f01a1.fl"		170	170	5E-53		probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) ; (U34740)
17661	ENU01455	"ANI61C8914 :293..604, ANI61S4152: 1..407"	42-68	359-384	MCEST	"g3d06a1.rl, g3d06a1.fl"		31	31	5.7		putative p450 monooxygenase [Emmericella nidulans] ANI61CM38315
17662	ENU01456	"ANI61C1010 :0..2843..2981, ANI61C7089: 71..481"	22-45	362-389	MCEST	"o6b02a1.rl, o6b02a1.fl"						ANI61CM41145
17663	ENU01457	"ANI61C6597 :1..72, ANI61C3524: 50..592"	60-87	332-353	MCEST	"j4f01a1.rl, j4f01a1.fl"		39	39	0.023		MOESIN ; (U14180) moesin [Lytechinus variegatus]
17664	ENU01458	"ANI61C6625 :201..1, ANI61C1899: 1665..1262"	22-47	359-379	MCEST	"n3f02a1.rl, n3f02a1.fl"		117	117	3E-26		protein disulfide isomerase precursor (PDI) ; protein disulfide-isomerase (EC 5.3.4.1) - Aspergillus niger ; (X89449) protein disulfide isomerase [Aspergillus niger] ; (X98797) protein disulfide isomerase [Aspergillus niger]

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17665	ENU01459	"ANI61C4700 :432..1, ANI61C1138 0:911..599"	22-49	268-287	MCEST	"h8f01a1.rl, h8f01a1.fl"			33	0.55		(Z99292) hypothetical protein [Schizosaccharomyces pombe]
17666	ENU01460	"ANI61C6726 :1200..1621, ANI61C4083: 99..417"	63-90	271-297	MCEST	"y3b09a1.rl, y3b09a1.fl"			30	5		ANI61CM52592
17667	ENU01461	"ANI61C9301 :798..1167, ANI61C9566: 1029..1512"	40-59	409-436	MCEST	"m6d04a1.rl, m6d04a1.fl"			34	0.86		(AF017250) vitellogenin precursor [Oreochromis aureus]
17668	ENU01462	"ANI61C2308 :840..543, ANI61C1899: 1653..1235"	22-45	365-384	MCEST	"m6b06a1.rl, m6b06a1.fl"			129	1E-29		protein disulfide isomerase precursor (PDI) ; protein disulfide-isomerase (EC 5.3.4.1) - Aspergillus niger ; (X89449) protein disulfide isomerase [Aspergillus niger] ; (X98797) protein disulfide isomerase [Aspergillus niger]
17669	ENU01463	"ANI61C1102 :9:691..1191, ANI61C346:2 933..3336"	22-45	360-382	MCEST	"f2b12a1.rl, f2b12a1.fl"			31	3.3		ANI61CM33599
17670	ENU01464	"ANI61C7184 :4690..4574, ANI61C9821: 6436..6132"	22-48	218-241	MCEST	"c6d06a1.rl, c6d06a1.fl"			205	2E-52		(U95045) velvet A [Emericella nidulans]
17671	ENU01465	"ANI61C6741 :1692..1918, ANI61C8333: 1318..1784"	27-54	421-440	MCEST	"u4c01a1.rl, u4c01a1.fl"			32	2.2		(D83390) connectin/titin [Gallus gallus]
17672	ENU01466	"ANI61C6814 :4164..3779, ANI61C971:4 473..4034"	22-46	382-401	MCEST	"d4h01a1.rl, d4h01a1.fl"			33	1.2		ANI61CM36803
17673	ENU01467	"ANI61C8310 :3802..3562, ANI61C1111 8:681..270"			MCEST	"z7h03a1.rl, z7h03a1.fl"						

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17682	ENU01476	ANI61C4101: 450..870	97-114	456-475	NAP		g2117305	135	48	0.00004			(Z95620) putative dna binding protein [Schizosaccharomyces pombe]
17683	ENU01477	ANI61S3147: 506..23	109-130	531-550	NAP		g4512655	622	135	2.00E-54	84	45	(AC007048) putative protein phosphatase 2C [Arabidopsis thaliana]
17684	ENU01478	ANI61C893:3 352..4027	77-97	691-710	NAP		g1723528	504	73	1.00E-12	36	21	hypothetical 53.0 KD protein C22E12.17C in chromosome I; (Z70043) unknown [Schizosaccharomyces pombe]
17685	ENU01479	ANI61C9776: 69..1349	90-113	1310-1329	NAP		g3766375	124	81	2.00E-14	29	39	"(AL031907) putative transcriptional regulation protein, trp-asp repeat containing [Schizosaccharomyces pombe]"
17686	ENU01480	ANI61C1110 7:10801..1114	65-84	345-365	NAP		g4455309	258	120	3.00E-27	47	48	(AL035528) hypothetical protein [Arabidopsis thaliana]
17687	ENU01481	ANI61C6001: 278..673	106-125	446-465	NAP		g2621995	463	128	2.00E-29	50	36	(AE000865) conserved protein [Methanobacterium thermoautotrophicum]
17688	ENU01482	ANI61S2131: 485..72	105-124	457-476	NAP		g731893	265	100	5.00E-21	35	25	putative transporter YIL166C; probable membrane protein YIL166c - yeast (Saccharomyces cerevisiae); (Z46921) unknown [Saccharomyces cerevisiae]
17689	ENU01483	ANI61C8084: 5381..5797	115-134	470-489	NAP		g114959	609	114	3.00E-25	48	18	Thermotable beta-glucosidase B (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase); beta-glucosidase (EC 3.2.1.21) B - Clostridium thermocellum; (X15644) bglB gene (AA1-754) [Clostridium thermocellum]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17690	ENU01484	ANI61C2517: 1000..557	42-64	424-443	NAP		g125727	247	84	2.00E-16			Killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase ; RF2 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1 ; (X07127) RF2 gene product (AA 1 - 1146) [Kluyveromyces lactis] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactis] ; (X01095) URFP2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactis] ; hypothetical 49.6 KD protein in ELM1-PR12 intergenic region ; hypothetical protein YKL046c precursor - yeast (Saccharomyces cerevisiae) ; (Z28046) ORF YKL046c [Saccharomyces cerevisiae]
17691	ENU01485	ANI61C5196: 111-130 1189..676	111-130	563-582	NAP		g549674	586	70	1.00E-11			hypothetical 49.6 KD protein in ELM1-PR12 intergenic region ; hypothetical protein YKL046c precursor - yeast (Saccharomyces cerevisiae) ; (Z28046) ORF YKL046c [Saccharomyces cerevisiae]
17692	ENU01486	ANI61C7556: 94-113 4782..4141	94-113	670-693	NAP		g2408015	246	51	0.000009	33	57	[Schizosaccharomyces pombe]
17693	ENU01487	ANI61C922:1 46-65 034..354	46-65	663-684	NAP		g1705437	538	126	5.00E-39	50	51	"Branched-chain amino acid aminotransferase, cytosolic (BCAT) (ECA39 protein) ; (U42443) MECA39 [Mus musculus] "
17694	ENU01488	ANI61C1319: 34-55 184..947	34-55	735-755	NAP		g3328190		42	0.004			(AF074266) proto-oncogene AF4 [Mus musculus]
17695	ENU01489	ANI61C8803: 54-76 1587..1194	54-76	1546-1567	NAP		g3121869		171	1.00E-41	42	30	Coronin-like protein ; (Z99753) hypothetical protein [Schizosaccharomyces pombe]
17696	ENU01490	ANI61C5193: 118-140 2292..233	118-140	2113-2134	NAP		g1166378	784	252	2.00E-77	34	59	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "
17697	ENU01491	ANI61S4436: 31-51 133..426	31-51	262-282	NAP								
17698	ENU01492	ANI61C8712: 122-141 171..491	122-141	383-400	NAP		g539913		42	0.001			peripheral-type benzodiazepine receptor 1 isoquinoline-binding protein - mouse ; (D21207) peripheral-type benzodiazepine receptor [Mus musculus]
17699	ENU01493	ANI61C5155: 100-120 3236..2870	100-120	404-423	NAP		g1399020	154	36	0.000004			(U34658) FKIF6 [Morone saxatilis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17700	ENU01494	ANI61C7145: 2421..1716	114-131	756-777	NAP		g3885836	128	44	0.001	33	18	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
17701	ENU01495	ANI61C1089 24-49	757-788		NAP		g3947740	1043	217	1.00E-55	67	47	(Y18476) NADH dehydrogenase subunit 2 [Trichophyton rubrum]
17702	ENU01496	ANI61C5157: 0:940..579	25-44	959-978	NAP		g585251	297	146	2.00E-34	29	62	Polyketide synthase HETM; hetM protein - Anabaena sp. (PCC 7120); (L22883) polyketide synthase [Anabaena sp.]
17703	ENU01497	ANI61C1117: 6205..9180	102-121	3016-3035	NAP		g399198	335	103	7.00E-41	28	26	cell division control protein 25; SKCDC25 protein - yeast (Saccharomyces kluyveri) (fragment); (M82964) CDC25 [Saccharomyces kluyveri]
17704	ENU01498	ANI61C7188: 111-129	3027-3045		NAP		g1166378	828	393	e-111	32	87	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "
17705	ENU01499	ANI61C1137 5879..2904	85-104	3010-3029	NAP		g3560268	538	141	4.00E-64	28	86	"(AL031535) putative transcription factor subunit, TPR domain ns [Schizosaccharomyces pombe] "
17706	ENU01500	ANI61C3679: 104-123	3035-3054		NAP		g4512618	665	245	3.00E-92	28	61	(AC004793) Strong similarity to gi 3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb AF080119 and is a member of the reverse transcriptase family PF 00078.
17707	ENU01501	ANI61C1132 1:726..375	122-142	412-431	NAP		g2959364		74	4.00E-13			(AL022117) putative o-methyltransferase [Schizosaccharomyces pombe]
17708	ENU01502	ANI61C6286: 2070..2522	91-109	477-501	NAP		g1653970	196	68	4.00E-11	33	33	(Y09020) fructosyl amino acid oxidase [Aspergillus terreus]
17709	ENU01503	ANI61S4271: 5..510	26-49	461-489	NAP		g2992164	491	179	1.00E-44	51	30	(AB012580) eIF3 p66 [Mus musculus]
17710	ENU01504	ANI61C3193: 578..58	122-144	579-600	NAP		g37174		42	0.003			(X05615) thyroglobulin [Homo sapiens]
17711	ENU01505	ANI61C9970: 1873..1332	117-138	629-648	NAP		g3116113	534	150	5.00E-36	46	26	(AL023286) probable atp-dependent rna helicase [Schizosaccharomyces pombe]
17712	ENU01506	ANI61C2497: 2277..3199	121-142	981-1000	NAP		g1658175	673	117	1.00E-47	41	56	(U74468) indole-3-acetaldehyde dehydrogenase [Ustilago maydis]

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17713	ENU01507	ANI61C9216: 1258..94	98-117	1202-1220	NAP		g2132247	517	201	8.00E-51	33	40	hypothetical protein YPL249c - yeast (Saccharomyces cerevisiae) ; (Z67751) putative protein [Saccharomyces cerevisiae] ; (Z73605) ORF YPL249c [Saccharomyces cerevisiae]
17714	ENU01508	ANI61C3460: 99-120 3079..1846	99-120	1271-1290	NAP		g2131417	996	337	7.00E-92	48	33	hypothetical protein YDR291w - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr291wp [Saccharomyces cerevisiae]
17715	ENU01509	ANI61C6244: 88-108 80..1353	88-108	1298-1319	NAP		g2498440	2193	734	0	98	87	"homogentisate 1,2-dioxygenase (homogentisicase) (homogentisate oxygenase) (homogentisic acid oxidase) ; 3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15) - Emericella nidulans ; (U30797) 2,5 dihydroxyphenylacetate oxidase [Emericella nidulans] ; (AJ001836) homogentisate dioxygenase [Emericella nidulans] "
17716	ENU01510	ANI61C7285: 109-128 4043..7025	109-128	3029-3049	NAP		g1723934	133	89	2.00E-16	27	51	hypothetical 41.6 KD protein in SUT1-RCK1 intergenic region ; probable membrane protein YGL159w - yeast (Saccharomyces cerevisiae) ; (Z72681) ORF YGL159w [Saccharomyces cerevisiae]
17717	ENU01511	ANI61C1056 68-87 0:80..269	68-87	225-244	NAP		g3169094	215	71	1.00E-12	41	28	(AL023706) small nuclear ribonucleoprotein
17718	ENU01512	ANI61C813:3 71-90 88..65	71-90	333-352	NAP		g3299812	206	82	1.00E-15	51	87	[Schizosaccharomyces pombe] (AB016006) ribosomal protein S31 homolog [Schizosaccharomyces pombe] ; (Z95620) 40s ribosomal protein s25 [Schizosaccharomyces pombe]
17719	ENU01513	ANI61C1510: 68-87 2260..1915	68-87	351-370	NAP		g4469025	158	69	8.00E-12	47	66	(AL035602) putative protein [Arabidopsis thaliana]
17720	ENU01514	ANI61C2772: 57-76 445..48	57-76	393-412	NAP		g2780359	462	141	2.00E-33	53	23	(AB010110) ascorbate oxidase [Acremonium sp.]
17721	ENU01515	ANI61C9732: 44-61 2295..1884	44-61	394-413	NAP		g2924502	625	32	2			(AL022019) lim domain protein [Schizosaccharomyces pombe]

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17722	ENU01516	ANI61C6821: 1019..570	52-71	440-459	NAP		g2133033	220	63	0.000000	36	89	"probable membrane protein YPR153w - yeast (<i>Saccharomyces cerevisiae</i>) ; (U40829) Note that this gene could be spliced, using an ATG beginning at 42644, a 5' splice site at 42648-9, and a 3' splice site at 42782-3 [Saccharomyces cerevisiae] "
17723	ENU01517	ANI61C5477: 2921..3377	43-64	439-457	NAP		g2315274	698	208	1.00E-53	62	43	(Y11113) endoglucanase IV [Hypocrea jecorina]
17724	ENU01518	ANI61C410:8 57-76 557..9022	57-76	461-480	NAP		g3136052	940	137	5.00E-32	42	28	(AL023592) acetamidase [Schizosaccharomyces pombe]
17725	ENU01519	ANI61S2176: 36..505	57-76	467-484	NAP		g2506666	902	287	1.00E-81	96	52	"hypothetical 32.3 KD protein in RHSE-NARV intergenic region (ORFB) ; (D90786) ORF_ID:o276#3; similar to [PIR Accession Number S11432] [Escherichia coli] ; (D90787) ORF_ID:o276#3; similar to [PIR Accession Number S11432] [Escherichia coli] ; (AE000243) orf, hypothetical protein [Escherichia coli] "
17726	ENU01520	ANI61C8626: 6085..5604	63-82	483-502	NAP		g1911486	999	139	1.00E-32	64	49	"(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger] "
17727	ENU01521	ANI61C9428: 1375..891	64-83	487-506	NAP		g3183173	657	224	2.00E-58	77	31	"Seryl-tRNA synthetase, cytoplasmic (serine--tRNA ligase) (SERRS) ; (Z97210) seryl-tma synthetase [Schizosaccharomyces pombe] "
17728	ENU01522	ANI61C4374: 6274..6761	56-75	481-500	NAP		g3242460	842	93	1.00E-18	42	9	(AB010467) multidrug resistance-associated protein (MRP)-like protein-2 (MLP-2) [Rattus norvegicus]
17729	ENU01523	ANI61C8728: 3084..2565	28-47	484-504	NAP		g1703215	915	123	1.00E-27	41	27	general alpha-glucoside permease; alpha-glucoside transport protein - yeast (<i>Saccharomyces cerevisiae</i>); (Z73074) ORF YGR289c
17730	ENU01524	ANI61C7581: 604..1128	48-67	511-530	NAP		g3257361	263	93	2.00E-20	44	60	[Saccharomyces cerevisiae] (AP000004) 249aa long hypothetical protein [Pyrococcus horikoshii]

Seq num	Seq id	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17731	ENU01525	ANI61S3483; 24-43	489-510	NAP		g3402674	751	233	7.00E-61	87	37	(AC004697) putative myrosinase-binding protein [Arabidopsis thaliana]
17732	ENU01526	ANI61C7029; 72-91 3312..2764	559-578	NAP		g1169238	935	119	2.00E-44	61	31	"glutamate decarboxylase (GAD); glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia; (L16797) glutamate decarboxylase [Petunia hybrida]; (L16977) glutamate decarboxylase [Petunia hybrida]" (Z68144) hypothetical protein [Schizosaccharomyces pombe]
17733	ENU01527	ANI61C9584; 56-75 586..28	553-572	NAP		g1103515	217	91	6.00E-18	36	86	GTP cyclohydrolase II; GTP cyclohydrolase II (ribA) homolog - Haemophilus influenzae (strain Rd KW20); (U32706) GTP cyclohydrolase II (ribA) [Haemophilus influenzae Rd]
17734	ENU01528	ANI61C1404; 65-84 2584..2024	564-583	NAP		g1169878		62	0.000000			proteolipid protein PPA1; probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae); (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae]; (U10399) Ppalp: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae] (AF021234) 3-oxoacyl-[acyl-carrier protein]-synthase [Neurospora crassa] (AF072709) unknown [Streptomyces lividans]
17735	ENU01529	ANI61C9912; 59-78 676..110	565-583	NAP		g130720	550	177	4.00E-50	71	71	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
17736	ENU01530	ANI61C1043 22-42 6:7075..7642	535-554	NAP		g2522482	1231	107	3.00E-30	54	39	[Schizosaccharomyces pombe]
17737	ENU01531	ANI61C5523; 22-44 988..407	541-560	NAP		g3293539	216	83	1.00E-15	55	46	protein [Neurospora crassa]
17738	ENU01532	ANI61C9745; 32-51 2018..1396	589-612	NAP		g3169083	212	45	0.0006	38	36	lividans
17739	ENU01533	ANI61C5924; 51-69 4449..3814	624-643	NAP		g4455778	860	100	8.00E-21			[Schizosaccharomyces pombe]

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17740	ENU01534	ANI61C8278: 22-42 809..149	22-42	621-640	NAP		g729566	1081	188	1.00E-48	57	41	"Secretory pathway GDP dissociation inhibitor ; GDP dissociation inhibitor GDI1 - yeast (Saccharomyces cerevisiae) ; (S69371) Gdi1p=GDP dissociation inhibitor [Saccharomyces cerevisiae, Peptide, 451 aa] [Saccharomyces cerevisiae] ; (U18916) Gdi1p: secretory pathway GDP dissociation inhibitor [Saccharomyces cerevisiae]"
17741	ENU01535	ANI61C8347: 39-58 693..1361	39-58	646-665	NAP		g1170136	449	200	7.00E-51	49	78	"endoglucanase V precursor (endo-1,4-beta-glucanase V) (cellULase V) (EG V) ; cellulase (EC 3.2.1.4) V precursor - fungus (Trichoderma reesei) (strain QM9414) ; (Z33381) endo-1,4-beta-glucanase V (EGV) [Hypocrea jecorina]"
17742	ENU01536	ANI61C1482: 59-78 918..1587	59-78	667-686	NAP		g4262216	491	170	9.00E-42	36	77	(AC006161) putative DNA binding protein [Arabidopsis thaliana] (Z95397) unknown
17743	ENU01537	ANI61C3946: 42-61 1682..2371	42-61	670-689	NAP		g2104460	645	81	9.00E-15	40	20	[Schizosaccharomyces pombe]
17744	ENU01538	ANI61C3736: 50-69 2629..1923	50-69	695-714	NAP		g461623	334	65	6.00E-10	31	23	"beta-galactosidase precursor (lactase) ; (L06037) beta-D-galactosidase [Aspergillus niger] ; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger] ; beta galactosidase [Aspergillus niger]"
17745	ENU01539	ANI61C842:1 72-91 216..1938	72-91	733-752	NAP		g1514667	227	79	5.00E-19	34	59	(X92509) crg1 [Ustilago maydis]
17746	ENU01540	ANI61C405:1 32-52 53..958	32-52	778-795	NAP		g3219304	1070	183	2.00E-75	69	25	(AB009461) MUS38 [Neurospora crassa]
17747	ENU01541	ANI61C1420: 57-76 36..853	57-76	813-832	NAP		g3913051	244	76	1.00E-20	31	54	putative flavin-containing monoamine oxidase MTV014.14 ; (AL021646) hypothetical protein Rv3170 [Mycobacterium tuberculosis]
17748	ENU01542	ANI61C4648: 47-66 1263..2101	47-66	824-843	NAP		g2389003	1358	264	7.00E-80	60	33	(Z98981) hypothetical protein [Schizosaccharomyces pombe]
17749	ENU01543	ANI61C7922: 22-44 1708..829	22-44	837-856	NAP		g3264834	341	71	1.00E-20	30	74	(AF072541) xyitol dehydrogenase; XDH [Galactocandida mastotermitis]
17750	ENU01544	ANI61C7526: 39-58 1573..2457	39-58	855-881	NAP		g3661541	166	48	0.00007	31	77	(AF091396) poly-zinc finger protein [Trypanosoma cruzi]

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17751	ENU01545	ANI61C9518: 1440...545	71-90	904-923	NAP		g2132224	294	89	4.00E-17	31	66	hypothetical protein YPL191c - yeast (Saccharomyces cerevisiae) ; (Z73547) ORF YPL191c [Saccharomyces cerevisiae]
17752	ENU01546	ANI61C6095: 66-89	66-89	910-929	NAP		g1351702	289	66	5.00E-10	26	54	hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
17753	ENU01547	ANI61C9283: 65-84	65-84	929-948	NAP		g3183125	1148	369	e-101	55	67	probable DNA PRIMase small subunit ; (Z98531) hypothetical dna primase [Schizosaccharomyces pombe]
17754	ENU01548	ANI61C8752: 47-67	47-67	919-938	NAP		g2257527	452	91	9.00E-18	43	63	(AB004537) HLJ1 protein [Schizosaccharomyces pombe]
17755	ENU01549	ANI61C1824: 51-70	51-70	945-964	NAP		g3764057	623	257	6.00E-68	45	75	(AF016246) purine nucleoside permease [Candida albicans]
17756	ENU01550	ANI61C1534: 22-41	22-41	918-937	NAP		g729859	1735	294	1.00E-82	49	40	Sexual differentiation process protein ISP4 ; isp4 protein - fission yeast (Schizosaccharomyces pombe) ; (D14061) ORF [Schizosaccharomyces pombe]
17757	ENU01551	ANI61C7241: 26-45	26-45	935-954	NAP		g3006143	98	52	0.000005	42	25	(AL022299) hypothetical protein [Schizosaccharomyces pombe]
17758	ENU01552	ANI61C8537: 33-52	33-52	945-964	NAP		g2665358	551	173	2.00E-42	30	40	(Y15774) copper amine oxidase [Bos taurus]
17759	ENU01553	ANI61C1033: 29-47	29-47	970-992	NAP		g416590	937	288	5.00E-77	51	38	AFG2 protein ; valosin-containing protein homolog AFG2 - yeast (Saccharomyces cerevisiae) ; (L14615) AFG2 [Saccharomyces cerevisiae] ; (U19729) Afg2p [Saccharomyces cerevisiae]
17760	ENU01554	ANI61C9762: 69-90	69-90	1013-1033	NAP		g950007		52	0.000005			(U26938) Tc1-like transposase [Drosophila virilis] ; (Z49253) Tc1-like transposase [Drosophila virilis]
17761	ENU01555	ANI61C2412: 35-54	35-54	982-1001	NAP		g2981103	512	101	1.00E-20	32	26	(AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe]

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17762	ENU01556	ANI61C8543: 23-42 4912..5920		970-989	NAP		g2388955	1037	253	7.00E-87	64	77	(Z98979) putative isopropyl malate dehydrogenase [Schizosaccharomyces pombe]
17763	ENU01557	ANI61C5900: 70-89 1169..84	1094- 1113		NAP		g3080523	1115	398	e-110	58	67	(AL022599) aspartate kinase [Schizosaccharomyces pombe]
17764	ENU01558	ANI61C1047 23-48 0:5194..4079	1078- 1097		NAP		g2414638	623	185	2.00E-54	43	70	(Z99260) putative microsomal dipeptidase precursor [Schizosaccharomyces pombe]
17765	ENU01559	ANI61C7992: 60-81 1138..7	1130- 1149		NAP		g3881525	227	112	5.00E-24	28	14	(Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357f10.5 comes from this gene [Caenorhabditis elegans]
17766	ENU01560	ANI61C6916: 71-90 50..1183	1143- 1162		NAP		g3080530	294	96	3.00E-19	38	30	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
17767	ENU01561	ANI61C1110 22-41 5:2100..901	1161- 1179		NAP		g730701	1749	347	e-137	79	77	adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (ADOHCYase); adenosylhomocysteinase (EC 3.3.1.1) - yeast (Saccharomyces cerevisiae); (U18796) Sam1p: Adenosylhomocysteinase [Saccharomyces cerevisiae]
17768	ENU01562	ANI61C9449: 47-66 75..1367	1278- 1298		NAP		g1730731	1037	288	2.00E-94	49	46	hypothetical 98.9 KD protein in COX5A-ALG11 intergenic region; hypothetical protein YNL049c - yeast (Saccharomyces cerevisiae); (U12141) Ynl2505p [Saccharomyces cerevisiae]; (Z71325) ORF YNL049c [Saccharomyces cerevisiae]; (AJ009783) Sfb2 [Saccharomyces cerevisiae]
17769	ENU01563	ANI61C919:4 67-86 6..1389	1349- 1368		NAP		g3236468	1583	593	e-169	69	58	(AF070481) minichromosome maintenance protein Mcm7p [Schizosaccharomyces pombe]; (AL031158) yeast cell division control protein 47 homologue [Schizosaccharomyces pombe]

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17770	ENU01564	ANI61C7722: 1954..528	26-45	1390-1410	NAP		g3915458	1728	458	e-154	65	62	putative ABC transporter C8C9.18 in chromosome 1
17771	ENU01565	ANI61C4806: 58-77		1433-1452	NAP		g2239229	2162	761	0	82	84	(Z97210) hypothetical protein [Schizosaccharomyces pombe]
17772	ENU01566	ANI61C1059: 24-45		1410-1429	NAP		g172707	811	193	6.00E-89	47	56	(M77274) SRP receptor alpha-chain homologue [Saccharomyces cerevisiae]
17773	ENU01567	ANI61C385:5 51-70		1470-1489	NAP		g1709487	945	372	e-102	54	59	"Origin recognition complex protein, subunit 1; (U38522) Orp1 [Schizosaccharomyces pombe]; (U40378) orc1+ protein [Schizosaccharomyces pombe]; (AL034463) origin recognition complex protein, subunit 1. [Schizosaccharomyces pombe]"
17774	ENU01568	ANI61C630:2 38-58		1525-1544	NAP		g4154090	329	75	2.00E-21	37	79	(Z99568) putative tma protein transferase [Schizosaccharomyces pombe]
17775	ENU01569	ANI61C7964: 64-84		1766-1784	NAP		g3023956	614	259	2.00E-74	38	30	Vegetative incompatibility protein HET-E-1; (L28125) beta transducin-like protein [Podospora anserina]
17776	ENU01570	ANI61C7672: 63-82		1936-1955	NAP		g2414651	665	207	2.00E-52	40	51	(Z99296) hypothetical protein [Schizosaccharomyces pombe]
17777	ENU01571	ANI61C1035 45-64		1926-1945	NAP		g4455171	305	148	2.00E-34	35	24	(AL035521) hypothetical protein [Arabidopsis thaliana]
17778	ENU01572	ANI61C1014 25-44		2011-2030	NAP		g3242651	2185	724	0	63	72	(AB015509) beta-mannosidase [Aspergillus aculeatus]
17779	ENU01573	ANI61C945:4 35-54		2049-2068	NAP		g2645229	388	167	3.00E-40	36	32	(U78597) kinesin light chain [Plectonema boryanum]
17780	ENU01574	ANI61C945:4 35-54		2049-2068	NAP		g2645229	388	167	3.00E-40	36	32	(U78597) kinesin light chain [Plectonema boryanum]
17781	ENU01575	ANI61C6394: 53-72		2078-2101	NAP		g3341488	853	367	e-100	42	75	(X99280) protein kinase [Schizosaccharomyces pombe]; (AL031798) protein kinase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17782	ENU01576	ANI61C4040: 69-91 2608..2210	2106-2125	2187-2204	NAP		g586542	939	310	e-104	43	70	general amino acid permease AGP2 ; probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae) ; (X75891) YBR1007 [Saccharomyces cerevisiae] ; (Z36001) ORF YBR132c [Saccharomyces cerevisiae] ; YBR1007 gene [Saccharomyces cerevisiae] (M77661) putative pol polypeptide [Magnaporthe grisea] Formamidase (formamide amidohydrolase) ; (X99632) formamidase [Methylophilus methylotrophus] Choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
17783	ENU01577	ANI61C554:3 22-47 698..1810	2187-2204	2187-2204	NAP		g538067	827	324	2.00E-87	33	39	hypothetical 90.6 KD protein C1D4.10 in chromosome I ; (Z69239) unknown [Schizosaccharomyces pombe] (AE000913) conserved protein [Methanobacterium thermoautotrophicum] (AC000133) GSP19 [Emericella nidulans] (A1011297) hypothetical protein [Emericella nidulans]
17784	ENU01578	ANI61C2603: 30-49 2357..58	2263-2287	2263-2287	NAP		g3913682	563	239	5.00E-62	56	29	l-aminocyclopropane-1-carboxylate synthase 2 (ACC synthase 2) (S-adenosyl-L-methionine methylthioadenosine-lyase 2) (ACS-2) ; l-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - tomato ; (X59139) l-aminocyclopropane 1-carboxylate synthase [Lycopersicon esculentum]
17785	ENU01579	ANI61C7999: 33-52 4536..2130	2378-2397	2378-2397	NAP		g117619		55	6.00E-14			
17786	ENU01580	ANI61C8896: 27-47 2811..248	2526-2545	2526-2545	NAP		g1723232	404	89	2.00E-16	27	87	
17787	ENU01581	ANI61C7000: 54-73 328..88	233-252	233-252	NAP		g2622649	174	73	5.00E-13	40	61	
17788	ENU01582	ANI61S1911: 71-91 293..32	272-290	272-290	NAP		g1870211	533	87	3.00E-17	94	71	
17789	ENU01583	ANI61C6801: 67-86 1072..783	295-314	295-314	NAP		g3647374	246	38	0.000002	80	67	
17790	ENU01584	ANI61C9457: 64-94 1374..1678	307-326	307-326	NAP		g584682	184	50	0.000005			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17791	ENU01585	ANI61C1107 3:11524..1185 9	70-89	340-363	NAP		g731476	441	169	6.00E-42	69	86	hypothetical 14.4 KD protein in RNR1-ALD3 intergenic region ; hypothetical protein YER072w - yeast (Saccharomyces cerevisiae) ; (U18813) Yer072wvp [Saccharomyces cerevisiae] hypothetical 16.6 KD protein in THI5-AGP3 intergenic region ; hypothetical protein YFL057c - yeast (Saccharomyces cerevisiae) ; (D50617) YFL057C [Saccharomyces cerevisiae] ; (D44603) unknown [Saccharomyces cerevisiae]
17792	ENU01586	ANI61C7942: 51-72 923..572	51-72	341-360	NAP		g1175961	493	156	4.00E-38	64	77	nucleoside diphosphate kinase (NDK) (NDP kinase) ; nucleoside-diphosphate kinase (EC 2.7.4.6) - yeast (Saccharomyces cerevisiae) ; (X75780) A153 [Saccharomyces cerevisiae] ; (D13562) nucleoside diphosphate kinase [Saccharomyces cerevisiae] ; (Z28067) ORF YKL067w [Saccharomyces cerevisiae] ; nucleoside diphosphate kinase [Saccharomyces cerevisiae]
17793	ENU01587	ANI61C584:8 44-65 08..1165	44-65	337-358	NAP		g548341	437	121	2.00E-27			[Saccharomyces cerevisiae] contains similarity to human OS-9 precurosor (GB:U41635) [Arabidopsis thaliana] (D64004) hypothetical protein [Synecocystis sp.] hypothetical 11.3 KD protein in MIR1-STE18 intergenic region ; probable membrane protein YJR085c - yeast (Saccharomyces cerevisiae) ; (Z49585) ORF YJR085c [Saccharomyces cerevisiae] ; (L47993) ORF YJR085c [Saccharomyces cerevisiae]
17794	ENU01588	ANI61C720:2 22-53 867..3240	22-53	333-352	NAP		g3047065	158	39	0.013			"NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 14K chain - Neurospora crassa ; (Z18945) NADH:ubiquinone oxidoreductase (NADH dehydrogenase), 14 kDa [Neurospora crassa] "
17795	ENU01589	ANI61C4190: 61-82 2037..1658	61-82	371-398	NAP		g1208451	217	59	0.000000 27 02	36		
17796	ENU01590	ANI61C9077: 24-55 3225..2844	24-55	338-363	NAP		g1352897	174	59	4.00E-12	40	100	
17797	ENU01591	ANI61C3388: 23-46 1278..1659	23-46	343-362	NAP		g630424	222	76	1.00E-13	44	90	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17798	ENU01592	ANI61C1120 7:145..533	63-82	389-409	NAP		g2492755	444	159	1.00E-38	55	46	sorbitol utilization protein SOU2 ; (AF002134) Sou2p [Candida albicans]
17799	ENU01593	ANI61C1111 6:655..251	71-94	414-433	NAP		g2132286	339	133	5.00E-31	52	15	"hypothetical protein YPR112c - yeast (Saccharomyces cerevisiae) ; (U32445) Similar to Polyadenylate-binding protein (Swiss Prot. accession number P04147) and other RNA binding proteins (e.g., Swiss Prot. accession number P19682 and P27476) [Saccharomyces cerevisiae] " (AL035581) hypothetical protein. [Schizosaccharomyces pombe]
17800	ENU01594	ANI61C1758: 49-68 8836..8430	49-68	394-413	NAP		g4468021	243	40	0.000000			[Schizosaccharomyces pombe]
17801	ENU01595	ANI61C629:1 03..513	44-63	391-412	NAP		g2501435	517	136	1.00E-36	72	67	ubiquitin-conjugating enzyme E2-20 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) ; (D85545) UcbP4 [Schizosaccharomyces pombe] ; (AL034564) ubiquitin conjugating enzyme [Schizosaccharomyces pombe]
17802	ENU01596	ANI61C1428: 45-68 932..520	45-68	396-415	NAP		g1346053	182	78	3.00E-14	31	82	"transcription initiation factor TFIID 19 KD subunit (TAFII-19) (TAFII19) ; FUN81 protein - yeast (Saccharomyces cerevisiae) ; (Z46660) FUN81 gene, len: 167, CAI: 0.10, FU81_yeast P11747 [Saccharomyces cerevisiae] " FAB1 protein - yeast (Saccharomyces cerevisiae) ; (D50617) FAB1 protein [Saccharomyces cerevisiae]
17803	ENU01597	ANI61C1309: 22-43 81..499	22-43	378-398	NAP		g1084543	644	182	8.00E-46	58	6	(D83125) secretory component [Sarcophaga peregrina]
17804	ENU01598	ANI61C6595: 38-61 4362..4789	38-61	403-423	NAP		g1402634	336	116	1.00E-25	41	24	putative serine/threonine protein phosphatase C22H10.04 ; (Z69730)
17805	ENU01599	ANI61C8417: 51-70 3133..3563	51-70	419-439	NAP		g1723460	1135	238	1.00E-62	73	46	putative phosphoprotein phosphatase [Schizosaccharomyces pombe]
17806	ENU01600	ANI61C7533: 35-54 2349..2779	35-54	403-423	NAP		g2133268	77	46	0.0001	29	14	DNA-binding protein amdA - Emericella nidulans ; (L28810) regulatory protein [Emericella nidulans]
17807	ENU01601	ANI61C7287: 66-87 91..522	66-87	435-455	NAP		g3393020	658	195	2.00E-49	75	24	(AL031174) t-complex protein 1 gamma subunit homolog [Schizosaccharomyces pombe]

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17808	ENU01602	ANI61C1042 0:1537..1969	31-50	399-421	NAP		g4160357	333	73	1.00E-12	29	29	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
17809	ENU01603	ANI61C9572: 49-73 1841..1410	49-73	422-441	NAP		g1174456	1680	168	3.00E-41	63	29	putative ATP-dependent RNA helicase - STE13; probable RNA helicase - fission yeast (Schizosaccharomyces pombe); (D29795) RNA helicase [Schizosaccharomyces pombe]; (AL035263) putative atp-dependent rna helicase ste13p [Schizosaccharomyces pombe]
17810	ENU01604	ANI61C1056 58-87 7:1708..2145	58-87	434-453	NAP		g2497061	229	106	1.00E-22	39	24	hypothetical 65.2 KD protein in COX14-HMGS intergenic region; probable membrane protein YML127w - yeast (Saccharomyces cerevisiae); (Z50178) unknown [Saccharomyces cerevisiae]
17811	ENU01605	ANI61C96:49 52-73 3..55	52-73	429-448	NAP		g2894293		86	1.00E-16			(AL021837) hypothetical protein [Schizosaccharomyces pombe]
17812	ENU01606	ANI61C4830: 63-82 42..481	63-82	442-459	NAP		g461699		57	0.000000 07			calcium binding protein; (U03413) calcium binding protein [Dictyostelium discoideum]
17813	ENU01607	ANI61C9039: 69-88 122..562	69-88	448-467	NAP		g4176522	357	127	4.00E-29	42	36	(AL035263) hypothetical protein [Schizosaccharomyces pombe]
17814	ENU01608	ANI61C1091 42-61 6:2577..3025	42-61	429-448	NAP		g1208451	287	89	1.00E-17	36	40	(D64004) hypothetical protein [Synecocystis sp.]
17815	ENU01609	ANI61C9222: 32-51 163..614	32-51	411-441	NAP		g2873363	564	66	8.00E-24	42	20	(U89492) arylsulfatase [Neurospora crassa]
17816	ENU01610	ANI61C2078: 38-63 3182..2730	38-63	429-448	NAP		g3915113	404	158	2.00E-38	52	42	Maleylacetate reductase; maleylacetate reductase - Pseudomonas cepacia; (U19883) maleylacetate reductase [Burkholderia cepacia]
17817	ENU01611	ANI61S1044: 44-64 488..32	44-64	436-458	NAP		g3219943	418	124	3.00E-28	50	36	hypothetical 46.4 KD protein C3A12.11C in chromosome I; (Z95395) hypothetical rna binding protein [Schizosaccharomyces pombe]

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17818	ENU01612	ANI61C6328: 52-71 1723..2180	52-71	436-467	NAP		g586336		59	0.000000 02			hypothetical 21.1 KD protein in HPC2-PYC2 intergenic region ; probable membrane protein YBR217w - yeast (Saccharomyces cerevisiae) ; (Z36086) ORF YBR217w [Saccharomyces cerevisiae] ; (AB017924) ORF YBR217w [Saccharomyces cerevisiae]
17819	ENU01613	ANI61C1006 59-79 3:598..1055	59-79	456-474	NAP		g586294	220	104	4.00E-22	34	48	hypothetical 35.8 KD protein in YSW1-RIB7 intergenic region ; hypothetical protein YBR151w - yeast (Saccharomyces cerevisiae) ; (Z36020) ORF YBR151w [Saccharomyces cerevisiae]
17820	ENU01614	ANI61C1122 31-52 3:562..100	31-52	433-451	NAP		g493580	1071	156	9.00E-38	51	20	(U09580) beta-D-glucoside glucohydrolase [Trichoderma reesei] putative ATP-dependent RNA helicase CDC28 ; (U48733) Cdc28p
17821	ENU01615	ANI61C9892: 61-80 2016..1553	61-80	463-482	NAP		g3913210	591	211	2.00E-54	68	15	[Schizosaccharomyces pombe] (AL023860) short chain dehydrogenase [Schizosaccharomyces pombe] (AL031179) importin beta subunit [Schizosaccharomyces pombe] (AL035540) Phospholipase like protein [Arabidopsis thaliana]
17822	ENU01616	ANI61C6:504 22-46 .38	22-46	427-446	NAP		g3218393	167	62	1.00E-12	38	43	
17823	ENU01617	ANI61C2355: 66-85 591..124	66-85	472-491	NAP		g3395584	301	83	1.00E-15	31	12	
17824	ENU01618	ANI61S336:5 69-94 15..47	69-94	465-495	NAP		g4467143	761	268	1.00E-71	98	30	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17825	ENU01619	ANI61C4983: 31-54 841..371	31-54	436-459	NAP		g2392291	311	96	2.00E-19			"Chain A, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain B, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain C, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain D, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain E, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain F, 2-Enoyl-CoA Hydratase, Data Collected At 100 K, Ph 6.5 ; Chain A, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain B, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain C, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain D, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain E, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA ; Chain F, Enoyl-CoA Hydratase Complexed With Octanoyl-CoA"
17826	ENU01620	ANI61C8671: 22-51 1667..2137	22-51	431-450	NAP		g1172532	295	45	3.00E-10			penicillolysin precursor (deuterolysin) ; penicillolysin - Penicillium citrinum ; (D25535) Penicillolysin [Penicillium citrinum]
17827	ENU01621	ANI61C7181: 22-55 3922..4392	22-55	431-450	NAP		g3916	334	74	7.00E-13	33	35	(X66371) MDM1-protein [Saccharomyces cerevisiae]
17828	ENU01622	ANI61C1034 22-53 7:1930..1457	22-53	421-453	NAP		g1705681	1089	172	1.00E-42	51	23	cell division control protein 4 ; (X96763) CDC4 [Candida albicans]
17829	ENU01623	ANI61C1052 44-64 4:549..72	44-64	452-478	NAP		g1711582	291	124	3.00E-28	53	87	succinyl-CoA synthetase beta chain (SCS-beta) ; sucC succinyl-coA synthetase beta-chain - Pseudomonas aeruginosa (fragment) ; (X84052) succinyl-coA synthetase beta-subunit from sucC [Pseudomonas aeruginosa]
17830	ENU01624	ANI61C9832: 59-78 2367..1890	59-78	470-494	NAP		g548509	1100	211	2.00E-54	95	48	"possible phosphate-non-repressible acid phosphatase precursor ; acid phosphatase, 35.6K - Emericella nidulans ; (M96993) acid phosphatase [Emericella nidulans]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17831	ENU01625	ANI61C30:45 80..4101	67-86	483-504	NAP		g2462677	141	48	0.00004	27	39	(Z99568) hypothetical protein. [Schizosaccharomyces pombe]
17832	ENU01626	..	69-89	490-512	NAP		g2909624		152	1.00E-36	44	33	(AL021942) hypothetical protein Rv0565c [Mycobacterium tuberculosis]
17833	ENU01627	ANI61C7014: 3929..4417	54-75	481-500	NAP		g1353008	148	35	0.3			hypothetical 53.5 KD protein in GCD14-POS18 intergenic region ; hypothetical protein YJL123c - yeast (Saccharomyces cerevisiae) ; (Z49398) ORF YJL123c [Saccharomyces cerevisiae]
17834	ENU01628	ANI61S4363: 554..66	37-65	462-483	NAP		g1352891	422	153	5.00E-37	44	40	putative glycosyltransferase HOC1 precursor ; probable membrane protein YJR075w - yeast (Saccharomyces cerevisiae) ; (Z49575) ORF YJR075w [Saccharomyces cerevisiae] ; (L47993) ORF YJR075w [Saccharomyces cerevisiae] ; (U62942) Hoc1p [Saccharomyces cerevisiae]
17835	ENU01629	ANI61C2320: 1370..1858	22-47	444-468	NAP		g2842511	966	177	5.00E-44	50	36	(AL021748) hypothetical [Schizosaccharomyces pombe]
17836	ENU01630	ANI61C347:2 134..2624	39-60	468-487	NAP		g3452329	194	93	1.00E-18	39	93	(AF072850) cytochrome p450 CYP4C19 [Lytechinus anamesis]
17837	ENU01631	ANI61C556:5 422..4929	23-56	453-473	NAP		g3116120	136	79	2.00E-14	27	15	(AL023287) probable helicase [Schizosaccharomyces pombe]
17838	ENU01632	ANI61C3163: 1048..555	41-72	457-492	NAP		g2773203	598	215	1.00E-55	61	30	(AF039713) Similar to phosphoglycerate mutase; coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk387c10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cm10f9; coded for by C. elegans cDNA cm18g...
17839	ENU01633	ANI61C3353: 162..656	66-86	492-518	NAP		g2851420	253	79	2.00E-14	33	16	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region ; (AE000443) orf, hypothetical protein [Escherichia coli] "
17840	ENU01634	ANI61C1118 5:8243..7747	52-71	478-506	NAP		g2330823	319	95	2.00E-24	65	65	(Z98530) ribosomal protein [Schizosaccharomyces pombe]

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17841	ENU01635	..	65-84	497-521	NAP		g2132957		75	3.00E-13	30	31	probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (AL023589) splicesome-associated protein [Schizosaccharomyces pombe] lymphocyte specific helicase - mouse ; (U25691) lymphocyte specific helicase [Mus musculus] (Z98601) diphosphomevalonate decarboxylase [Schizosaccharomyces pombe] binding protein [Schizosaccharomyces pombe] (Z92774) fadD3 [Mycobacterium tuberculosis] (Y17393) prefoldin subunit 2 [Mus musculus] (L47106) kinesin [Neurospora crassa] (AF015825) unknown [Bacillus subtilis] ; (Z99110) yj1B [Bacillus subtilis] (AL023794) putative proline oxidase precursor [Schizosaccharomyces pombe] fruit protein PKIW1501 ; hypothetical protein - kiwi fruit ; (L27810) pKIWI501 [Actinidia deliciosa] (D64003) hypothetical protein [Synechocystis sp.] "omega-6 fatty acid desaturase, endoplasmic reticulum (delta-12 desaturase) ; (L26296) delta-12 desaturase [Arabidopsis thaliana] " "(AB018078) oligo-1,4 - 1,4- glucantransferase / amylo-1,6- glucosidase [Saccharomyces cerevisiae] "
17842	ENU01636	ANI61C4567: 48-74 607..1106		486-505	NAP		g3135996	589	120	8.00E-27	41	32	
17843	ENU01637	ANI61S483:3 27-50 4..534		466-485	NAP		g2137490	465	185	2.00E-46	54	27	
17844	ENU01638	ANI61C2329: 27-47 4237..4740		457-488	NAP		g2330786	969	152	2.00E-36	47	40	
17845	ENU01639	ANI61C5098: 56-75 1101..598		498-517	NAP		g3738207	339	147	5.00E-35	43	50	
17846	ENU01640	ANI61C2362: 28-48 791..1296		470-490	NAP		g1877292	206	52	9.00E-12	30	32	
17847	ENU01641	ANI61C7547: 44-72 1875..2380		473-507	NAP		g3212116	127	63	0.000000	30	91	
17848	ENU01642	ANI61C6627: 54-71 155..661		499-518	NAP		g1947184	579	122	4.00E-41	81	14	
17849	ENU01643	ANI61C1152: 23-54 509..1		466-489	NAP		g2612899	147	52	5.00E-10	35	95	
17850	ENU01644	ANI61C7562: 23-46 360..869		462-490	NAP		g3192023	187	101	5.00E-21	36	33	
17851	ENU01645	ANI61C2007: 22-49 90..603		474-493	NAP		g1170600	140	36	0.14	30	91	
17852	ENU01646	ANI61C4822: 66-93 45..558		506-537	NAP		g1001214	443	156	1.00E-37	45	33	
17853	ENU01647	ANI61S344:1 33-54 2..526		475-505	NAP		g1169598	954	370	e-102	98	44	
17854	ENU01648	ANI61C5920: 62-81 821..305		505-536	NAP		g3986291	544	152	9.00E-41	57	9	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17855	ENU01649	ANI61C9533: 2666..2148	64-83	514-540	NAP		g4185903	922	202	3.00E-62	83	27	(AJ132432) fimbrin [Gibberella pulicaris]
17856	ENU01650	ANI61C4266: 42-67	42-67	500-519	NAP		g118774	1172	177	5.00E-44	60	21	DNA ligase (polydeoxyribonucleotide synthase (ATP)) ; DNA ligase (ATP) (EC 6.5.1.1) - fission yeast [Schizosaccharomyces pombe] ; (X05107) DNA ligase [Schizosaccharomyces pombe]
17857	ENU01651	ANI61C8612: 72-90	72-90	528-550	NAP		g2131348	383	56	1.00E-16	39	26	hypothetical protein YDL156w - yeast [Saccharomyces cerevisiae] ; (X97751) D1536 [Saccharomyces cerevisiae] ; (Z74204) ORF YDL156w [Saccharomyces cerevisiae]
17858	ENU01652	ANI61C6664: 68-87	68-87	531-550	NAP		g4538926	357	124	5.00E-28	43	23	putative phosphatidylserine decarboxylase [Arabidopsis thaliana]
17859	ENU01653	ANI61C7770: 41-65	41-65	505-526	NAP		g2494301	1373	271	3.00E-72	78	39	eukaryotic translation initiation factor 2 gamma subunit (EIF-2-gamma) ; (U37354) initiation factor eIF-2 gamma subunit [Schizosaccharomyces pombe]
17860	ENU01654	ANI61C4206: 49-68	49-68	508-534	NAP		g3560221	328	143	8.00E-34	43	50	(AL031523) hypothetical protein [Schizosaccharomyces pombe]
17861	ENU01655	ANI61C3455: 22-55	22-55	490-511	NAP		g585222	485	182	2.00E-45	60	90	glutathione peroxidase homolog YBR244W ; probable glutathione peroxidase (EC 1.1.1.9) - yeast [Saccharomyces cerevisiae] ; (Z36113) ORF YBR244w [Saccharomyces cerevisiae]
17862	ENU01656	ANI61C3754: 56-75	56-75	525-545	NAP		g586542	855	149	1.00E-35	41	29	general amino acid permease AGP2 ; probable amino acid transport protein YBR132c - yeast [Saccharomyces cerevisiae] ; (X75891) YBR1007 [Saccharomyces cerevisiae] ; (Z36001) ORF YBR132c [Saccharomyces cerevisiae] ; YBR1007 gene [Saccharomyces cerevisiae]

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17863	ENU01657	ANI61C7497: 22-41 932..400		492-512	NAP		g729611	807	189	9.00E-48			vanadate resistance protein GOG5/VRG4/VAN2 ; vanadate resistance protein VAN2 - yeast (Saccharomyces cerevisiae) ; (L33915) vanadate resistant protein [Saccharomyces cerevisiae] ; (U15599) Van2p [Saccharomyces cerevisiae] ; (Z72747) ORF YGL225w [Saccharomyces cerevisiae] ; VRG4 gene [Saccharomyces cerevisiae] (AF036546) protein kinase CK2 beta subunit [Candida albicans] hypothetical 27.4 KD protein in HYR1 3 region ; hypothetical protein YIR042c - yeast (Saccharomyces cerevisiae) ; (Z46902) unknown [Saccharomyces cerevisiae] lactam utilization protein LAMB ; lactam utilization protein lamB - Emericella nidulans ; (M77283) lamB [Emericella nidulans] (AL031545) putative coatmer delta subunit [Schizosaccharomyces pombe] putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe] (Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana] (AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa] RTA1 protein ; RTA1 protein - yeast (Saccharomyces cerevisiae) ; (Z72998) ORF YGR213c [Saccharomyces cerevisiae] ; (X84736) RTA1 [Saccharomyces cerevisiae]
17864	ENU01658	ANI61C9506: 61-82 865..743		531-551	NAP		g3093417	512	173	6.00E-43	58		
17865	ENU01659	ANI61C9637: 25-46 5288..5822		498-517	NAP		g731928	393	163	7.00E-40	46	73	
17866	ENU01660	ANI61C8632: 50-78 1385..855		525-544	NAP		g585381	1296	257	4.00E-84	94	68	
17867	ENU01661	ANI61C1444: 66-85 1040..1577		542-561	NAP		g3581908	589	122	5.00E-49	70	67	
17868	ENU01662	ANI61C2252: 22-52 70..606		490-517	NAP		g1351714	103	47	0.00008	22	32	
17869	ENU01663	ANI61C2212: 29-51 2027..2565		506-525	NAP		g3549879	768	124	5.00E-28	49	30	
17870	ENU01664	ANI61C1102 45-64 7:562..22		522-543	NAP		g3600039	183	95	4.00E-19	30	23	
17871	ENU01665	ANI61C9234: 52-71 1247..707		531-550	NAP		g2970667	215	56	8.00E-15	41	46	
17872	ENU01666	ANI61C322:4 53-73 374..4922		538-559	NAP		g1710802	199	75	3.00E-13	33	56	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17873	ENU01667	ANI61C8425: 1..551	22-46	498-530	NAP		g466190	551	213	5.00E-55	54	80	ribosomal large subunit pseudouridine synthase B (pseudouridylate synthase) (uracil hydrolyase); hypothetical protein X13 - Bacillus subtilis; (L09228) ORFX13 [Bacillus subtilis]; (Z99116) similar to hypothetical proteins [Bacillus subtilis] (X82490) unnamed protein product [Fusarium oxysporum] (AL023590) Glutathione S-transferase [Schizosaccharomyces pombe] histidine biosynthesis bifunctional amidotransferase / cyclase; amidotransferase HIS7 (EC 2.4.2.-) / cyclase HIS7 - yeast (Saccharomyces cerevisiae); (Z36117) ORF YBR248c [Saccharomyces cerevisiae] hypothetical 57.2 KD protein in MET8-HPC2 intergenic region; hypothetical protein YBR214w - yeast (Saccharomyces cerevisiae); (Z36083) ORF YBR214w [Saccharomyces cerevisiae]
17874	ENU01668	ANI61C461:8 54-74 58..1409	54-74	539-563	NAP		g2274947	177	79	2.00E-14	28	61	myo-inositol transporter 1; (X98622) myo-inositol transporter [Schizosaccharomyces pombe] (Y11113) endoglucanase IV [Hypocrea jecorina] probable membrane protein YPL224c - yeast (Saccharomyces cerevisiae); (Z73580) ORF YPL224c [Saccharomyces cerevisiae] probable oxidoreductase YJR096W; aldehyde reductase homolog YJR096w - yeast (Saccharomyces cerevisiae); (Z49596) ORF YJR096w [Saccharomyces cerevisiae] (U88308) C32E8.5 gene product [Caenorhabditis elegans] (AF053318) CCR4-associated factor 1 [Homo sapiens]
17875	ENU01669	ANI61C2346: 57-87 2599..2045	57-87	550-569	NAP		g3136036	189	68	1.00E-14	33	58	
17876	ENU01670	ANI61C6107: 62-94 5339..4783	62-94	555-576	NAP		g585255	588	231	2.00E-60	70	29	
17877	ENU01671	ANI61C3450: 72-96 677..120	72-96	566-587	NAP		g586334	307	77	8.00E-14	37	35	
17878	ENU01672	ANI61C1133 68-87 8:560..3	68-87	563-583	NAP		g2500938	380	127	7.00E-31	46	32	
17879	ENU01673	ANI61C7642: 62-81 157..716	62-81	560-579	NAP		g2315274	220	87	7.00E-17	38	52	
17880	ENU01674	ANI61C3041: 22-46 202..762	22-46	521-540	NAP		g2133005	317	71	8.00E-19	38	36	
17881	ENU01675	ANI61C8628: 41-60 2821..2259	41-60	536-561	NAP		g1176340	313	94	9.00E-21	36	57	
17882	ENU01676	ANI61C6429: 35-56 7156..7718	35-56	523-555	NAP		g1825727	407	138	3.00E-32	43	60	
17883	ENU01677	ANI61C7861: 22-49 82..644	22-49	522-542	NAP		g4106061	534	169	1.00E-41	58	51	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17884	ENU01678	ANI61C1228: 45-64 1995..1429		541-569	NAP		g1706503	2105	135	3.00E-31	41	12	DNA polymerase alpha (DNA polymerase I) ; DNA-directed DNA polymerase (EC 2.7.7.7) - yeast (Saccharomyces cerevisiae) ; (Z50161) DNA Polymerase I [Saccharomyces cerevisiae] ; (Z71378) ORF YNL102w [Saccharomyces cerevisiae] (U73857) betaine-aldehyde dehydrogenase [Escherichia coli] verprolin ; verprolin - yeast (Saccharomyces cerevisiae) ; (U19028) Vrp1p [Saccharomyces cerevisiae] ; MDP2 gene [Saccharomyces cerevisiae] glucose transporter (sugar carrier) ; glucose transport protein STP1 - Arabidopsis thaliana ; (X55350) glucose transporter [Arabidopsis thaliana] probable monooxygenase MTCY31.20 ; (Z73101) hypothetical protein Rv0892 [Mycobacterium tuberculosis] lactate 2-monooxygenase (lactate oxidase) ; lactate 2-monooxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monooxygenase [Mycobacterium smegmatis] tropomyosin ; tropomyosin - yeast (Schizosaccharomyces pombe) ; (L04126) tropomyosin [Schizosaccharomyces pombe] lysophospholipase precursor (phospholipase B) ; lysophospholipase (EC 3.1.1.5) - Penicillium notatum (fragment) ; (X60348) lysophospholipase [Penicillium chrysogenum]
17885	ENU01679	ANI61C9640: 55-78 4633..5199		558-579	NAP		g1657510	1307	201	3.00E-51	52	37	
17886	ENU01680	ANI61C7173: 48-68 69..266		559-578	NAP		g2507155	179	59	0.000000	34	19	
17887	ENU01681	ANI61C7819: 72-91 2860..3435		586-605	NAP		g134976	359	45	0.0004			
17888	ENU01682	ANI61C652:5 52-71 55..1132		562-586	NAP		g1731385	334	96	2.00E-19	37	33	
17889	ENU01683	ANI61C5538: 22-41 424..1004		537-558	NAP		g125886	475	77	1.00E-23	38	47	
17890	ENU01684	ANI61C1189: 36-63 8185..8765		554-574	NAP		g401205	288	86	2.00E-16	41	97	
17891	ENU01685	ANI61C8980: 22-48 466..1045		542-561	NAP		g730338	1174	262	2.00E-69	67	30	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17892	ENU01686	ANI61C5264; 143..724	60-79	577-599	NAP		g1666269	328	149	2.00E-35	41	74	(Z82021) cytochrome P450 [Agaricus bisporus]
17893	ENU01687	ANI61C1059 25-55 2:3355..3939	543-566		NAP		g125399	724	214	3.00E-55			serine/threonine-protein kinase KIN28; probable protein kinase KIN28 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae); (X04423) protein kinase [Saccharomyces cerevisiae]; (X95644) ORF 2330 [Saccharomyces cerevisiae]; (Z74156) ORF YDL108w [Saccharomyces cerevisiae]; protein kinase [Saccharomyces cerevisiae]
17894	ENU01688	ANI61C2075; 1..584	22-46	539-563	NAP		g1170905	777	157	6.00E-38	61	50	24 KD metalloproteinase precursor (deuterolysin); metalloproteinase (EC 3.4.-.-) 23K - Aspergillus flavus; (L37524) metalloproteinase [Aspergillus flavus]
17895	ENU01689	ANI61C2888; 24-44 6274..5689	24-44	537-567	NAP		g2498527	234	97	9.00E-20	36	21	dimethylglycine dehydrogenase precursor (ME2GLYDH); dimethylglycine dehydrogenase - rat; (X55995) dimethylglycine dehydrogenase [Rattus norvegicus] (Z98533) rho gdp dissociation inhibitor. [Schizosaccharomyces pombe]
17896	ENU01690	ANI61C8417; 58-78 4649..4059	58-78	585-606	NAP		g2330853	351	119	2.00E-26	45	74	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
17897	ENU01691	ANI61C8659; 70-98 1179..588	70-98	602-619	NAP		g3080529	223	101	6.00E-21	37	64	hypothetical 143.6 KD protein C26A3.09C in chromosome I; (Z69240) hypothetical protein [Schizosaccharomyces pombe]
17898	ENU01692	ANI61C8489; 23-42 699..107	23-42	551-573	NAP		g1723237	148	62	2.00E-12	31	12	"OVCA1=candidate tumor suppressor [human, fetal brain, Peptide, 443 aa]"
17899	ENU01693	ANI61C754; 7 26-46 86..194	26-46	553-576	NAP		g1438796	1015	245	1.00E-64	61	43	

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17900	ENU01694	ANI61C6597: 68-87 8113..8706		600-619	NAP		g132744	474	146	3.00E-38			"60S ribosomal protein L17 ; ribosomal protein L23.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (X01694) ribosomal protein L17 [Saccharomyces cerevisiae] ; (X79489) L23 B x-137 [Saccharomyces cerevisiae] ; (Z35848) ORF YBL087c [Saccharomyces cerevisiae] ; (U18916) Rpl17bp: Ribosomal protein, large subunit [Saccharomyces cerevisiae] ; (U15653) ribosomal protein L17B [Saccharomyces cerevisiae] "
17901	ENU01695	ANI61C6603: 36-55 707..1303		571-590	NAP		g3426129	717	152	2.00E-36	47	13	"(AL031307) leptomycin B resistance protein, ABC transporter [Schizosaccharomyces pombe] "
17902	ENU01696	ANI61C2370: 63-82 113..709		598-617	NAP		g3915530	223	76	1.00E-13	25	17	hypothetical 118.4 KD protein in WRS1-PKH2 intergenic region ; hypothetical protein YOL098c - yeast (Saccharomyces cerevisiae) ; (Z48149) similarity with D. melanogaster insulinase [Saccharomyces cerevisiae] ; (Z74840) ORF YOL098c [Saccharomyces cerevisiae]
17903	ENU01697	ANI61C2471: 55-74 34..631		589-610	NAP		g3885329	560	210	7.00E-54	47	46	(AC005623) alien-like protein [Arabidopsis thaliana]
17904	ENU01698	ANI61C7526: 23-42 105..703		557-579	NAP		g3413964	458	161	5.00E-39	55	36	(AB011003) UDP-N-acetylglucosamine pyrophosphorylase [Candida albicans]
17905	ENU01699	ANI61C8576: 23-44 459..1057		560-579	NAP		g464422	491	176	1.00E-43			probable 1-acyl-SN-glycerol-3-phosphate acyltransferase (1-AGP acyltransferase) (1-AGPAT) (lysophosphatidic acid acyltransferase) (LPAAAT) ; probable sn2-acylglyceride fatty acyltransferase (EC 2.3.1.-) - yeast (Saccharomyces cerevisiae) ; (L13282) acyltransferase [Saccharomyces cerevisiae] ; (Z74100) ORF YDL052c [Saccharomyces cerevisiae]

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17906	ENU01700	ANI61C1038 1:517..1115	22-55	556-578	NAP		g585972	461	161	5.00E-39	48	58	SCO2 protein precursor ; SCO1 protein homolog SCO2 - yeast (Saccharomyces cerevisiae) ; (X76078) YBR0308 [Saccharomyces cerevisiae] ; (Z35893) ORF YBR024w [Saccharomyces cerevisiae] ; ORF YBR0308 [Saccharomyces cerevisiae] peptidyl-prolyl cis-trans isomerase (PPIASE) (rotamase) (cyclophilin) (cyclosporin A-binding protein) (CPH) ; peptidylprolyl isomerase (EC 5.2.1.8) A - fission yeast (Schizosaccharomyces pombe) ; (X53223) cyclophilin (AA 1-162) [Schizosaccharomyces pombe] ; (D83992) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
17907	ENU01701	ANI61C9637: 72-91 4153..4752	72-91	604-629	NAP		g118109	560	214	3.00E-55			glutamate-cysteine ligase regulatory subunit [Mus musculus] (AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis] (D87078) similar to D.melanogaster pumilio protein (S22026): similar to human KIAA0099 protein(D43951) [Homo sapiens]
17908	ENU01702	ANI61C8628: 22-44 1396..794	22-44	563-582	NAP		g2088561	165	84	9.00E-16	31	60	urea hydro-lyase) ; cyanamide hydratase (EC 4.2.1.69) - fungus (Myrothecium verrucaria) ; (M59078) cyanamide hydratase [Myrothecium verrucaria] (AL022070) mago-nashi homolog [Schizosaccharomyces pombe]
17909	ENU01703	ANI61C5399: 71-92 2873..3476	71-92	603-632	NAP		g2808725		48	0.00004			putative ribosomal protein L15 [Aspergillus niger]
17910	ENU01704	ANI61C4146: 22-48 733..130	22-48	561-583	NAP		g1944416	617	134	5.00E-31	40	21	norsolorinic acid reductase [Aspergillus parasiticus]
17911	ENU01705	ANI61C8125: 22-53 838..233	22-53	560-584	NAP		g117800	730	211	4.00E-54	60	73	
17912	ENU01706	ANI61C9584: 22-53 2303..1697	22-53	553-586	NAP		g2950474	340	96	2.00E-19	57	97	
17913	ENU01707	ANI61C5212: 72-97 1243..636	72-97	611-638	NAP		g3850093	294	86	2.00E-16	33	36	
17914	ENU01708	ANI61C1119 4:1398..788	68-90	617-636	NAP		g3122672	798	155	5.00E-54	91	77	
17915	ENU01709	ANI61C1135 2:991..1603	29-49	576-598	NAP		g1200177	916	85	3.00E-32	42	47	

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17916	ENU01710	ANI61C1038 0:3175..3787	22-54	571-591	NAP		g1730665	121	61	0.000000	24	90	hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region ; probable membrane protein YNR018w - yeast (Saccharomyces cerevisiae) ; (Z71633) ORF YNR018w [Saccharomyces cerevisiae] aspartic proteinase 3 precursor (YAPSIN 1) ; aspergillopepsin I (EC 3.4.23.18) YAP3 precursor - yeast (Saccharomyces cerevisiae) ; (U53877) Yap3p: aspartic proteinase [Saccharomyces cerevisiae] ; (X89514) Aspartyl protease [Saccharomyces cerevisiae] ; (Z73292) ORF YLR120c [Saccharomyces cerevisiae] (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] succinate dehydrogenase (ubiquinone) iron-sulphur protein precursor (IP) ; (AF042062) succinate dehydrogenase iron-sulphur protein [Mycosphaerella graminicola] putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe] putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe] "(Z98978) SPAC27E2.03c, putative gtp-binding protein, len:392a a, similar eg. to YBR025C, YBN5_yeast, P38219, hypothetical 1 44.2 kd protein, (394aa), fasta scores, opt:1664, E():0, (63.7% identity in 391 aa overlap), also sim..." (AL032681) alcohol dehydrogenase [Schizosaccharomyces pombe]
17917	ENU01711	ANI61C8430: 55-73 2220..1605	55-73	609-628	NAP		g2507240	213	88	6.00E-17	39	31	
17918	ENU01712	ANI61C4637: 56-76 59..675	56-76	611-630	NAP		g2276352	429	173	1.00E-42	47	49	
17919	ENU01713	ANI61C9863: 22-44 1144..528	22-44	571-596	NAP		g3334166	904	276	8.00E-74	81	57	
17920	ENU01714	ANI61C9609: 26-47 625..7	26-47	582-602	NAP		g1351714	695	115	3.00E-26	36	40	
17921	ENU01715	ANI61C9609: 26-47 625..7	26-47	582-602	NAP		g1351714	695	115	3.00E-26	36	40	
17922	ENU01716	ANI61C6570: 24-52 625..5	24-52	582-601	NAP		g2388943	659	204	5.00E-52	53	52	
17923	ENU01717	ANI61C9806: 25-44 193..816	25-44	584-606	NAP		g3810864	422	66	2.00E-18	36	53	

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17924	ENU01718	ANI61C3200: 3021..2396	47-66	597-630	NAP		g2498268	143	61	0.000000	36	36	copper transport protein CTR3 (copper transporter 3) ; probable membrane protein YLR411w - yeast (Saccharomyces cerevisiae) ; (U20162) Ctr3p [Saccharomyces cerevisiae] ; (U81482) copper transporter 3 [Saccharomyces cerevisiae] probable eukaryotic translation initiation factor 3 beta subunit (EIF-3 beta) ; (Z70691) eukaryotic translation initiation factor 3 beta subunit [Schizosaccharomyces pombe] (AL022117) putative o-methyltransferase [Schizosaccharomyces pombe] (Z99162) farnesyltransferase beta subunit [Schizosaccharomyces pombe] (AL031545) hypothetical ryanodine receptor domain containing protein [Schizosaccharomyces pombe] signal recognition particle 54 KD protein homolog ; signal recognition particle 54K protein homolog - Aspergillus niger ; (L38317) srpA gene product [Aspergillus niger] ; srpA gene [Aspergillus niger] (AF030296) ubiquitin conjugating enzyme UBC1 [Glomerella cingulata] (AF012091) cysteine rich protein [Metarhizium anisopliae] "endo-1,4-beta-xylanase 2 precursor (xylanase 2) (1,4-beta-D-xylan xylanohydrolase 2) ; endo-1,4-beta-xylanase (EC 3.2.1.8) 2 precursor - Emericella nidulans ; (Z49893) xylanase [Emericella nidulans] "hypothetical protein YOL151w - yeast (Saccharomyces cerevisiae) ; (Z48239) orf2 [Saccharomyces cerevisiae] ; (Z74893) ORF YOL151w [Saccharomyces cerevisiae]
17925	ENU01719	ANI61C5549: 60-81 191..818	60-81	622-644	NAP		g1723536	633	110	4.00E-39	42	25	
17926	ENU01720	ANI61C1131 35-55 2:847..220	35-55	600-619	NAP		g2959364	299	136	1.00E-31	41	70	
17927	ENU01721	ANI61C4472: 58-79 796..170	58-79	611-642	NAP		g2408017	229	78	7.00E-22	41	39	
17928	ENU01722	ANI61C9766: 48-73 2644..3270	48-73	613-632	NAP		g3581910	562	155	2.00E-37	45	48	
17929	ENU01723	ANI61C1069 22-47 1:2644..3271	22-47	588-607	NAP		g3334345	2295	333	6.00E-91	92	39	
17930	ENU01724	ANI61C1043 63-82 5:4737..5368	63-82	632-652	NAP		g3323498	654	132	1.00E-51	94	80	
17931	ENU01725	ANI61C3265: 67-88 1748..1480	67-88	639-658	NAP		g2352898	780	116	1.00E-49	52	50	
17932	ENU01726	ANI61C1074 46-65 6:1250..615	46-65	617-639	NAP		g1722902	1116	250	5.00E-98	96	88	
17933	ENU01727	ANI61C7309: 63-82 1500..864	63-82	626-657	NAP		g2132023	300	93	3.00E-20	33	55	

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17934	ENU01728	ANI61C3091: 44-64 1737..2374		617-638	NAP		g131622	281	65	4.00E-20			"phosphoribosylglycinamide formyltransferase (GART) (GAR transformylase) (5'-phosphoribosylglycinamide transformylase) ; ADE8 protein - yeast (Saccharomyces cerevisiae) ; (M36585) ADE8 gene product [Saccharomyces cerevisiae] ; (U32274) Ade8p: glycineamide ribotide transformylase, EC number 2.1.2.2; YDR408C; CAI: 0.12 [Saccharomyces cerevisiae] ; ADE8 gene [Saccharomyces cerevisiae] ; ADE8 gene [Saccharomyces cerevisiae] "
17935	ENU01729	ANI61C468:2 30-49 580..3217		605-624	NAP		g1351673	423	141	4.00E-33	42	57	hypothetical 37.7 KD protein C1F7.12 in chromosome I ; hypothetical protein SPAC1F7.12 - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown
17936	ENU01730	ANI61C7926: 39-58 7341..6705		609-633	NAP		g2388903	558	210	7.00E-54	57	37	[Schizosaccharomyces pombe] (Z98974) putative cytochrome p450 [Schizosaccharomyces pombe]
17937	ENU01731	ANI61C1107 32-51 8:2079..1440		607-629	NAP		g2132219	249	72	7.00E-22	40	100	hypothetical protein YPL170w - yeast (Saccharomyces cerevisiae) ; (Z73526) ORF YPL170w [Saccharomyces cerevisiae] ; (X96770) P2515 protein [Saccharomyces cerevisiae]
17938	ENU01732	ANI61C6672: 56-76 758..119		629-653	NAP		g1730734	144	68	8.00E-11	24	17	hypothetical 128.1 KD protein in OMP2-MSG5 intergenic region ; probable membrane protein YNL054w - yeast (Saccharomyces cerevisiae) ; (U12141) Ynl2467p [Saccharomyces cerevisiae] ; (Z71330) ORF YNL054w [Saccharomyces cerevisiae]
17939	ENU01733	ANI61S4240: 23-54 2..642		594-621	NAP		g2244937	997	334	3.00E-99	95	40	(Z97339) hypothetical protein [Arabidopsis thaliana]
17940	ENU01734	ANI61C354:1 35-54 045..401		619-638	NAP		g3850084	483	133	9.00E-31	41	61	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]

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17941	ENU01735	ANI61C1069 1:1390..744	49-68	634-653	NAP		g2132301	219	62	0.000000	30	84	hypothetical protein YPR143w - yeast (Saccharomyces cerevisiae); (U40829) Note that there is an overlapping ORF on the other strand (27648-27085) [Saccharomyces cerevisiae]
17942	ENU01736	ANI61C1646: 72-91 650..4		641-676	NAP		g3581866	298	137	6.00E-32	40	76	(AL031541) putative dehydrogenase [Streptomyces coelicolor]
17943	ENU01737	ANI61C1050 23-55 5:10224..1087 6		611-633	NAP		g1083640	186	85	6.00E-16	26	39	cytochrome P450III - rat; (X79991) cytochrome P450III [Rattus norvegicus]; (D38381) P450 6beta-2 [Rattus norvegicus]; cytochrome P450 [Rattus norvegicus]
17944	ENU01738	ANI61C1116 55-77 0:1150..1803		646-666	NAP		g3219917	212	64	4.00E-18	28	84	hypothetical 27.4 KD protein C30D10.14 in chromosome II; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]
17945	ENU01739	ANI61C8325: 22-45 773..1431		612-638	NAP		g2131352	336	101	5.00E-21	48	87	hypothetical protein YDL166c - yeast (Saccharomyces cerevisiae); (Z67750) putative protein [Saccharomyces cerevisiae]; (Z74214) ORF YDL166c [Saccharomyces cerevisiae]
17946	ENU01740	ANI61C7771: 30-50 2257..2894		629-646	NAP		g2493387	2647	458	e-128	98	43	[Saccharomyces cerevisiae] probable sterigmatocystin biosynthesis P450 monooxygenase STCS (cytochrome P450 59); (U34740) putative p450 monooxygenase [Emicella nidulans]
17947	ENU01741	ANI61C8376: 57-75 39..700		657-676	NAP		g1352268	911	325	1.00E-88	77	60	Deoxyhypusine synthase; (U22400) deoxyhypusine synthase [Neurospora crassa]
17948	ENU01742	ANI61C744:7 32-54 3..735		632-651	NAP		g1723438	219	74	8.00E-13	43	19	hypothetical 52.3 KD protein C56F8.06C in chromosome I precursor; (Z69728) unknown [Schizosaccharomyces pombe]
17949	ENU01743	ANI61C9987: 23-43 115..777		624-643	NAP		g2462674	356	122	2.00E-27	32	57	(Z95395) hypothetical protein [Schizosaccharomyces pombe]
17950	ENU01744	ANI61C2574: 22-54 4710..4048		620-642	NAP		g3702646	276	104	6.00E-22	34	36	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
17951	ENU01745	ANI61C3010: 49-69 256..920		651-670	NAP		g2131405	462	150	7.00E-36	51	51	hypothetical protein YDR267c - yeast (Saccharomyces cerevisiae); (U51030) Ydr267cp [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17952	ENU01746	ANI61C9890: 49-68 1427..2093		652-673	NAP		g549768	133	55	0.000000 5			hypothetical 61.1 KD protein in YPT52-DBP7 intergenic region ; hypothetical protein YKR016w - yeast (Saccharomyces cerevisiae) ; (Z28241) ORF YKR016w [Saccharomyces cerevisiae]
17953	ENU01747	ANI61C4162: 23-46 4593..3927		627-647	NAP		g3913152	919	336	1.00E-91	70	66	"alpha-L-arabinofuranosidase precursor (arabinoxylan arabinofuranohydrolase) ; (Z78010) (1,4)-beta-D-arabinoxylan arabinofuranohydrolase [Aspergillus tubingensis]"
17954	ENU01748	ANI61C8530: 43-63 2774..2107		647-668	NAP		g2492755	704	113	5.00E-50	54	72	sorbitol utilization protein SOU2 ; (AF002134) Sou2p [Candida albicans]
17955	ENU01749	ANI61C7365: 37-56 1551..882		629-664	NAP		g2330856	841	75	5.00E-17	32	18	(Z98533) putative rna-directed rna polymerase [Schizosaccharomyces pombe]
17956	ENU01750	ANI61C3463: 67-86 1301..1975		674-699	NAP		g2131494	346	91	8.00E-18	35	38	hypothetical protein YDR440w - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr440wp; CAI: 0.13 [Saccharomyces cerevisiae]
17957	ENU01751	ANI61C8563: 22-44 428..1104		632-656	NAP		g626251	280	47	1.00E-11			citrate transport protein - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2039-ORF [Saccharomyces cerevisiae] ; (Z36160) ORF YBR291c [Saccharomyces cerevisiae] ; ORF YBR2039 [Saccharomyces cerevisiae]
17958	ENU01752	ANI61C319:4 24-51 177..4854		637-659	NAP		g2414577	431	88	1.00E-34	40	69	(Z99292) hypothetical protein [Schizosaccharomyces pombe]
17959	ENU01753	ANI61C3311: 40-59 4708..5389		660-679	NAP		g1333636	197	43	0.003			(L47321) glycoprotein 150 [Murine herpesvirus 68] ; (Y09060) serine threonine rich glycoprotein [murine herpesvirus 68] ; (U97553) glycoprotein 150 [murine herpesvirus 68]
17960	ENU01754	ANI61C737:1 25-48 037..353		648-667	NAP		g266564	1297	343	e-124	96	41	M-phase inducer phosphatase ; protein-tyrosine-phosphatase (EC 3.1.3.48) nimT - Emericella nidulans ; (X64601) NIMT/CDC25 [Emericella nidulans] (AL023776) hypothetical protein [Schizosaccharomyces pombe]
17961	ENU01755	ANI61C8708: 32-59 3206..2521		656-675	NAP		g3184056	76	46	0.0002			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17962	ENU01756	ANI50C6889_1:1734..1049	47-66	665-690	NAP		g2132389		233	1.00E-60	57	73	"phosphate transport protein, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X92441) YOR50-12 [Saccharomyces cerevisiae] ; (Z75130) ORF YOR222w [Saccharomyces cerevisiae]"
17963	ENU01757	ANI61C7024 89..1802	22-45	645-667	NAP		g2496730	369	169	2.00E-41	40	55	hypothetical protein Y4OU precursor ; (AE000089) Y4oU [Rhizobium sp. NGR234]
17964	ENU01758	ANI61C7798: 790..101	28-47	656-675	NAP		g2132397	344	134	5.00E-31	44	42	POS5 protein - yeast (Saccharomyces cerevisiae) ; (Z73544) ORF YPL188w [Saccharomyces cerevisiae]
17965	ENU01759	ANI61C8193: 3049..2356	22-48	642-673	NAP		g1351368	360	100	2.00E-35			RNA polymerase II holoenzyme cyclin-like subunit ; cyclin homolog UME3 - yeast (Saccharomyces cerevisiae) ; (U20635) Ssn8p [Saccharomyces cerevisiae] ; (U20221) RNA polymerase II holoenzyme cyclin-like subunit [Saccharomyces cerevisiae] ; (U16248) cyclin [Saccharomyces cerevisiae] ; (Z71301) ORF YNL025c [Saccharomyces cerevisiae] ; RNA polymerase II regulatory protein [Saccharomyces cerevisiae]
17966	ENU01760	ANI61C5471: 2354..1658	22-41	657-676	NAP		g1703215	283	129	2.00E-29	29	36	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
17967	ENU01761	ANI61C9593: 1..698	22-49	655-677	NAP		g731806	707	270	5.00E-72	56	20	"probable calcium-transporting ATPase 7 ; probable membrane protein YIL048w - yeast (Saccharomyces cerevisiae) ; (Z38060) orf, len: 1151, CAI: 0.17, similar to S30768 S30768 probable ATPase - yeast (saccharomyces cerevisiae) [Saccharomyces cerevisiae]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17968	ENU01762	ANI61C1070 6:8487..9184	60-79	696-715	NAP		g1730823	610	136	2.00E-31	38	36	probable mannosyltransferase ALG9; probable membrane protein YNL219c - yeast (Saccharomyces cerevisiae); (Z71495) ORF YNL219c [Saccharomyces cerevisiae]; (X96417) putative mannosyltransferase [Saccharomyces cerevisiae] general amino acid permease AGP2; probable amino acid transport protein YBR132c - yeast (Saccharomyces cerevisiae); (X75891) YBR1007 [Saccharomyces cerevisiae]; (Z36001) ORF YBR132c [Saccharomyces cerevisiae]; YBR1007 gene [Saccharomyces cerevisiae] (U70619) heroin esterase [Rhodococcus sp.] lactose permease; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (AL035226) major facilitator superfamily protein [Schizosaccharomyces pombe] (AL023589) membrane transporter [Schizosaccharomyces pombe] hypothetical 26.1 KD protein in POP4- SHM1 intergenic region; hypothetical protein YBR261c - yeast (Saccharomyces cerevisiae); (X70529) ORF YBR1729 [Saccharomyces cerevisiae]; (Z36130) ORF YBR261c [Saccharomyces cerevisiae] unknown; (AF046024) UBA3 [Homo sapiens]; (AB012190) Nedd8- activating enzyme hUba3 [Homo sapiens] (AL035396) SRG1-like protein [Arabidopsis thaliana] (AF069492) SONA [Emmericella nidulans]
17969	ENU01763	ANI61C7105: 22-44 1769..1069	22-44	652-680	NAP		g586542	859	95	1.00E-41	46	36	
17970	ENU01764	ANI61C3637: 28-63 100..802	28-63	669-688	NAP		g2088525	352	83	4.00E-18	37	64	
17971	ENU01765	ANI61C1020: 53-76 706..3	53-76	695-714	NAP		g125935	137	65	5.00E-10	32	19	
17972	ENU01766	ANI61C4189: 35-54 2709..2005	35-54	674-697	NAP		g4160574	519	63	2.00E-18	33	40	
17973	ENU01767	ANI61C8086: 56-76 2503..1797	56-76	701-720	NAP		g3135989	619	183	1.00E-45	39	40	
17974	ENU01768	ANI61C7151: 24-45 490..1197	24-45	670-689	NAP		g586379	359	120	6.00E-36	40	98	
17975	ENU01769	ANI61C8423: 39-59 208..916	39-59	686-705	NAP		g4507765	660	204	5.00E-52	46	53	
17976	ENU01770	ANI61C2775: 71-91 2225..1517	71-91	715-737	NAP		g4454019		45	0.00007			
17977	ENU01771	ANI61C9647: 36-55 1724..1014	36-55	681-704	NAP		g3202044	1440	496	e-140	98	65	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17978	ENU01772	ANI61C7619; 1340..630	70-89	711-738	NAP		g729968	889	301	3.00E-81	60	53	"saccharopine dehydrogenase [NADP+, L-glutamate forming]; saccharopine dehydrogenase (NADP+, L-glutamate-forming) (EC 1.5.1.10) - yeast (Saccharomyces cerevisiae); (X77363) saccharopine dehydrogenase (NADP+, L-glutamate forming) [Saccharomyces cerevisiae]; (Z71665) ORF YNR050c [Saccharomyces cerevisiae]"
17979	ENU01773	ANI61C1147 1:36..747	57-79	706-726	NAP		g2624697	823	266	5.00E-76	76	53	Pectin Lyase A
17980	ENU01774	ANI61C8541; 3665..2954	54-76	704-723	NAP		g1709941	298	106	2.00E-22	27	35	proline-specific permease; proline transport protein - yeast (Saccharomyces cerevisiae); (X95720) O6345 [Saccharomyces cerevisiae]; (Z75256) ORF YOR348c [Saccharomyces cerevisiae] (AL023518) hypothetical protein [Schizosaccharomyces pombe]
17981	ENU01775	ANI61C6911: 35-56 1061..347	35-56	687-707	NAP		g3130055	90	41	0.000000	28	64	"hypothetical 23.7 KD protein C13G6.14 in chromosome I; hypothetical protein SPAC13G6.14 - fission yeast (Schizosaccharomyces pombe); hypothetical protein SPAC24B11.03 - fission yeast (Schizosaccharomyces pombe); (Z54308) hypothetical protein [Schizosaccharomyces pombe]; (Z67757) unknown [Schizosaccharomyces pombe]; (AF125215) diadenosine 5', 5'''-P1,P6-hexaphosphate hydrolase [Schizosaccharomyces pombe]"
17982	ENU01776	ANI61C578:8 22-41 1..798	22-41	678-697	NAP		g1175461	212	75	5.00E-13			RAS-2 protein; (D16137) NC-ras-2 protein [Neurospora crassa]
17983	ENU01777	ANI61C1120 22-41 8:2075..1355	22-41	680-699	NAP		g2500078	676	151	2.00E-55	68	94	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17984	ENU01778	ANI61C1029 4:9723..9004	22-51	680-699	NAP		g1730800	334	120	1.00E-37	37	85	hypothetical 28.8 KD protein in PSD1-SKO1 intergenic region; hypothetical protein YNL168c - yeast (Saccharomyces cerevisiae) ; (X92517) N1696 [Saccharomyces cerevisiae] ; (Z71444) ORF YNL168c [Saccharomyces cerevisiae] (D64052) cytochrome P450 like TBP [Nicotiana tabacum] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe] xanthine dehydrogenase (purine hydroxylase I) ; xanthine dehydrogenase (EC 1.1.1.204) - Emericella nidulans ; (X82827) xanthine dehydrogenase [Emericella nidulans] hypothetical 143.7 KD protein C11D3.15 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] (AE000680) glutaryl-tRNA (Gln) amidotransferase subunit A [Aquifex aeolicus] (AP000003) 388aa long hypothetical amino acid amidohydrolase [Pyrococcus horikoshii] (AJ001909) transcriptional activator [Aspergillus niger] O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) ; (U81806) OMST-oxidoreductase [Aspergillus flavus] ; (U81807) OMST-oxidoreductase [Aspergillus flavus]
17985	ENU01779	ANI61C1253: 68-87 7171..6449	68-87	728-748	NAP		g1545805	653	102	9.00E-27	66	44	
17986	ENU01780	ANI61C4046: 58-83 3414..2689	58-83	706-741	NAP		g3560142	680	132	3.00E-30	34	38	
17987	ENU01781	ANI61C6939: 61-80 556..1285	61-80	729-748	NAP		g2493965	729	218	5.00E-70	64	15	
17988	ENU01782	ANI61C6754: 25-45 3042..3771	25-45	693-712	NAP		g1351711	3300	181	9.00E-72	59	18	
17989	ENU01783	ANI61C177:2 43-62 2..753	43-62	713-732	NAP		g2635242	234	93	2.00E-18	31	61	
17990	ENU01784	ANI61C6621: 25-44 2002..2734	25-44	696-715	NAP		g2982954	658	139	1.00E-32	42	44	
17991	ENU01785	ANI61C1038 24-43 8:6660..7392	24-43	689-714	NAP		g3257130	388	109	2.00E-23	35	57	
17992	ENU01786	ANI61C380:1 26-49 856..2589	26-49	698-717	NAP		g2808634	545	150	1.00E-35	46	20	
17993	ENU01787	ANI61C124:7 27-47 ..741	27-47	700-719	NAP		g3914244	70	70	2.00E-15			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
17994	ENU01788	ANI61C3719: 67-90 885..149		741-761	NAP		g1352938	479	188	4.00E-47	43	61	hypothetical 39.7 KD protein in HOM6-PMT4 intergenic region ; hypothetical protein YJR142w - yeast (Saccharomyces cerevisiae) ; (Z49642)
													ORF YJR142w [Saccharomyces cerevisiae]
17995	ENU01789	ANI61C846:2 22-49 341..1602		700-719	NAP		g1351369	850	275	3.00E-73	60	41	meiotic mRNA stability protein kinase UME5 ; (U20222) Srb10p [Saccharomyces cerevisiae] ; RNA polymerase II regulatory protein [Saccharomyces cerevisiae]
17996	ENU01790	ANI61C8292: 22-57 1872..1132		699-720	NAP		g118066	495	186	1.00E-46	41	45	cyclohexanone monooxygenase ; (M19029) cyclohexanone monooxygenase [Acinetobacter sp.]
17997	ENU01791	ANI61C2524: 60-80 55..796		738-759	NAP		g2493572	414	175	2.00E-43	41	45	putative CDP-diacylglycerol--serine O-phosphatidyltransferase (phosphatidylserine synthase) ; (Z86109) unknown [Saccharomyces pastorianus]
17998	ENU01792	ANI61C1071 32-51 7:1722..975		713-737	NAP		g2842695	79	58	0.000000	23	17	hypothetical 150.9 KD protein C6G9.04 in chromosome I ; (Z81317) hypothetical protein [Schizosaccharomyces pombe]
17999	ENU01793	ANI61C3292: 63-83 816..69		749-769	NAP		g2330659	222	59	2.00E-14	29	16	(Z98595) putative snf2 family helicase [Schizosaccharomyces pombe]
18000	ENU01794	ANI61S1000: 52-71 160..66		738-759	NAP		g117619		76	3.00E-13	30	37	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18001	ENU01795	ANI61C5352: 28..781	57-83	748-768	NAP		g3123159	493	202	1.00E-51	45	60	hypothetical 40.4 KD TRP-ASP repeats containing protein C14B1.4 in chromosome III ; (Z37139) similar to guanine nucleotide binding protein; cDNA EST EMBL:T00917 comes from this gene; cDNA EST CEMSE07F comes from this gene; cDNA EST EMBL:T00918 comes from this gene; cDNA EST EMBL:D70900 comes from this gene; cD...
18002	ENU01796	ANI61C6476: 6018..6773	68-89	750-781	NAP		g2804298	680	92	6.00E-31	37	39	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous] (AC000133) ORF [Emericella nidulans]
18003	ENU01797	ANI61C1116 6:120..876	61-80	749-775	NAP		g1870210	1452	481	e-135	98	53	(AL031174) beta-transducin [Schizosaccharomyces pombe]
18004	ENU01798	ANI61C1060 4:70..826	65-87	758-779	NAP		g3393019	791	194	5.00E-81	60	53	putative seryl--TRNA synthetase YHR011W (serine--TRNA ligase (SERRS) ; serine--tRNA ligase homolog - yeast (Saccharomyces cerevisiae) ; (U10400) Yhr011wp [Saccharomyces cerevisiae]
18005	ENU01799	ANI61C8864: 2659..1903	58-77	751-772	NAP		g731635	551	189	2.00E-47	44	53	"(AL031532) yeast gtr2 homolog, novel small GTPase subfamily protein [Schizosaccharomyces pombe]" putative flavin-containing monoamine oxidase MTV014.14 ; (AL021646) hypothetical protein Rv3170 [Mycobacterium tuberculosis] (AF097728) pyruvate carboxylase [Aspergillus terreus]
18006	ENU01800	ANI50C2350 0_1:82..845	23-58	720-744	NAP		g3560242	251	251	2.00E-67	55	75	RAS-related protein RAB-11B ; GTP-binding protein Rab11b - mouse ; (L26528) Rab11b [Mus musculus] "(D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii]"
18007	ENU01801	ANI61C1420: 1..764	22-47	724-743	NAP		g3913051	244	76	3.00E-13	30	55	
18008	ENU01802	ANI61C6541: 1379..2143	22-44	723-744	NAP		g3806120	3163	392	e-108	89	19	
18009	ENU01803	ANI61C1003 4:100..870	22-56	726-750	NAP		g1172815	699	251	6.00E-74	78	91	
18010	ENU01804	ANI50C6358 _1:803..33	47-73	756-775	NAP		g1437475	151	151	3.00E-42	40	80	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18011	ENU01805	ANI61C8273: 4655..3882	72-91	771-803	NAP		g1346665	128	53	0.000002	35	33	"N-terminal acetyltransferase 2 (amino-terminal, alpha-amino, acetyltransferase 2) ; protein N-yeast (Saccharomyces cerevisiae) ; (X85807) ORF G6630 [Saccharomyces cerevisiae] ; (Z72932) ORF YGR147c [Saccharomyces cerevisiae] " probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (Y17243) cytochrome P450 [Gibberella fujikuroi] (AL021839) myb family DNA binding protein [Schizosaccharomyces pombe] phosphoribosylaminoimidazole carboxylase (AIR carboxylase) (AIRC) ; (U70673) phosphoribosylaminoimidazole carboxylase [Filobasidiella neoformans]
18012	ENU01806	ANI61C3339: 3593..2819	54-73	756-786	NAP		g2132957	768	271	5.00E-72	53	49	
18013	ENU01807	ANI61C3910: 207..982	51-70	765-784	NAP		g4127832	220	106	2.00E-22	32	46	
18014	ENU01808	ANI61C1094: 2:150..216	43-62	743-778	NAP		g2894269	225	68	8.00E-11	44	29	
18015	ENU01809	ANI61C9734: 2103..1324	54-73	758-790	NAP		g2500019	1081	123	5.00E-29	48	39	
18016	ENU01810	ANI61C9817: 902..122	35-54	748-773	NAP		g1352887	525	157	7.00E-43	51	70	
18017	ENU01811	ANI61C8177: 14..795	35-54	755-774	NAP		g4507053	223	85	5.00E-16	34	45	
18018	ENU01812	ANI61C7083: 90..875	38-58	762-781	NAP		g459243	155	86	3.00E-16	33	29	
18019	ENU01813	ANI61C1049: 4:4220..5005	37-57	758-780	NAP		g2826769		83	2.00E-15			
18020	ENU01814	ANI61C1857: 2322..2414	39-58	765-783	NAP		g3368	2245	207	8.00E-53	41	28	
18021	ENU01815	ANI61C5906: 1318..531	27-46	753-772	NAP		g3192038	395	129	3.00E-29	32	74	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18022	ENU01816	ANI61C9151: 22-53 4849..4060	22-53	751-769	NAP		g2500768	963	190	5.00E-66	61	66	Septin homolog SPN2 ; (U29888) septin homolog [Schizosaccharomyces pombe]
18023	ENU01817	ANI61C9777: 58-78 1870..1082	58-78	782-805	NAP		g2665711		82	1.00E-19			(AF035413) AgaG [Agrobacterium tumefaciens]
18024	ENU01818	ANI61C9875: 52-71 79..875	52-71	783-806	NAP		g1705594	1074	327	6.00E-89	67	47	peroxisome assembly protein CAR1 (peroxin-2) ; car1 protein - Podospora anserina ; (X87329) peroxisome assembly factor [Podospora anserina]
18025	ENU01819	ANI61C6977: 22-46 1666..868	22-46	759-778	NAP		g1077411	721	240	8.00E-67	56	20	hypothetical protein YLR189c - yeast (Saccharomyces cerevisiae) ; (U17246) Ylr189cp [Saccharomyces cerevisiae]
18026	ENU01820	ANI61C1134: 22-43 3715..2917	22-43	759-778	NAP		g3341417		62	2.00E-20			(AJ009657) Mu3 subunit of clathrin-associated protein complex AP-3 [Drosophila melanogaster]
18027	ENU01821	ANI61C1485: 25-44 1557..2356	25-44	761-782	NAP		g135160	639	165	3.00E-40	40	51	"asparaginyl-TRNA synthetase, mitochondrial precursor (asparagine--TRNA ligase) (ASNRS) ; hypothetical protein YCR024c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR024c, len:492 [Saccharomyces cerevisiae] "
18028	ENU01822	ANI61C5728: 24-46 4582..3771	24-46	773-792	NAP		g3925768	675	115	9.00E-34	46	70	(AL034352) putative GTP-binding protein [Schizosaccharomyces pombe]
18029	ENU01823	ANI61C8692: 56-75 967..157	56-75	793-824	NAP		g3873259	1526	257	5.00E-68	58	56	(AF095899) PDI related protein A [Aspergillus niger]
18030	ENU01824	ANI61C7436: 58-77 2475..3286	58-77	807-827	NAP		g127218	924	257	5.00E-68	57	66	mitochondrial import receptor subunit TOM40 (MOM38 protein) (translocase of outer membrane 40 KD subunit) ; mitochondrial import receptor MOM38 - Neurospora crassa ; (X56883) outer membrane protein [Neurospora crassa] ; outer membrane protein MOM38 [Neurospora crassa]
18031	ENU01825	ANI61C3438: 22-45 1120..309	22-45	772-791	NAP		g1168396	833	298	2.00E-80	58	50	actin interacting protein 2 ; AIP2 protein - yeast (Saccharomyces cerevisiae) ; (U35667) Aip2p [Saccharomyces cerevisiae] ; (Z67750) putative protein [Saccharomyces cerevisiae] ; (Z74226) ORF YDL178w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18032	ENU01826	ANI61C1214: 24-52 148..966	24-52	780-799	NAP		g130806	249	56	0.000000	35	22	pre-mRNA processing RNA helicase PRP5 ; pre-mRNA processing protein PRP5 - yeast (Saccharomyces cerevisiae) ; (M33191) PRP5 [Saccharomyces cerevisiae] ; (Z36106) ORF YBR237w [Saccharomyces cerevisiae]
18033	ENU01827	ANI61C5721: 22-51 93..912	22-51	769-799	NAP		g2498971	369	56	4.00E-28	36	54	putative sterigmatocystin biosynthesis monoxygenase STCW ; (U34740) putative FAD-containing monoxygenase [Emicella nidulans] putative sterigmatocystin biosynthesis monoxygenase STCW ; (U34740) putative FAD-containing monoxygenase [Emicella nidulans] (AC006223) hypothetical protein [Arabidopsis thaliana] putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) ; (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe]
18034	ENU01828	ANI61C5721: 22-51 93..912	22-51	769-799	NAP		g2498971	369	56	4.00E-28	36	54	
18035	ENU01829	ANI61C9612: 22-53 1449..630	22-53	767-799	NAP		g4263703	221	101	2.00E-23	33	53	
18036	ENU01830	ANI61C1628: 31-53 1198..2025	31-53	793-816	NAP		g1710663	2331	428	e-119	72	23	
18037	ENU01831	ANI61C7971: 22-51 856..1690	22-51	783-813	NAP		g3947884	625	146	2.00E-34	48	70	
18038	ENU01832	ANI61C1061: 52-70 861..26	52-70	810-845	NAP		g4588080	616	175	3.00E-43	35	56	(AF095286) guanine deaminase GDA [Homo sapiens] "catalase (PXP-9) ; catalase (EC 1.11.1.6), peroxisomal - yeast (Candida tropicalis) ; (X13978) catalase (AA 1 - 485) [Candida tropicalis] ; (X066660) catalase (AA 1 - 485) [Candida tropicalis] ; peroxisomal catalase [Candida tropicalis]"
18039	ENU01833	ANI61C5959: 51-70 934..93	51-70	827-849	NAP		g115699	1548	226	2.00E-90	58	57	
18040	ENU01834	ANI61C9843: 55-74 696..1539	55-74	837-856	NAP		g2414656	694	234	7.00E-61	47	54	(Z99261) putative aminotransferase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18041	ENU01835	ANI61C1438: 24-45 1368..522	24-45	807-826	NAP		g2127591	137	57	0.000000	29	81	N-acetylphosphinothricin-tripetide-deacetylase - Streptomyces viridochromogenes ; (X65195) N-acetylphosphinothricin-tripetide-deacetylase [Streptomyces viridochromogenes]
18042	ENU01836	ANI61C1600: 24-43 1195..346	24-43	811-831	NAP		g2293194	289	89	2.00E-32			(AF0082220) yteR [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18043	ENU01837	ANI61C6951: 26-45 582..1433	26-45	816-835	NAP		g4050050	648	159	8.00E-72	54	82	(AF102147) putative dimethyladenosine transferase [Homo sapiens]
18044	ENU01838	ANI61C9308: 32-55 2353..1501	32-55	817-842	NAP		g3395556	676	66	2.00E-32	51	59	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
18045	ENU01839	ANI61C7122: 57-77 49..878	57-77	845-867	NAP		g730864	506	152	3.00E-38	53	71	sporulation protein SPS19 (sporulation-specific protein SPX19) ; sporulation protein SPS19 - yeast (Saccharomyces cerevisiae) ; (X78898) N1362 [Saccharomyces cerevisiae] ; (Z71479) ORF YNL202w [Saccharomyces cerevisiae]
18046	ENU01840	ANI61C1011 68-87 9:2048..1195	68-87	860-879	NAP		g2494910	1455	255	3.00E-67	47	33	hypothetical 91.7 KD TRP-ASP repeats containing protein in NUP116-FAR3 intergenic region ; probable membrane protein YMR049c - yeast (Saccharomyces cerevisiae) ; (Z49703) unknown [Saccharomyces cerevisiae] (Z75526) Weak similarity to Staphylococcus autolysin gene (TR:G765072); cDNA EST EMBL:M89336 comes from this gene; cDNA EST yk505d12.3 comes from this gene [Caenorhabditis elegans] (AC004850) vacuolar assembly protein VPS41 homolog (S53) [Homo sapiens]
18047	ENU01841	ANI61C122:1 47-69 400..546	47-69	840-859	NAP		g3874039	295	90	2.00E-17	42	27	mutS (E. coli) homolog 3 ; (U61981) hMSH3 [Homo sapiens] (U09352) 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenes]
18048	ENU01842	ANI61C8569: 40-65 66..921	40-65	834-853	NAP		g4309891	317	124	7.00E-28	37	33	
18049	ENU01843	ANI61C2388: 49-69 1763..2619	49-69	843-863	NAP		g4505249	1372	278	4.00E-74	48	25	
18050	ENU01844	ANI61C3304: 22-45 3423..2567	22-45	814-836	NAP		g517205	305	149	3.00E-35	33	47	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18051	ENU01845	ANI61C924:4 9..911	70-92	867-890	NAP		g3810847	341	161	8.00E-39	39	37	(AL032684) zinc finger protein [Schizosaccharomyces pombe]
18052	ENU01846	ANI61C8857: 29-48 1188..2055	29-48	824-854	NAP		g2492894	1809	331	5.00E-90	56	13	adenylate cyclase (ATP pyrophosphatase) (adenylyl cyclase) ; adenylyate cyclase (EC 4.6.1.1) - Podospira anserina ; (L43413) adenylyl cyclase [Podospira anserina]
18053	ENU01847	ANI61C4219: 44-68 925..57	44-68	850-869	NAP		g2132252	703	74	1.00E-12	28	40	hypothetical protein YPL263c - yeast (Saccharomyces cerevisiae) ; (Z73619) ORF YPL263c [Saccharomyces cerevisiae]
18054	ENU01848	ANI61C5719: 49-79 921..50	49-79	856-878	NAP		g1717749	522	153	1.00E-45	41	32	"potassium transport protein ; (Z69369) SPAC3F10.02c, potassium transport gene, len: 841, conflict with PIR:S50225 potassium transport protein homolog at position 4549 causes frameshift near N-terminus [Schizosaccharomyces pombe] "
18055	ENU01849	ANI61C6777: 50-69 874..1	50-69	854-881	NAP		g1175428	583	229	3.00E-59	41	89	hypothetical 37.2 KD protein C12C2.09C in chromosome II ; (Z54140) conserved hypothetical protein [Schizosaccharomyces pombe]
18056	ENU01850	ANI61C8505: 59-79 2230..1356	59-79	870-891	NAP		g3080508	510	168	4.00E-41	45	68	(AL022598) UDP-galactose transporter homologue [Schizosaccharomyces pombe]
18057	ENU01851	ANI61C8544: 72-93 103..977	72-93	880-904	NAP		g3136060	281	145	5.00E-34	34	59	(AL023592) zinc finger protein [Schizosaccharomyces pombe]
18058	ENU01852	ANI61C7094: 42-61 1117..236	42-61	863-882	NAP		g113382	323	50	0.00002	36	58	alcohol dehydrogenase III ; alcohol dehydrogenase (EC 1.1.1.1) III - Emericella nidulans ; (X02764) alcohol dehydrogenase 3 [Emericella nidulans] (U94348) acetyl-coenzyme A synthetase [Pyrobaculum aerophilum] (U38783) orf of unknown function; Method: conceptual translation supplied by author
18059	ENU01853	ANI61C5249: 26-45 176..1059	26-45	848-867	NAP		g4100125	317	89	3.00E-34	40	37	[Schizosaccharomyces pombe] (Z69254) alpha-galactosidase [Hypocrea jecorina]
18060	ENU01854	ANI61C1107 33-57 8:47..931	33-57	856-875	NAP		g1145409	110	76	3.00E-13	26	42	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
18061	ENU01855	ANI61C1082 43-62 1:1936..1052	43-62	857-885	NAP		g1580818	1121	439	e-122	67	39	
18062	ENU01856	ANI61C1077 42-62 5:2172..1288	42-62	865-884	NAP		g3850084	543	86	2.00E-35	44	72	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	%id	% cvrg	Description
18063	ENU01857	ANI61C5563: 25-45 970..85	846-868	NAP			g3873847	153	89	3.00E-17	35	29	(Z82256) cDNA EST EMBL:D67325 comes from this gene; cDNA EST EMBL:C13315 comes from this gene; cDNA EST EMBL:D37596 comes from this gene; cDNA EST EMBL:D69512 comes from this gene; cDNA EST EMBL:C11315 comes from this gene; cDN...
18064	ENU01858	ANI61C9914: 59-78 1844..2729	883-902	NAP			g1723213	499	146	2.00E-34	40	54	hypothetical 51.5 KD protein C3H8.02 in chromosome I ; (Z69086) unknown [Schizosaccharomyces pombe]
18065	ENU01859	ANI61C4664: 24-43 653..1545	854-874	NAP			g3080538	623	182	2.00E-45	48	61	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
18066	ENU01860	ANI61C1025 22-53 5:1471..2366	855-875	NAP			g3915186	197	103	2.00E-21	39	57	ubiquitin-conjugating enzyme E2-21 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) (peroxin-4) ; (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta]
18067	ENU01861	ANI61C7946: 52-74 2004..1107	888-907	NAP			g2414602	434	85	8.00E-16	37	56	(Z99295) pre-mrna splicing factor [Schizosaccharomyces pombe]
18068	ENU01862	ANI61C1054 34-56 8:1613..720	873-892	NAP			g2764949	1252	334	3.00E-96	97	43	(X98931) heat shock protein 70 [Emicella nidulans]
18069	ENU01863	ANI61C5778: 39-58 1808..2712	871-901	NAP			g2500938	988	238	4.00E-62	41	52	myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
18070	ENU01864	ANI61C2559: 67-86 227..1131	905-930	NAP			g1063421		99	4.00E-20			(L48797) toxin pump [Cochliobolus carbonum]
18071	ENU01865	ANI61C257:1 22-53 317..410	861-886	NAP			g2306977	1117	124	1.00E-41	56	42	(AF010145) hexose transporter [Aspergillus parasiticus]
18072	ENU01866	ANI61C5632: 22-47 31..938	868-887	NAP			g732227	502	80	4.00E-32	42	79	hypothetical 40.7 KD protein in OPDE 3'region (ORF2) ; hypothetical protein 2 - Pseudomonas aeruginosa ; (Z14064) ORF2 [Pseudomonas aeruginosa]
18073	ENU01867	ANI61C1078 54-73 4:1116..209	900-919	NAP			g1351673	521	174	7.00E-43	42	66	hypothetical 37.7 KD protein CIF7.12 in chromosome I ; hypothetical protein SPAC1F7.12 - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown [Schizosaccharomyces pombe]

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18074	ENU01868	ANI61C1004	67-86	921-940	NAP		g2842513	139	49	4.00E-14	25	90	(AL021748) superoxide dismutase [Schizosaccharomyces pombe]
18075	ENU01869	8:3049..2134 ANI61C562:8 308..9223	71-91	925-944	NAP		g134297	482	155	4.00E-47	40	70	SCJ1 protein - yeast (Saccharomyces cerevisiae) ; (X58679) SCJ1 [Saccharomyces cerevisiae] ; (Z49809) unknown [Saccharomyces cerevisiae] ; heat shock protein [Saccharomyces cerevisiae] (AL021748) superoxide dismutase [Schizosaccharomyces pombe] C-24(28) sterol reductase ; probable transport protein ERG4 - yeast (Saccharomyces cerevisiae) ; (Z72534) ORF YGL012w [Saccharomyces cerevisiae]
18076	ENU01870	ANI61C1004	67-86	921-940	NAP		g2842513	139	49	4.00E-14	25	90	(AL021748) superoxide dismutase [Schizosaccharomyces pombe]
18077	ENU01871	8:3049..2134 ANI61C924:2 097..3013	72-91	911-946	NAP		g1706692	1046	206	1.00E-52	52	61	transport protein ERG4 - yeast (Saccharomyces cerevisiae) ; (Z72534) ORF YGL012w [Saccharomyces cerevisiae]
18078	ENU01872	ANI61C7696: 39-59 18..936	39-59	896-915	NAP		g2598593		39	0.034			(Y15369) MtN12 [Medicago truncatula]
18079	ENU01873	ANI61C1754: 57-78 4729..3810	57-78	909-934	NAP		g3368		96	8.00E-26			(X63998) aminopeptidase yscII [Saccharomyces cerevisiae]
18080	ENU01874	ANI61C6862: 22-46 229..1154	22-46	882-905	NAP		g1791305	610	149	1.00E-57	43	70	(U83489) septin B [Emicella nidulans]
18081	ENU01875	ANI50C1_17 41:3..929	24-43	889-908	NAP		g1703202		168	4.00E-41	38	68	sterigmatocystin biosynthesis regulatory protein ; sterigmatocystin synthesis transcriptional regulator afIR - Emicella nidulans ; (U34740) pathway specific transcription factor [Emicella nidulans]
18082	ENU01876	ANI61C352:9 95..69	23-42	888-907	NAP		g1176004	480	192	4.00E-48	39	82	hypothetical 40.4 KD protein in PES4-HIS2 intergenic region ; (D50617) YFR024C [Saccharomyces cerevisiae]
18083	ENU01877	ANI61C4038: 71-93 1117..188	71-93	936-957	NAP		g2160185	299	101	8.00E-21	26	42	(AC000132) Similar to S. pombe ISP4 (gb D83992). [Arabidopsis thaliana]
18084	ENU01878	ANI61C1100 6:1241..312	32-53	897-919	NAP		g585251		77	1.00E-13			Polyketide synthase HETM ; hetM protein - Anabaena sp. (PCC 7120) ; (L22883) polyketide synthase [Anabaena sp.]
18085	ENU01879	ANI61C8862: 22-54 1064..135	22-54	888-910	NAP		g3006183	381	97	9.00E-38	37	67	(AL022304) trp-ast repeats containing protein [Schizosaccharomyces pombe]
18086	ENU01880	ANI61C1020 9:2555..1619	34-59	907-926	NAP		g2330840	417	118	1.00E-41	38	90	(Z98531) hypothetical protein [Schizosaccharomyces pombe]

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18087	ENU01881	ANI61C5467: 1083..828	22-46	902-921	NAP		g2494694	431	158	6.00E-38	34	63	Cutinase gene palindrome-binding protein (PBP) ; palindrome-binding protein - fungus (<i>Fusarium solani</i>) ; (U23722) cutinase gene palindrome-binding protein [<i>Fusarium solani</i> f. sp. <i>pisi</i>] (Z68218) K01H12.1 [<i>Caenorhabditis elegans</i>] (Z30582) SmX4 protein [Saccharomyces cerevisiae] (AC000133) ORF [Emericella nidulans]
18088	ENU01882	ANI61C1058: 59-80	59-80	186-219	NAP		g3878134	201	75	8.00E-14	47	84	DNA-directed RNA polymerase I 13.7 KD polypeptide (A12.2) ; DNA-directed RNA polymerase (EC 2.7.7.6) I chain A12.2 - yeast (<i>Saccharomyces cerevisiae</i>) ; (L00708) RNA polymerase I subunit A12.2 [Saccharomyces cerevisiae] ; (L35564) RNA polymerase I A12.2 subunit [Saccharomyces cerevisiae] ; (Z49563) ORF YJR063w [Saccharomyces cerevisiae] ; (L47993) ORF YJR063w [Saccharomyces cerevisiae]
18089	ENU01883	ANI61C1068: 55-74	55-74	221-240	NAP		g732947		37	0.018			alcohol dehydrogenase (acceptor) ; alcohol dehydrogenase - <i>Pseudomonas oleovorans</i> ; (X65936) alcohol dehydrogenase [<i>Pseudomonas oleovorans</i>] (AF036424) mucin-like protein [Trypanosoma cruzi]
18090	ENU01884	ANI61C1103: 66-85	66-85	313-332	NAP		g1870220	221	88	2.00E-17	42	76	probable isovaleryl-CoA dehydrogenase (IVD) ; C02D5.1 protein - <i>Caenorhabditis elegans</i> ; (L16622) homology with isovaleryl-CoA dehydrogenase protein; putative [<i>Caenorhabditis elegans</i>]
18091	ENU01885	ANI61C9818: 52-71	52-71	343-362	NAP		g417695	203	57	0.000000			
18092	ENU01886	ANI61C8397: 48-67	48-67	372-391	NAP		g416604	205	74	5.00E-13			
18093	ENU01887	ANI61C1044: 53-72	53-72	381-400	NAP		g3064176		33	0.81			
18094	ENU01888	ANI61C458: 4 55-73	55-73	400-420	NAP		g462428	143	68	2.00E-11	33	39	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18095	ENU01889	ANI61C7499; 1412..1003	69-87	418-435	NAP		g2127839	180	65	2.00E-10	32	82	"deoxycytidine triphosphate deaminase homolog - Methanococcus jannaschii ; (U67553) deoxycytidine triphosphate deaminase, putative (dcd) [Methanococcus jannaschii]"
18096	ENU01890	ANI61C3183; 32-51 568..985	32-51	388-407	NAP		g400513	33	0.0007				NADH-ubiquinone oxidoreductase B22 subunit (complex I-B22) (CI-B22) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B22 - bovine ; (X64836) NADH-ubiquinone oxidoreductase complex B22 subunit [Bos taurus]
18097	ENU01891	ANI61C1610; 36-56 1312..1732	36-56	395-414	NAP		g1078673	1228	40	0.006	31	13	gamma-adaptin - smut fungus (Ustilago maydis) ; (Z46804) gamma-adaptin [Ustilago maydis]
18098	ENU01892	ANI61C4480; 22-44 445..24	22-44	382-401	NAP		g2465151	111	53	0.000001	40	74	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
18099	ENU01893	ANI61C6633; 66-83 880..1308	66-83	434-452	NAP		g3646455	432	61	0.000000	77	53	(AL031603) 60s ribosomal protein [Schizosaccharomyces pombe]
18100	ENU01894	ANI61C2205; 30-49 4095..4526	30-49	400-419	NAP		g2493389	179	56	0.000000	39	21	probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) ; (U34740) putative p450 monooxygenase [Emmericella nidulans]
18101	ENU01895	ANI61C6093; 31-49 2385..2822	31-49	409-426	NAP		g2132183	760	138	3.00E-32	50	42	hypothetical protein YPL088w - yeast (Saccharomyces cerevisiae) ; (U43281) Lpg20p [Saccharomyces cerevisiae]
18102	ENU01896	ANI61C1021 1:862..1299	53-72	429-448	NAP		g3024608	488	138	3.00E-44	63	69	Scytalone dehydratase ; (D86079) scytalone dehydratase [Colletotrichum lagenarium]
18103	ENU01897	ANI61C1106 5:3087..3525	56-75	433-452	NAP		g1730822	804	157	3.00E-38	52	24	hypothetical 66.5 KD protein in ALG9-RAP1 intergenic region ; probable membrane protein YNL218w - yeast (Saccharomyces cerevisiae) ; (Z71494) ORF YNL218w [Saccharomyces cerevisiae]
18104	ENU01898	ANI61C1828; 55-72 420..860	55-72	434-453	NAP		g3687238	493	176	7.00E-44	57	53	(AC005169) hypothetical protein [Arabidopsis thaliana]
18105	ENU01899	ANI61C3632; 30-51 9..456	30-51	416-435	NAP		g538067	189	97	6.00E-20	36	10	(M77661) putative pol polyprotein [Magnaporthe grisea]

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18106	ENU01900	ANI61C1108: 4975..4527	58-77	445-463	NAP		g731968	426	141	2.00E-33	50	45	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region ; hypothetical protein YJL213w - yeast (Saccharomyces cerevisiae) ; (Z34098) ORF [Saccharomyces cerevisiae] ; (Z49488) ORF YJL213w [Saccharomyces cerevisiae] Metal resistance protein YCF1 (yeast cadmium factor 1) ; (L35237) metal resistance protein [Saccharomyces cerevisiae] (AF026204) No definition line found [Caenorhabditis elegans] "60S ribosomal protein YL16B ; ribosomal protein L6.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (U22382) Rpl16bp: 60S ribosomal protein YL16B [Saccharomyces cerevisiae] "
18107	ENU01901	ANI61C4859: 71-90 2706..2254		462-481	NAP		g731347		56	7.00E-17			"Interferon-induced GTP-binding protein MX ; Mx resistance protein homolog - perch (fragment) ; (M27252) [Perca fluviatilis gene with homology to murine Mx genes, partial cds.], gene product [Perca fluviatilis] "
18108	ENU01902	ANI61C3691: 40-59 301..754		432-451	NAP		g2435542	89	45	0.0004	37	70	(AL023518) hypothetical protein [Schizosaccharomyces pombe]
18109	ENU01903	ANI61C9317: 25-44 5033..4573		419-443	NAP		g1346942	399	125	2.00E-28	50	84	hypothetical 31.6 KD protein C2E12.03C in chromosome I ; (Z69726) unknown [Schizosaccharomyces pombe]
18110	ENU01904	ANI61C1116 63-83 4:4277..4747		472-491	NAP		g127568	292	82	3.00E-15	31	51	(U31884) aromatic L-amino acid decarboxylase [Rattus norvegicus] Nitrate reductase 3 (NR) ; (U20450) nitrate reductase [Zea mays] (AF088906) clock-controlled gene-9 protein [Neurospora crassa]
18111	ENU01905	ANI61C1389: 72-98 74..545		481-501	NAP		g3130056	206	80	7.00E-15	37	22	
18112	ENU01906	ANI61C3296: 61-80 747..266		479-500	NAP		g1723416	297	104	4.00E-22	39	50	
18113	ENU01907	ANI61C3109: 41-58 2704..3193		470-488	NAP		g975309	802	103	2.00E-31	49	29	
18114	ENU01908	ANI61C3335: 36-55 2067..2558		465-484	NAP		g1352497	1224	112	5.00E-28	42	18	
18115	ENU01909	ANI50C844_ 1:539..45		460-479	NAP		g3746895		63	0.000000 001			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18116	ENU01910	ANI61C1026 2:32..534	53-72	494-513	NAP		g465665	310	135	2.00E-31	41	68	"hypothetical 27.1 KD protein UFD4-CAP1 intergenic region ; hypothetical protein YKL009w - yeast (Saccharomyces cerevisiae) ; (S53418) ribosomal protein L10 homolog [Saccharomyces cerevisiae=yeast, Peptide, 236 aa] [Saccharomyces cerevisiae] ; (Z28009) ORF YKL009w [Saccharomyces cerevisiae] "
18117	ENU01911	ANI61C9065: 58-76 3388..2883	58-76	502-521	NAP		g1491795	503	159	2.00E-38	41	18	"(U39812) beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus] "
18118	ENU01912	ANI61C1043 2:628..120	51-68	498-517	NAP		g4107287	459	50	0.000000 001			(AL035076) putative allantoin permease [Schizosaccharomyces pombe]
18119	ENU01913	ANI61C3562: 55-73 1373..862	55-73	505-524	NAP		g4586977	3318	176	1.00E-43	47	7	(AB018382) Mok13; Mok13 is homologous to Mok1 which is an alpha-glucan synthase [Schizosaccharomyces pombe]
18120	ENU01914	ANI61C5666: 49-67 639..1163	49-67	512-531	NAP		g3122291	661	161	4.00E-48	70	49	Inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) (PPASE) ; (AJ001000) inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) [Pichia pastoris]
18121	ENU01915	ANI61C3340: 68-87 670..136	68-87	541-560	NAP		g1723227	109	39	0.017			hypothetical 16.6 KD protein in ATL 5'region (ORF3) ; (D17366) ORF3 [Staphylococcus aureus] ; (L41499) ORF3 [Staphylococcus aureus]
18122	ENU01916	ANI61C7507: 50-69 420..959	50-69	528-547	NAP		g687834	45	39	0.023			"(U21319) similar to alcohol dehydrogenase, highest similarity to B. japonicum FIXR protein (SP-FIXR_BRAJA, P05406) [Caenorhabditis elegans] "
18123	ENU01917	ANI61C1802: 24-44 3..545	24-44	505-524	NAP		g1870209	332	104	3.00E-22	41	32	(AC000133) ORF [Emmericella nidulans]
18124	ENU01918	ANI61C4995: 54-71 681..137	54-71	537-556	NAP		g2498711	230	99	2.00E-20	34	31	"origin recognition complex protein, subunit 2 ; (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe] ; (AL049474) origin recognition complex protein, subunit 2. [Schizosaccharomyces pombe] "

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18125	ENU01919	ANI61C4995: 681..137	54-71	537-556	NAP		g2498711	230	99	2.00E-20	34	31	"origin recognition complex protein, subunit 2 ; (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe] ; (AL049474) origin recognition complex protein, subunit 2. [Schizosaccharomyces pombe] " cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Saccharomyces cerevisiae) ; (X03215) cytochrome b2 precursor [Saccharomyces cerevisiae] ; (Z46729) cytochrome b2 precursor [Saccharomyces cerevisiae] (AL022070) hsp grpe homolog [Schizosaccharomyces pombe] 66 kD stress protein (P66) ; (U86011) 66-kDa stress protein p66 [Physarum polycephalum] "High affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae] " (Y16261) CRO1 protein [Podospora anserina] "AMP deaminase (myoadenylate deaminase) ; AMP deaminase (EC 3.5.4.6) - yeast (Saccharomyces cerevisiae) ; (Z46659) AMD1 gene, len: 810, CAI: 0.19, AMP deaminase [Saccharomyces cerevisiae] " (Z99532) myo-inositol transporter [Schizosaccharomyces pombe]
18126	ENU01920	ANI61C8394: 24-43 2048..1504	24-43	507-526	NAP		g117804	244	119	1.00E-26			
18127	ENU01921	ANI61C7977: 62-81 136..680	62-81	545-564	NAP		g2950485	313	137	5.00E-32	45	73	
18128	ENU01922	ANI61C7152: 41-58 4725..5234	41-58	525-545	NAP		g3123032	275	125	2.00E-28	32	30	
18129	ENU01923	ANI61C3573: 37-61 742..1290	37-61	523-542	NAP		g1709181	434	45	0.000000 02	27	27	
18130	ENU01924	ANI61C8580: 31-52 6502..7054	31-52	522-541	NAP		g2808541	871	108	2.00E-23	39	25	
18131	ENU01925	ANI61C8962: 65-84 786..231	65-84	559-578	NAP		g1351916	1951	272	1.00E-72	68	22	
18132	ENU01926	ANI61C1026 38-57 3:17..588	38-57	548-567	NAP		g2440196	487	147	6.00E-35	48	64	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18133	ENU01927	ANI61C6374: 6285..6856	59-78	570-588	NAP		g140499	649	184	5.00E-46	57	67	"putative 30.7 KD methyltransferase in TSM1-ARE1 intergenic region ; hypothetical protein YCR047c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR047c, len:275 [Saccharomyces cerevisiae]"
18134	ENU01928	ANI61C8578: 55-73 5303..4712	55-73	585-604	NAP		g2493143	440	121	4.00E-27	71	88	Vacuolar ATP synthase 16 KD proteolipid subunit ; (U02877) vacuolar ATPase subunit c [Candida tropicalis] (Z99126) putative mannosyl transferase [Schizosaccharomyces pombe]
18135	ENU01929	ANI61C3426: 51-70 302..895	51-70	583-602	NAP		g2398816	312	103	9.00E-22	30	46	(U78597) kinesin light chain [Plectonema boryanum]
18136	ENU01930	ANI61C1156: 37-61 3124..3720	37-61	572-591	NAP		g2645229	156	67	9.00E-11	32	40	probable peroxisomal membrane protein PMP20 (allergen ASP F 3) ; (U58050) peroxisomal-lke protein [Aspergillus fumigatus]
18137	ENU01931	ANI61C5927: 63-81 1059..457	63-81	604-623	NAP		g3914384	536	90	5.00E-45	65	86	cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe) ; (X78799) cdc7 [Schizosaccharomyces pombe] ; (AL035537) cell division control protein 7 [Schizosaccharomyces pombe]
18138	ENU01932	ANI61C823:4 7..654	68-87	614-633	NAP		g1168817	236	60	1.00E-18	33	16	[Schizosaccharomyces pombe] "5- methyltetrahydropteroyltriglutamate--- homocysteine methyltransferase (methionine synthase, vitamin-B12 independent isozyme) (cobalamin-independent methionine synthase) (delta-P8 protein) ; 5- methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase (EC 2.1.1.14) - yeast (Saccharomyces cerevisiae) ; (U18839) Met6p: 5- methyltetrahydropteroyl triglutamate-- homocysteine methyltransferase [Saccharomyces cerevisiae] ; (U32508) N5-methyltetrahydrofolate homocysteine methyltransferase [Saccharomyces cerevisiae]"
18139	ENU01933	ANI61C5908: 71-90 760..1378	71-90	628-647	NAP		g730018	1750	317	4.00E-86	77	26	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18140	ENU01934	ANI61C3096: 2148..1528	49-67	608-627	NAP		g3929350	3103	259	1.00E-68	65	22	Peroxisomal hydratase-dehydrogenase-epimerase (HDE) (multifunctional beta-oxidation protein) [contains: 2-enoyl-CoA hydratase ; D-3-hydroxyacyl CoA dehydrogenase] ; multifunctional beta-oxidation protein - Neurospora crassa ; (X80052) multifunctional beta-oxidation protein [Neurospora crassa]
18141	ENU01935	ANI61C6914: 51-71 684..64	51-71	610-629	NAP		g4501859	550	101	4.00E-44			"acyl-Coenzyme A dehydrogenase, short/branched chain precursor ; acyl-CoA dehydrogenase, short/branched chain specific precursor (SBCAD) (2-methyl branched chain acyl-CoA dehydrogenase) (2-MEBCAD) ; short/branched chain acyl-CoA dehydrogenase (EC 1.3.-.-) precursor - human ; (U12778) acyl-CoA dehydrogenase [Homo sapiens] " (AF034089) calcineurin subunit B [Neurospora crassa]
18142	ENU01936	ANI61C1103 49-68 7.5341..4717	49-68	612-631	NAP		g2645886	627	210	5.00E-54	87	92	quinatate permease (quinatate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans]
18143	ENU01937	ANI61C8512: 47-67 26..652	47-67	611-631	NAP		g131768	252	73	9.00E-16	32	31	(AL031262) hypothetical protein [Schizosaccharomyces pombe]
18144	ENU01938	ANI61C6933: 39-58 1260..629	39-58	608-627	NAP		g3417428	214	75	3.00E-13	31	29	cytochrome B ; ubiquinol--cytochrome b reductase (EC 1.10.2.2) cytochrome b - Emericella nidulans mitochondrion (SGC3) ; (J01389) apocytochrome b [Emericella nidulans]
18145	ENU01939	ANI61C3548: 33-56 918..286	33-56	593-623	NAP		g117840	1057	320	5.00E-87	98	54	(AB009078) L-2,3-butanediol dehydrogenase [Brevibacterium saccharolyticum]
18146	ENU01940	ANI61C7842: 28-45 137..774	28-45	604-623	NAP		g4062842	290	80	1.00E-14	41	69	casein kinase II beta chain (CK II) ; (X74274) casein kinase II beta subunit [Schizosaccharomyces pombe]
18147	ENU01941	ANI61C4563: 50-71 1004..363	50-71	631-649	NAP		g729881	641	226	1.00E-58	58	85	

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18148	ENU01942	ANI61C9471: 43..685	64-83	645-664	NAP		g1718099	846	254	5.00E-67	76	54	vacuolar ATP synthase subunit AC39 (V-ATPase AC39 subunit) (V-ATPase 41 KD subunit) ; (U36470) vacuolar ATPase 41 kDa subunit [Neurospora crassa]
18149	ENU01943	ANI61C2909: 45-62 756..108	45-62	628-651	NAP		g1723727	481	115	1.00E-31	62	42	hypothetical 41.0 KD protein in YIP1-CBP4 intergenic region ; hypothetical protein YGR173w - yeast (Saccharomyces cerevisiae) ; (Z72958) ORF YGR173w [Saccharomyces cerevisiae]
18150	ENU01944	ANI61C6178: 32-51 682..24	32-51	625-648	NAP		g2894179	356	148	4.00E-35	43	65	(AJ223998) PCZA361.15 [Amycolatopsis orientalis]
18151	ENU01945	ANI61C1138 53-72 3:2574..1916	53-72	650-669	NAP		g3810873	144	55	0.000000	32	45	(AB010465) lactonohydrolase [Fusarium oxysporum]
18152	ENU01946	ANI61C8219: 50-69 742..81	50-69	650-669	NAP		g1902911		89	4.00E-17			(D83988) reductase [Colletotrichum lagenarium]
18153	ENU01947	ANI61C7493: 67-84 4028..3367	67-84	667-686	NAP		g2494090	208	62	1.00E-11	37	55	hypothetical 33.3 KD protein in PERR-ARGF intergenic region ; (AE000134) putative lyase/synthase [Escherichia coli]
18154	ENU01948	ANI61C1055 31-50 7:133..538	31-50	635-653	NAP		g3023956	885	189	1.00E-47	42	16	vegetatible incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserina]
18155	ENU01949	ANI61C3688: 39-58 4356..3691	39-58	643-662	NAP		g2983787	238	86	3.00E-16	39	46	"(AE000737) fructose-1,6-bisphosphate aldolase class II [Aquifex aeolicus]"
18156	ENU01950	ANI61C8586: 39-58 1110..441	39-58	647-666	NAP		g3004863	967	262	2.00E-69	57	27	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"
18157	ENU01951	ANI61C2388: 56-75 4438..5116	56-75	673-692	NAP		g1170278	510	194	5.00E-49	56	62	ATP phosphoribosyltransferase (EC phosphoribosyltransferase (EC 2.4.2.17) - yeast (Candida albicans) ; (X83871) ATP phosphoribosyltransferase [Candida albicans]
18158	ENU01952	ANI61C508:5 69-88 005..4326	69-88	687-706	NAP		g825440	927	183	2.00E-82	92	87	(L42299) RAS [Aspergillus fumigatus]

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18159	ENU01953	ANI61C2966: 2334..1644	50-67	677-697	NAP		g127568	224	112	2.00E-24	37	58	"interferon-induced GTP-binding protein MX; Mx resistance protein homolog - perch (fragment); (M27252) [Perca fluviatilis gene with homology to murine Mx genes, partial cds.], gene product [Perca fluviatilis]"
18160	ENU01954	ANI61C7836: 51-70	51-70	687-705	NAP		g2687850	659	116	4.00E-45	45	34	(Y15839) fatty acid transporter protein [Cochliobolus heterostrophus]
18161	ENU01955	ANI61C1016: 36-55	36-55	671-690	NAP		g1526987	423	110	3.00E-45	49	89	(U13050) pectate lyase D [Fusarium solani f. sp. pisi]
18162	ENU01956	ANI61C2322: 66-85	66-85	706-725	NAP		g4481956	290	100	8.00E-28	51	36	(AL035637) putative uracil kinase-cytosine deaminase-bifunctional enzyme [Schizosaccharomyces pombe]
18163	ENU01957	ANI61C7012: 49-68	49-68	689-709	NAP		g995557		36	0.21			(X89453) DRPLA [Rattus norvegicus]
18164	ENU01958	ANI61C1806: 27-46	27-46	671-695	NAP		g280478	446	117	2.00E-39	55	96	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 22K chain precursor - Neurospora crassa
18165	ENU01959	ANI61C6073: 22-45	22-45	675-694	NAP		g1351299	260	126	1.00E-28	36	24	putative potassium transport protein C1F5.12; (Z68136) unknown [Schizosaccharomyces pombe]
18166	ENU01960	ANI61C3790: 68-87	68-87	721-741	NAP		g1711561	304	122	3.00E-27	31	41	sugar transporter STL1; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae); (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
18167	ENU01961	ANI61C905:4 60-79	60-79	731-750	NAP		g2494905	618	178	4.00E-44	48	49	microtubule-associated protein YTM1; hypothetical protein YOR272w - yeast (Saccharomyces cerevisiae); (X89633) hypothetical protein [Saccharomyces cerevisiae]; (Z75180) ORF YOR272w [Saccharomyces cerevisiae]; (U92821) microtubule-associated protein [Saccharomyces cerevisiae]

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18168	ENU01962	ANI61C6665: 2181..2920	47-66	723-744	NAP		g1723254	673	130	1.00E-29	55	63	probable phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase ; (Z69369) putative phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerases [Schizosaccharomyces pombe]
18169	ENU01963	ANI61C2704: 70-89 61..806	70-89	754-773	NAP		g115595	225	67	4.00E-16	34	69	F-actin capping protein alpha subunit ; actin-capping protein alpha chain - yeast (Saccharomyces cerevisiae) ; (X61398) Capping Protein Alpha Subunit [Saccharomyces cerevisiae] ; (Z28007) ORF YKL007w [Saccharomyces cerevisiae] ; (S59773) CAP1 [Saccharomyces cerevisiae] transposase - fungus (Cochliobolus carbonum) (AL023794) hypothetical protein [Schizosaccharomyces pombe] unknown ; (AF075599) ubiquitin conjugating enzyme 12 [Homo sapiens] ; (AB012191) Nedd8-conjugating enzyme hUbc12 [Homo sapiens] (Z97050) ilvD [Mycobacterium tuberculosis]
18170	ENU01964	ANI50C1415 22-50 4_1:81..842	22-50	722-741	NAP		g2133335		221	5.00E-57	42	47	
18171	ENU01965	ANI61C7152: 72-91 1895..2662	72-91	778-797	NAP		g3192028	312	113	1.00E-24	36	85	
18172	ENU01966	ANI61C1188: 41-60 2035..2807	41-60	752-771	NAP		g4507791	510	148	8.00E-47	56	96	
18173	ENU01967	ANI61C1125 70-89 1:2244..1466	70-89	787-806	NAP		g2213526	342	121	7.00E-27	33	42	
18174	ENU01968	ANI61C1023 61-83 1:66..846	61-83	781-798	NAP		g731527	265	67	3.00E-23	37	51	hypothetical 49.5 KD protein in UBP3-PET122 intergenic region ; hypothetical protein YER152c - yeast (Saccharomyces cerevisiae) ; (U18917) Yer152cp [Saccharomyces cerevisiae] (AF080235) reductase homolog [Streptomyces cyanogenus]
18175	ENU01969	ANI61C3627: 40-59 1765..977	40-59	767-786	NAP		g4240421		97	3.00E-22			

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18176	ENU01970	ANI61C3268: 376..1168	71-90	801-821	NAP		g121146	1021	293	1.00E-78	66	47	geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (dimethylallyltransferase / geranyltransferase / farnesyltransferase ; geranylgeranyl pyrophosphate synthetase - Neurospora crassa ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]
18177	ENU01971	ANI61C9212: 65-84 877..84	65-84	791-816	NAP		g1168269	414	131	5.00E-30	41	76	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) ; (L23430) endo-1,5-alpha-L-arabinase [Aspergillus niger] ; endo-1,5-alpha-L-arabinase [Aspergillus niger] " transcription initiation protein SPT6 ; SPT6 protein - yeast (Saccharomyces cerevisiae) ; (M34391) SPT6 protein [Saccharomyces cerevisiae] ; (Z72899) ORF YGR116w [Saccharomyces cerevisiae]
18178	ENU01972	ANI61C1330: 2725..1930	66-84	800-819	NAP		g134854	907	123	4.00E-41	37	17	transcription initiation protein SPT6 ; SPT6 protein - yeast (Saccharomyces cerevisiae) ; (M34391) SPT6 protein [Saccharomyces cerevisiae] ; (Z72899) ORF YGR116w [Saccharomyces cerevisiae]
18179	ENU01973	ANI61C8126: 66-86 1627..828	66-86	804-823	NAP		g1805251	1222	311	4.00E-84	55	47	transposase [Aspergillus awamori]
18180	ENU01974	ANI61C9741: 67-85 6301..7100	67-85	805-824	NAP		g1020413	119	83	2.00E-15	26	42	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
18181	ENU01975	ANI61C9072: 37-57 2093..1289	37-57	780-799	NAP		g3860264	344	68	5.00E-22	39	54	(AC005824) unknown protein [Arabidopsis thaliana]
18182	ENU01976	ANI61C8695: 63-82 2561..3363	63-82	809-830	NAP		g1351702	765	129	2.00E-29	36	40	hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
18183	ENU01977	ANI61C1015 66-85 8..1184..373	66-85	816-835	NAP		g3355628	557	111	1.00E-37	35	15	(X91867) CPC3 protein [Neurospora crassa]
18184	ENU01978	ANI50C1469 36-55 2..1:889..75	36-55	785-808	NAP		g1168784		83	7.00E-30	37	45	catalase ; catalase (EC 1.11.1.6) - Haemophilus influenzae (strain Rd KW20) ; (U32774) catalase (hktE) [Haemophilus influenzae Rd]
18185	ENU01979	ANI61C3072: 28-47 716..1534	28-47	781-804	NAP		g4454690		54	0.000001			(AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]

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18186	ENU01980	ANI61C1073 4:1983..1164	70-87	828-847	NAP		g1351671	165	83	3.00E-15			hypothetical 25.4 KD protein C1F7.10 in chromosome I ; hypothetical protein SPAC1F7.10 - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown [Schizosaccharomyces pombe]
18187	ENU01981	ANI61C4097: 56-75 234..1054	56-75	814-834	NAP		g586299	630	203	2.00E-51	50	67	hypothetical oxidoreductase in RPB5-CDC28 intergenic region ; probable membrane protein YBR159w - yeast (Saccharomyces cerevisiae) ; (Z36028) ORF YBR159w [Saccharomyces cerevisiae]
18188	ENU01982	ANI61C6237: 71-91 1362..2188	71-91	836-855	NAP		g732189	735	157	9.00E-38	37	61	hypothetical 49.1 KD protein in SSB2-SPX18 intergenic region ; hypothetical protein YNL207w - yeast (Saccharomyces cerevisiae) ; (X78898) N1342 [Saccharomyces cerevisiae] ; (Z71483) ORF YNL207w [Saccharomyces cerevisiae]
18189	ENU01983	ANI61C1754: 22-44 3010..2181	22-44	790-809	NAP		g466171	827	215	3.00E-79	89	96	"GTP-binding protein YPT1 ; GTP-binding protein ypt1 - Neurospora crassa ; (S51252) NCYPT1=putative small GTP-binding protein [Neurospora crassa, Peptide, 203 aa] [Neurospora crassa] ; small GTP-binding protein [Neurospora crassa] " (AL035210) halotolerance protein [Schizosaccharomyces pombe]
18190	ENU01984	ANI61C9551: 26-45 5918..5071	26-45	812-831	NAP		g4160397	782	257	5.00E-68	49	76	putative sterigmatocystin biosynthesis monoxygenase STCW ; (U34740) putative FAD-containing monoxygenase [Emericella nidulans] (Z98602) putative siroheme synthase [Schizosaccharomyces pombe]
18191	ENU01985	ANI61C7226: 42-61 967..1825	42-61	839-858	NAP		g2498971	2547	599	e-171	99	58	(AL021815) putative cis-muonate cycloisomerase [Schizosaccharomyces pombe]
18192	ENU01986	ANI61C7492: 49-68 456..1329	49-68	851-880	NAP		g2330809	571	217	7.00E-57	50	96	
18193	ENU01987	ANI61C6496: 42-61 695..61	42-61	868-887	NAP		g2879855	954	179	2.00E-44	48	45	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18194	ENU01988	ANI61C1410: 58-77 1629..735	58-77	891-910	NAP		g3024813	280	125	3.00E-28	3		"vanillyl-alcohol oxidase (aryl-alcohol oxidase) (4-allylphenol oxidase) ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With Isoeugenol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With Isoeugenol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With P-Cresol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With P-Cresol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 2-Nitro-P-Cresol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 2-Nitro-P-Cresol ; Chain A, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 4-(1-Heptenyl)phenol ; Chain B, Structure Of The Octameric Flavoenzyme Vanillyl-Alcohol Oxidase In Complex With 4-(1-Heptenyl)phenol "
18195	ENU01989	ANI61C9556: 36-57 5217..6111	36-57	869-888	NAP		g3451313	242	65	1.00E-15	34	77	protein [Schizosaccharomyces pombe]
18196	ENU01990	ANI61C298:1 60-79 948..1050	60-79	897-916	NAP		g3024443	464	160	1.00E-38	38	92	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Zalerion arboricola ; (U33266) pyrroline carboxylate reductase [Zalerion arboricola]

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18197	ENU01991	ANI61C8349: 420..1320	64-83	903-922	NAP		g3738171	507	145	3.00E-40	44	87	"(AL031856) atp synthase gamma chain, mitochondrial precursor [Schizosaccharomyces pombe] "
18198	ENU01992	ANI61C8021: 70-89 399..1303	70-89	913-932	NAP		g2498731	206	50	2.00E-18	39	64	probable NADP-dependent oxidoreductase P1 ; zeta-crystallin homolog - Arabidopsis thaliana ; (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
18199	ENU01993	ANI61C3602: 22-46 5355..4435	22-46	881-900	NAP		g730689	261	75	1.00E-12	32	89	RTM1 protein ; RTM1 protein - yeast (Saccharomyces cerevisiae) ; (U02618)
18200	ENU01994	ANI61C9410: 53-72 112..1032	53-72	912-931	NAP		g3718005	1054	387	e-107	62	52	RTM1 gene product [Saccharomyces cerevisiae] (AJ006852) alternative NADH-dehydrogenase [Yarrowia lipolytica]
18201	ENU01995	ANI61C9218: 46-65 3037..2106	46-65	915-934	NAP		g1709438	621	242	3.00E-63			lipamide acyltransferase component precursor of branched-chain alpha-keto acid dehydrogenase complex (E2) (Dihydrolipoamide branched chain transacylase) (BCKAD E2 subunit) ; dihydrolipoamide transacylase precursor - mouse ; (L42996) acyltransferase [Mus musculus] ; branched chain alpha-ketoacid dehydrogenase:subunit=E2 [Mus musculus]
18202	ENU01996	ANI61C3555: 61-80 1251..314	61-80	937-956	NAP		g1001835	320	145	5.00E-34	33	79	(D64005) nitrilase [Synechocystis sp.]
18203	ENU01997	ANI61C8559: 50-75 990..50	50-75	929-948	NAP		g4432914	896	128	1.00E-51	59	46	(D45894) thiamine-4 [Neurospora crassa]
18204	ENU01998	ANI61C980:2 72-89 743..3684	72-89	952-972	NAP		g2909465	235	100	2.00E-20	29	96	(AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis]
18205	ENU01999	ANI61C7233: 47-64 1570..626	47-64	930-949	NAP		g4539600	403	88	5.00E-31	52	70	(AL049522) hypothetical protein [Schizosaccharomyces pombe]
18206	ENU02000	ANI61C5362: 42-62 1181..233	42-62	931-948	NAP		g173177	577	210	1.00E-53	40	52	(L02869) VPS17 [Saccharomyces cerevisiae]
18207	ENU02001	ANI61C1208: 25-44 4167..5117	25-44	913-933	NAP		g119714	150	53	0.000002	29	33	Extensin precursor (cell wall hydroxyproline-rich glycoprotein) ; hydroxyproline-rich glycoprotein precursor - common tobacco ; (X13885) extensin (AA 1-620) [Nicotiana tabacum]

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18208	ENU02002	ANI61C1065 6:1262..2213	43-62	933-952	NAP		g1708797	445	96	4.00E-19	39	22	LET1 protein ; LET1 protein - yeast (Kluyveromyces marxianus var. lactis) ; (X70373) LET1 [Kluyveromyces lactis]
18209	ENU02003	ANI61C1708; 595..1553	27-46	924-943	NAP		g3661614	2806	579	e-164	88	41	(AF093142) aconitase [Aspergillus terreus]
18210	ENU02004	ANI61C859:1 34..1093	70-90	968-987	NAP		g1169587	994	294	6.00E-99	60	65	"fructose-2,6-BISphosphatase ; fructose-2,6-bisphosphate 2-phosphatase (EC 3.1.3.46) - yeast (Saccharomyces cerevisiae) ; (Z49430) ORF YJL155c [Saccharomyces cerevisiae]"
18211	ENU02005	ANI50C721_ 1:18..977	38-57	936-955	NAP		g2239208		132	4.00E-30	35	30	(Z97209) hypothetical protein [Schizosaccharomyces pombe]
18212	ENU02006	ANI61C9205; 4292..3314	45-64	963-982	NAP		g140459	376	49	4.00E-14	51	74	"hypothetical 30.7 KD protein in RVS161-ADP1 intergenic region ; hypothetical protein YCR010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR010c, len:283 [Saccharomyces cerevisiae]"
18213	ENU02007	ANI61C1116 1:459..29	46-66	967-986	NAP		g1938424	274	85	3.00E-34	41	21	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
18214	ENU02008	ANI61C7920: 1937..949	69-87	994-1015	NAP		g112790	456	199	3.00E-50	33	90	3-dehydroshikimate dehydratase (DHS dehydratase) ; 3-dehydroshikimate dehydratase - Neurospora crassa ; (X14603) DHS dehydratase [Neurospora crassa] ; (M10139) 3-dehydroshikimate dehydratase [Neurospora crassa]
18215	ENU02009	ANI50C1679 9_1:1996..1007	39-62	967-986	NAP		g2228748		90	3.00E-17	23	52	(U93867) RNA polymerase III subunit [Homo sapiens]
18216	ENU02010	ANI61C142:1 893..901	72-94	1002-1022	NAP		g2735428		54	0.000002			(U94913) H-K-ATPase alpha 2b subunit [Rattus norvegicus]

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18217	ENU02011	ANI61C5215: 39-58 6805..5806	44-64	977-996	NAP		g4093186	247	71	2.00E-11	30	91	"(AF106583) contains similarity to domains present in ubiquitin-regulatory proteins (Pfam: PF00789, Score=79.3, E=7.8e-20, N=1), C2H2-type zinc finger domain (Pfam: PF00096, Score=9.5, E=6.2, N=1) and ubiquitin-associated domains (Pfam: PF000... " (D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18218	ENU02012	ANI61C1002 44-64 4:2643..1636	986-1008		NAP		g1167523	219	62	1.00E-20	26	24	"hypothetical 76.1 KD protein in UNG1-OST6 intergenic region ; hypothetical protein YML020w - yeast (Saccharomyces cerevisiae) ; (Z46659) unknown orf, len: 664, CAI: 0.13 [Saccharomyces cerevisiae] "
18219	ENU02013	ANI61C9368: 45-64 349..1367	1001-1021		NAP		g2497103	512	138	4.00E-39	42	43	(U81606) mixed-linked glucanase precursor [Cochliobolus carbonum] vegetative incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]
18220	ENU02014	ANI61C6615: 22-53 232..1254	982-1001		NAP		g2326188	654	235	5.00E-61	46	92	"glutamate decarboxylase, 67 KD isoform (GAD-67) (67 KD glutamic acid decarboxylase) ; glutamate decarboxylase (EC 4.1.1.15) 1 - cat ; (M18629) glutamic acid decarboxylase [Felis catus] "
18221	ENU02015	ANI61C5217: 49-68 336..1358	1010-1029		NAP		g3023956	264	90	1.00E-22	33	21	splicing factor U2AF homolog - mouse ; (X64587) orf [Mus musculus] putative transcriptional regulatory protein in MKK2-COX11 intergenic region ; hypothetical protein YPL133c - yeast (Saccharomyces cerevisiae) ; (U43703) Lpi12p [Saccharomyces cerevisiae]
18222	ENU02016	ANI61C3697: 40-59 2366..1340	1006-1024		NAP		g416884	658	253	1.00E-66	40	54	hypothetical 63.5 KD protein C3H1.06C in chromosome I ; (Z68144) putative major facilitator superfamily transporter [Schizosaccharomyces pombe]
18223	ENU02017	ANI61C6281: 70-90 131..1170	1045-1065		NAP		g110998	451	178	2.00E-49	42	61	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18224	ENU02018	ANI61C3002: 63-82 1264..224	1041-1061		NAP		g1730882	529	152	5.00E-54	41	69	
18225	ENU02019	ANI61C1025 64-83 4:1149..108	1044-1063		NAP		g1351690	393	73	2.00E-19	30	55	
18226	ENU02020	ANI61C1002 44-64 4:2643..1589	1036-1055		NAP		g1167523	219	62	1.00E-20	26	25	

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18227	ENU02021	ANI61C6760: 1769..2823	63-85	1055-1075	NAP		g538067	1738	217	8.00E-56	36	24	(M77661) putative pol polyprotein [Magnaporthe grisea]
18228	ENU02022	ANI61C1099 42-61 6:2471..3529	42-61	1039-1058	NAP		g3912972	328	125	9.00E-29	33	94	alcohol dehydrogenase II (ADH I); (AF008244) alcohol dehydrogenase II [Pichia stipitis]
18229	ENU02023	ANI61C3608: 44-63 1176..1114	44-63	1045-1064	NAP		g2408068	769	159	3.00E-77	51	67	(Z99165) hypothetical protein [Schizosaccharomyces pombe]
18230	ENU02024	ANI61C4301: 42-61 3496..2431	42-61	1046-1065	NAP		g2791498	176	111	8.00E-24	35	97	(AL021246) hypothetical protein Rv2458 [Mycobacterium tuberculosis]
18231	ENU02025	ANI61C8515: 49-66 1422..2488	49-66	1054-1073	NAP		g543962	525	173	2.00E-42	45	88	cell division control protein 16; cdc16 protein - fission yeast (Schizosaccharomyces pombe); (X71605) cdc16 [Schizosaccharomyces pombe]; (Z98981) cell division control protein 16 [Schizosaccharomyces pombe]
18232	ENU02026	ANI61C9037: 39-58 2449..3529	39-58	1047-1077	NAP		g2385382	586	116	3.00E-52	42	97	(AJ001428) D-mandelate dehydrogenase [Rhodotorula graminis]; (AJ001429) D-mandelate dehydrogenase [Rhodotorula graminis] putative transporter C11D3.18C; (Z68166) unknown [Schizosaccharomyces pombe]
18233	ENU02027	ANI61C3359: 70-88 3940..2858	70-88	1091-1110	NAP		g1351714	236	81	2.00E-14	27	62	"GNS1 protein; probable membrane protein YCR034w - yeast (Saccharomyces cerevisiae); (X56909) YCR521 [Saccharomyces cerevisiae]; (S78624) YCR521 [Saccharomyces cerevisiae=yeast, Peptide, 347 aa] [Saccharomyces cerevisiae]; (X59720) YCR034w, len:347 [Saccharomyces cerevisiae]; (AF012655) v-snare bypass mutant [Saccharomyces cerevisiae]"
18234	ENU02028	ANI61C2496: 63-82 254..1336	63-82	1084-1103	NAP		g140489	700	158	3.00E-69			(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
18235	ENU02029	ANI61C9101: 63-82 3505..2422	63-82	1084-1104	NAP		g3114719	587	109	2.00E-49	43	16	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18236	ENU02030	ANI61C8453: 3017..1910	60-81	1106-1125	NAP		g1352980	846	215	8.00E-85	50	30	ATP-dependent RNA helicase DOB1 (MRNA transport regulator MTR4) ; SKI2 protein homolog YJL050w - yeast (Saccharomyces cerevisiae) ; (Z49325) ORF YJL050w [Saccharomyces cerevisiae]
18237	ENU02031	ANI61C119:1 22-56	1069-1088	1069-1088	NAP		g2133335	329	53	0.000003	27	64	transposase - fungus (Cochliobolus carbonum)
18238	ENU02032	ANI61C360:2 60-83	1120-1139	1120-1139	NAP		g1293655	589	132	4.00E-30	37	53	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
18239	ENU02033	ANI61C7661: 58-75	1123-1142	1123-1142	NAP		g1658175	809	279	1.00E-86	45	72	(U74468) indole-3-acetaldehyde dehydrogenase [Ustilago maydis]
18240	ENU02034	ANI61C7147: 54-72	1125-1144	1125-1144	NAP		g3122300	1980	602	0	98	82	calcium/calmodulin-dependent protein kinase (CMPK) ; Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans ; (M74120) calmodulin-dependent protein kinase [Emericella nidulans] ; (AF054580) calmodulin-dependent protein kinase [Emericella nidulans]
18241	ENU02035	ANI61C1107 44-63	1117-1136	1117-1136	NAP		g2498702	196	109	3.00E-23	33	30	sterigmatocystin 7-O-methyltransferase precursor ; (L25835) O-methyltransferase [Aspergillus flavus] ; (L25834) O-methyltransferase [Aspergillus parasiticus] ; (L22091) O-methyltransferase [Aspergillus parasiticus]
18242	ENU02036	ANI61C7320: 49-68	1129-1148	1129-1148	NAP		g3355742	47	0.0003				(AL031128) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=404.95; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P46821; 2-match_description=microtubule-associated protein ... (Z25485) ACR1-protein [Saccharomyces cerevisiae]
18243	ENU02037	ANI61C6437: 22-40	1130-1147	1130-1147	NAP		g396595	782	236	7.00E-81	61	96	(Z99165) hypothetical protein [Schizosaccharomyces pombe]
18244	ENU02038	ANI61C7645: 22-46	1130-1149	1130-1149	NAP		g2408062	531	164	1.00E-39	35	58	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18245	ENU02039	ANI61C2531: 1202..24	62-81	1179-1198	NAP		g2833229	626	116	4.00E-52	36	70	Laccase (benzenediol:oxygen oxidoreductase) (urishiol oxidase) (diphenol oxidase)
18246	ENU02040	ANI61C6864: 32-51		1151-1170	NAP		g854534	764	184	1.00E-45	45	39	(X87634) oxidative stress resistance [Saccharomyces cerevisiae]
18247	ENU02041	1215..2395 ANI61C292:9 70-89		1199-1218	NAP		g2853081	416	99	2.00E-28	38	96	(AL021768) ATP binding protein-like [Arabidopsis thaliana]
18248	ENU02042	263..8070 ANI61C2972: 52-71 4997..3793		1194-1213	NAP		g4507229	1009	242	e-102	47	74	"Succinic semialdehyde dehydrogenase ; (Y11192) NAD+ dependent succinic semialdehyde dehydrogenase [Homo sapiens] ; (AL031230) dI73M23.2 (NAD+-dependent succinic semialdehyde dehydrogenase (SSADH, EC 1.2.1.24)) [Homo sapiens] "
18249	ENU02043	ANI61C1069 39-58 0:2234..1027		1185-1204	NAP		g728904	1065	177	1.00E-43	47	31	calcium-transporting ATPase 2 (vacuolar CA2+-ATPase) ; Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae) ; (U03060) calcium ATPase [Saccharomyces cerevisiae] ; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
18250	ENU02044	ANI61C7104: 51-70 217..1431		1204-1223	NAP		g2950489	309	69	8.00E-11	45	53	(AL022072) possible transmembrane protein [Schizosaccharomyces pombe]
18251	ENU02045	ANI61C3347: 44-63 4411..3196		1198-1217	NAP		g401172	183	107	2.00E-22	28	96	Tetracycline resistance protein (transposon TN4351 / TN4400) ; NADP-requiring oxidoreductase - Bacteroides fragilis ; (M37699) tetracycline resistance protein [Transposon Tn4351]
18252	ENU02046	ANI61C9152: 24-46 752..1976		1188-1206	NAP		g4581522	614	153	2.00E-36	32	42	(AL049559) hypothetical protein [Schizosaccharomyces pombe]
18253	ENU02047	ANI61C1022 22-42 0:3714..2488		1187-1206	NAP		g1723847	313	159	4.00E-38	32	93	hypothetical 43.5 KD protein in RPB9-ALG2 intergenic region ; hypothetical protein YGL067w - yeast (Saccharomyces cerevisiae) ; (Z72589) ORF YGL067w [Saccharomyces cerevisiae]

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18254	ENU02048	ANI61C8681: 2888..1653	45-64	1219-1238	NAP		g2499619	179	68	7.00E-15	32	21	probable serine/threonine-protein kinase YMR216C ; probable membrane protein YMR216c - yeast (Saccharomyces cerevisiae) ; (Z49809)
18255	ENU02049	ANI61C3355: 22-41 2535..3770	22-41	1195-1215	NAP		g418150	856	122	1.00E-56			unknown [Saccharomyces cerevisiae] GABA-specific permease (GABA-specific transport protein) ; GABA transport protein - yeast (Saccharomyces cerevisiae) ; (X66472) GABA-specific permease [Saccharomyces cerevisiae] ; (X99000) GABA transporter protein [Saccharomyces cerevisiae] ; (Z74258) ORF YDL210w [Saccharomyces cerevisiae] ; GABA transport protein [Saccharomyces cerevisiae] hypothetical 48.4 KD protein in ARP9-IMP2 intergenic region ; probable membrane protein YMR034c - yeast (Saccharomyces cerevisiae) ; (Z49213) unknown [Saccharomyces cerevisiae] (Z97052) hypothetical protein [Schizosaccharomyces pombe] "PRPD protein ; (U73857) similar to yqjP of B. subtilis [Escherichia coli] ; (AE000140) orf, hypothetical protein [Escherichia coli] " (AB012140) aryl/esterase [Acetobacter pasteurianus] hypothetical 48.0 KD protein C1B3.08 in chromosome I ; (Z98598) hypothetical protein [Schizosaccharomyces pombe] (Y10403) RNA-directed RNA polymerase [Lycopersicon esculentum] (AL033391) hypothetical membrane protein [Candida albicans] (M20319) aminotriazole resistance protein [Saccharomyces cerevisiae] (AB012604) squalene synthase [Candida utilis]
18256	ENU02050	ANI61C6437: 60-79 5220..6462	60-79	1241-1260	NAP		g2497127	440	182	3.00E-45	32	90	
18257	ENU02051	ANI61C1135 69-89 6:3899..2651	69-89	1256-1275	NAP		g2213553	595	183	3.00E-45	39	56	
18258	ENU02052	ANI61C7225: 64-82 243..1497	64-82	1257-1276	NAP		g2497946	1369	279	e-120	62	77	
18259	ENU02053	ANI61C4189: 39-59 1681..422	39-59	1237-1256	NAP		g2978332	172	57	0.000000	33	51	
18260	ENU02054	ANI61C4716: 50-69 2104..841	50-69	1252-1271	NAP		g3183362	339	103	3.00E-21	38	74	
18261	ENU02055	ANI61C1046 33-52 7:49..1313	33-52	1237-1255	NAP		g4038592	308	154	1.00E-36	30	32	
18262	ENU02056	ANI61C2205: 27-46 2038..772	27-46	1231-1250	NAP		g3850125	458	131	8.00E-30	32	75	
18263	ENU02057	ANI61C7041: 25-44 373..1647	25-44	1238-1257	NAP		g171124	387	78	1.00E-25	29	74	
18264	ENU02058	ANI61C9605: 43-62 1866..3148	43-62	1263-1283	NAP		g3341974	931	360	9.00E-99	47	92	

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18265	ENU02059	ANI61C8226: 84..1376	67-87	1298-1317	NAP		g4584836	424	150	1.00E-35	33	54	(AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum]
18266	ENU02060	ANI61C8226: 67-87		1298-1317	NAP		g4584836	424	150	1.00E-35	33	54	(AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum]
18267	ENU02061	ANI61C1064 47-66 84..1376 0:634..1928		1280-1299	NAP		g2565329	694	278	7.00E-77	45	88	(AF025290) cAMP-dependent protein kinase catalytic subunit [Ustilago maydis]
18268	ENU02062	ANI61C4192: 24-43 2279..3576		1261-1279	NAP		g4160579	227	99	5.00E-20	37	49	(AL035218) hypothetical protein [Schizosaccharomyces pombe]
18269	ENU02063	ANI61C5216: 48-68 1371..69		1288-1307	NAP		g2661608	1696	246	e-118	53	69	(AL009197) hypothetical ctp synthase [Schizosaccharomyces pombe]
18270	ENU02064	ANI61C2416: 23-43 166..1500		1296-1315	NAP		g2239198	636	178	1.00E-62	55	99	(Z97209) putative tricarboxylate transport protein protein [Schizosaccharomyces pombe]
18271	ENU02065	ANI61C7568: 53-72 50..1400		1339-1361	NAP		g1709181	503	136	9.00E-39	34	70	"high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae] "
18272	ENU02066	ANI61C1128 23-48 1:3304..1949		1317-1336	NAP		g2132491	152	44	5.00E-11	34	68	Probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr284cp [Saccharomyces cerevisiae]
18273	ENU02067	ANI61C1016 22-41 3:5840..4475		1326-1345	NAP		g1169782	556	206	5.00E-60	37	91	Fusca protein FUS6 ; (L26498) FUS6 [Arabidopsis thaliana]
18274	ENU02068	ANI61C3255: 44-63 1532..167		1348-1367	NAP		g3023683	1913	560	e-180	90	86	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) ; 6beta-hydroxyhyocyanine epoxidase (EC 1.14.1.14) - Aspergillus oryzae ; (D63941) enolase [Aspergillus oryzae] ; (D64113) enolase [Aspergillus oryzae] ; enolase [Aspergillus oryzae] putative tartrate transporter ; (U32375) membrane protein [Agrobacterium vitis]
18275	ENU02069	ANI61C1080 62-81 4:2281..892		1389-1408	NAP		g4033481	233	63	2.00E-21	30	84	
18276	ENU02070	ANI61C7689: 71-90 1478..81		1408-1426	NAP		g3882261	375	98	8.00E-25	31	54	(AB018313) KIAA0770 protein [Homo sapiens]

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18277	ENU02071	ANI61C9422: 124..1524	40-63	1379-1398	NAP		g4406656	214	102	4.00E-21	29	45	Unknown [Homo sapiens] (AF131820)
18278	ENU02072	ANI61C3006: 40-59 2192..782	40-59	1388-1407	NAP		g2493484	1127	342	e-110	53	81	glycerol kinase (ATP:glycerol 3-phosphotransferase) (glycerokinase) (GK); (U48403) glycerol kinase [Mus musculus]
18279	ENU02073	ANI61C6597: 44-63 4933..6344	44-63	1393-1413	NAP		g417699	1559	321	e-171			"histone deacetylase RPD3 (transcriptional regulatory protein RPD3); transcription regulator RPD3 - yeast (Saccharomyces cerevisiae); (S66438) RPD3 [Saccharomyces cerevisiae, Peptide, 433 aa] [Saccharomyces cerevisiae]; (X83226) global transcriptional regulator [Saccharomyces cerevisiae]; (Z71606) ORF YNL330c [Saccharomyces cerevisiae]"
18280	ENU02074	ANI61C1223: 24-45 39..1450	24-45	1374-1393	NAP		g3023717	1095	437	e-121	58	86	ESA1 protein; hypothetical protein YOR244w - yeast (Saccharomyces cerevisiae); (Z75152) ORF YOR244w [Saccharomyces cerevisiae] (U39201) acetolactate synthase [Magnaporthe grisea] (AF027868) Yoan [Bacillus subtilis]; (Z99114) similar to hypothetical proteins [Bacillus subtilis] (U73857) galactoside O-acetyltransferase [Escherichia coli] (AL032671) predicted using Genefinder [Caenorhabditis elegans] (AC004473) Contains similarity to goliath protein gblM97204 from D. melanogster. [Arabidopsis thaliana] Isotrichodermin C-15 hydroxylase (cytochrome P450 65A1); (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides] (AF041050) 4-coumarate:CoA ligase [Populus tremuloides] (Z98529) conserved hypothetical protein [Schizosaccharomyces pombe]
18281	ENU02075	ANI61C1029 69-87 6:9675..8253	69-87	1431-1450	NAP		g1072104	2199	628	e-180	70	68	
18282	ENU02076	ANI61C7367: 47-64 1181..2615	47-64	1420-1439	NAP		g2619026	699	153	8.00E-73	43	96	
18283	ENU02077	ANI61C1141 45-65 4:1586..135	45-65	1436-1454	NAP		g1657538	206	51	3.00E-14	40	26	
18284	ENU02078	ANI50C5820 72-89 3:1:2193..737	72-89	1467-1486	NAP		g3873654		43	0.005			
18285	ENU02079	ANI61C8228: 57-80 3484..2028	57-80	1452-1471	NAP		g3249088	134	76	6.00E-13	25	27	
18286	ENU02080	ANI61C1073 41-59 3:4685..3217	41-59	1448-1467	NAP		g3915140	448	73	2.00E-19	33	74	
18287	ENU02081	ANI61C8810: 23-40 3452..1970	23-40	1443-1462	NAP		g3258637	442	128	3.00E-50	37	64	
18288	ENU02082	ANI61C3730: 52-71 613..19	52-71	1484-1501	NAP		g3859776		62	0.000000	41	38	

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18289	ENU02083	ANI61C3730: 6371..4872	72-91	1510-1529	NAP		g2648302	239	115	6.00E-25	43	49	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]"
18290	ENU02084	ANI61C2434: 1017..2538	23-41	1481-1500	NAP		g1661227	633	234	1.00E-60	32	62	(U75973) NAAG-peptidase; NAALADase; prostate specific membrane antigen; PSM; PSMA [Rattus norvegicus]; (AF040256) glutamate carboxypeptidase II [Rattus norvegicus]
18291	ENU02085	ANI61C1714: 3069..1536	24-43	1496-1515	NAP		g547880	693	102	7.00E-58	43	78	LYSINE-specific permease; (U00007) lysine-specific permease [Escherichia coli]; Lys permease [Escherichia coli] (AF017990) Fkbp39p
18292	ENU02086	ANI61C5953: 1675..3225	24-43	1512-1532	NAP		g3406742	509	157	2.00E-37	45	72	[Schizosaccharomyces pombe]; (AL035548) Peptidyl Prolyl cis-trans isomerase [Schizosaccharomyces pombe]
18293	ENU02087	ANI61C1758: 3547..5098	24-45	1514-1533	NAP		g464369	566	118	7.00E-26	26	35	phenol 2-monooxygenase (phenol hydroxylase); (L04488) phenol hydroxylase [Trichosporon cutaneum] (X98309) ARI protein [Drosophila melanogaster]; (X98310) ARI protein [Drosophila melanogaster]
18295	ENU02089	ANI61C3068: 814..971	24-43	1582-1601	NAP		g130117	639	137	3.00E-39	35	80	phosphate-repressible phosphate permease; phosphate-repressible phosphate permease - Neurospora crassa; (M31364) phosphate permease [Neurospora crassa]
18296	ENU02090	ANI61C4335: 1165..2805	45-64	1624-1643	NAP		g1706439	651	220	1.00E-65	35	81	Dicarboxylic amino acid permease; dicarboxylic amino acid permease DIP5 - yeast (Saccharomyces cerevisiae); (X95802) dicarboxylic amino acids Dip5p permease [Saccharomyces cerevisiae]; (Z73621) ORF YPL265w [Saccharomyces cerevisiae]
18297	ENU02091	ANI61C5680: 3598..1952	53-73	1638-1657	NAP		g2498564	186	60	0.000000	39	42	MLO3 protein; (L42551) ORF [Schizosaccharomyces pombe]; (Z98270) Mlo3p [Schizosaccharomyces pombe]

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18298	ENU02092	32-51	ANI61C1080	1618-1637	NAP		g4033481	233	63	4.00E-22	29	90	putative tartrate transporter ; (U32375) membrane protein [Agrobacterium vitis]
18299	ENU02093	53-72	ANI61C8511: 1134..2788	1672-1691	NAP		g2494913	923	369	e-101	40	98	hypothetical 57.3 KD TRP-ASP repeats containing protein in POM152-REC114 intergenic region ; hypothetical protein YMR131c - yeast (Saccharomyces cerevisiae) ; (Z48622) unknown [Saccharomyces cerevisiae] "(U24701) beta-1,2-D-glucosidase [Septoria lycopersici] ; (U35462) tomatinase [Septoria lycopersici] ; beta2 tomatinase [Septoria lycopersici] "
18300	ENU02094	34-53	ANI61C7716: 2276..594	1655-1674	NAP		g799150	1915	531	e-150	54	69	"(U24701) beta-1,2-D-glucosidase [Septoria lycopersici] ; (U35462) tomatinase [Septoria lycopersici] ; beta2 tomatinase [Septoria lycopersici] "
18301	ENU02095	53-72	ANI61C5161: 3587..5276	1680-1700	NAP		g2132493	1168	379	e-104	51	86	probable membrane protein YDR294c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr294cp [Saccharomyces cerevisiae]
18302	ENU02096	63-83	ANI61C1048	1692-1713	NAP		g2131317		40	0.04			hypothetical protein YDL037c - yeast (Saccharomyces cerevisiae) ; (Z71781) unknown [Saccharomyces cerevisiae] ; (Z74085) ORF YDL037c [Saccharomyces cerevisiae]
18303	ENU02097	56-74	ANI61C5282: 3209..1499	1705-1724	NAP		g3258635	526	219	3.00E-61	32	99	(AF041049) 4-coumarate:CoA ligase [Populus tremuloides]
18304	ENU02098	41-60	ANI61C1054	1693-1713	NAP		g2921400	606	257	1.00E-74	33	90	(AF036097) flavocytochrome b subunit [Bos taurus]
18305	ENU02099	47-66	ANI61C154:2	1713-1731	NAP		g1405353	614	100	3.00E-55	35	30	(D86086) canalicular multispecific organic anion transporter [Rattus norvegicus]
18306	ENU02100	71-90	ANI61C7473: 2074..3826	1762-1781	NAP		g2760084	228	126	4.00E-28	31	49	(Y16045) leucine-rich repeat protein [Arabidopsis thaliana]
18307	ENU02101	68-87	ANI61C1883: 3449..1696	1760-1779	NAP		g2492816	1271	176	e-114	50	84	Uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe]
18308	ENU02102	68-88	ANI61C1014	1821-1852	NAP		g3336839	795	100	4.00E-78	40	95	(Y16834) hexose transporter [Candida albicans]
18309	ENU02103	71-90	ANI61C9693: 5173..3318	1864-1883	NAP		g731909	427	85	2.00E-30	36	31	hypothetical 87.0 KD protein in PAN1-PR1 intergenic region ; hypothetical protein YIR007w - yeast (Saccharomyces cerevisiae)

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18310	ENU02104	ANI61C5240: 755..2676	67-86	1924-1946	NAP		g1613878	1680	499	e-140	45	49	(U7236) ModA [Dictyostelium discoideum]
18311	ENU02105	ANI61C1118: 46-63		1924-1946	NAP		g3877738	122	44	0.003			(Z74473) predicted using GeneFinder [Caenorhabditis elegans]
18312	ENU02106	ANI61C5898: 50-69		1995-2013	NAP		g3702646	601	135	4.00E-63	34	73	(AL031825) putative membrane transport protein
18313	ENU02107	ANI61C1125: 52-71		2051-2070	NAP		g129307	885	272	e-101	39	93	[Schizosaccharomyces pombe] L-amino acid oxidase precursor (LAO) ; L-amino-acid oxidase (EC 1.4.3.2) precursor - Neurospora crassa
18314	ENU02108	ANI61C9178: 35-54		2034-2053	NAP		g3417415	462	102	2.00E-48	44	50	(AL031261) phosphoserine phosphatase [Schizosaccharomyces pombe]
18315	ENU02109	ANI61C466:4	53-76	2060-2079	NAP		g2501570	395	137	1.00E-36	35	71	hypothetical 51.4 KD protein in RAR1-SCJ1 intergenic region ; hypothetical protein YMR210w - yeast (Saccharomyces cerevisiae) ; (Z49809) unknown [Saccharomyces cerevisiae] probable membrane protein YDL074c - yeast (Saccharomyces cerevisiae) ; (Z74122) ORF YDL074c [Saccharomyces cerevisiae]
18316	ENU02110	ANI61C1122	34-53	2050-2068	NAP		g2132428	356	153	4.00E-36	28	40	[Saccharomyces cerevisiae] (AL034490) hypothetical protein [Schizosaccharomyces pombe]
18317	ENU02111	ANI61C1062	24-45	2080-2098	NAP		g4008552	334	100	4.00E-26	35	57	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum]"
18318	ENU02112	ANI61C7956: 63-82		2145-2164	NAP		g119830	757	661	0	47	36	"hypothetical 77.5 KD protein in PRP1-STE3 intergenic region ; hypothetical protein YKL179c - yeast (Saccharomyces cerevisiae) ; (X74151) previously orf13 and orf14 [2], now merged; homologous to human CENP-E [Saccharomyces cerevisiae] ; (Z28179) ORF YKL179c [Saccharomyces cerevisiae]"
18319	ENU02113	ANI61C4756: 22-57		2132-2151	NAP		g549740	469	113	4.00E-41	28	94	(AL021747) hypothetical protein [Schizosaccharomyces pombe]
18320	ENU02114	ANI61C6804: 61-80		2201-2219	NAP		g2842464	260	63	0.000000	26	93	[Schizosaccharomyces pombe]
		3811..6011								008			

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18321	ENU02115	ANI61S2760: 316..1	43-62	2188-2207	NAP		g2072788		89	1.00E-16	27	20	(U64574) cell cycle inhibitor Nif1 [Schizosaccharomyces pombe] ; (AL035065) cell cycle inhibitor nif1. [Schizosaccharomyces pombe] Ribonucleoside-diphosphate reductase large chain (ribonucleotide reductase) ; CDC22 protein - fission yeast (Schizosaccharomyces pombe) ; (Z67998) Cdc22p [Schizosaccharomyces pombe] lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (M59935) negative-acting regulatory protein [Emmericella nidulans] ; (M77664) repressor protein [Emmericella nidulans] Maltose permease MAL3T (maltose transport protein MAL3T) ; maltose transport protein MAL3T - yeast (Saccharomyces cerevisiae) ; (Z36167) ORF YBR298c [Saccharomyces cerevisiae] hypothetical 175.8 KD protein in GND1-IK11 intergenic region ; hypothetical protein YHR186c - yeast (Saccharomyces cerevisiae) ; (U00030) Yhr186cp [Saccharomyces cerevisiae] (X86780) polyketide synthase [Streptomyces hygroscopicus] probable membrane protein YPL217c - yeast (Saccharomyces cerevisiae) ; (Z73573) ORF YPL217c [Saccharomyces cerevisiae] "probable glucan 1,3-beta-glucosidase precursor (exo-1,3-beta-glucanase) ; (Z70721) putative 1,3-beta-d-glucanohydrolase [Schizosaccharomyces pombe] "
18322	ENU02116	ANI61C3865: 3362..5583	38-57	2198-2217	NAP		g1350600	3129	1186	0	77	88	
18323	ENU02117	ANI61C2081: 2294..71	54-73	2213-2235	NAP		g125935	437	195	1.00E-48	28	70	
18324	ENU02118	ANI61C9003: 3491..1222	63-85	2272-2291	NAP		g168082	1305	439	e-140	40	78	
18325	ENU02119	ANI61C594:1 322..3685	67-86	2369-2388	NAP		g585446	772	120	1.00E-83	37	70	
18326	ENU02120	ANI61C1055 3:212..2637	52-71	2415-2434	NAP		g731756	867	236	6.00E-79	37	42	
18327	ENU02121	ANI61C8706: 1514..3962	66-85	2452-2472	NAP		g987102	493	132	2.00E-62	36	8	
18328	ENU02122	ANI61C1003 7:2585..99	72-90	2497-2516	NAP		g2133002	2342	503	e-141	45	65	
18329	ENU02123	ANI61C1125 2:685..3171	72-91	2498-2516	NAP		g1706727	841	332	7.00E-90	42	48	

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18330	ENU02124	ANI61C1003 7:2585..99	72-90	2497- 2516	NAP		g2133002	2342	503	e-141	45	65	probable membrane protein YPL217c - yeast (Saccharomyces cerevisiae) ; (Z73573) ORF YPL217c [Saccharomyces cerevisiae]
18331	ENU02125	ANI61C9304: 24-47 4815..2302	24-47	2476- 2495	NAP		g2132957	207	51	0.000000 01	42	14	probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae]
18332	ENU02126	ANI61C3630: 62-81 2030..1942	62-81	2518- 2537	NAP		g1002380		39	0.14			[Saccharomyces cerevisiae] (U24189) RRM-type RNA binding protein [Caenorhabditis elegans]
18333	ENU02127	ANI61C648:2 58-77 735..34	58-77	2698- 2717	NAP		g4502897	719	222	1.00E-80	40	47	cleft lip and palate associated transmembrane protein 1 ; (AF037338) cleft lip and palate transmembrane protein 1 [Homo sapiens] ; (AF037339) cleft lip and palate transmembrane protein 1 [Homo sapiens]
18334	ENU02128	ANI61C7559: 67-86 126..2828	67-86	2707- 2727	NAP		g2833114	361	92	1.00E-17	26	25	(AL021766) hypothetical protein [Schizosaccharomyces pombe]
18335	ENU02129	ANI61C220:2 49-69 821..82	49-69	2727- 2745	NAP		g3913731	1354	504	e-156	42	82	probable mannosyl-oligosaccharide glucosidase (processing A-glucosidase I) ; (Z98603) hypothetical protein [Schizosaccharomyces pombe]
18336	ENU02130	ANI61C8057: 45-66 4763..1860	45-66	2887- 2906	NAP		g4176548	1115	288	e-109	54	57	(AL035259) putative Ca-calmodulin-dependent serine-threonine-protein kinase [Schizosaccharomyces pombe]
18337	ENU02131	ANI61C1412: 66-85 847..1046	66-85	203-223	NAP		g133186	400	111	6.00E-25	71	65	Guanyl-specific ribonuclease PB1 ; ribonuclease T1 (EC 3.1.27.3) - Penicillium brevicompactum ; RNase [Penicillium brevicompactum]
18338	ENU02132	ANI61C1055 30-50 0:3487..3286	30-50	163-189	NAP		g2493874	127	64	9.00E-11	42	94	cytochrome C oxidase assembly protein COX17 ; COX17 protein - yeast (Saccharomyces cerevisiae) ; (L75948) approximately 300 nucleotides distal from helicase gene [Saccharomyces cerevisiae] ; (Z73114) ORF YLL009c [Saccharomyces cerevisiae]

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18339	ENU02133	ANI61C1360: 22-50 1556..1353	22-50	164-183	NAP		g2833211	238	46	0.000000	62	50	NADH-ubiquinone oxidoreductase (complex I) (CI) ; 10.5 KD subunit (ubiquinone) NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 10.5K chain - Neurospora crassa ; (X69929) NUO-10.5 [Neurospora crassa]
18340	ENU02134	ANI61C480:4 55-77 32..223	55-77	202-222	NAP		g99521	416	137	1.00E-32	91	45	nad5 intron 1 protein 459 - Sugar beet mitochondrion (fragment) ; (X55786) ORF459 [Beta vulgaris] (AC000104) EST gb[T45093 comes from this gene. [Arabidopsis thaliana] phenol hydroxylase - imperfect fungus (Trichosporon beigeli) "(AE000352) orf, hypothetical protein [Escherichia coli] " "mitochondrial 60S ribosomal protein L33 (YML33) ; ribosomal protein L30, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49704) Mrp133p [Saccharomyces cerevisiae] " 30S ribosomal protein S15 (BS18) ; (Z80835) ribosomal protein S15 [Bacillus subtilis] ; (Z99112) ribosomal protein S15 (BS18) [Bacillus subtilis] (AL031179) splicing factor [Schizosaccharomyces pombe] (AJ011295) hypothetical protein [Emeticella nidulans] "DNA-directed RNA polymerase I, II, and III 7.7 KD polypeptide (ABC10-alpha) ; DNA-directed RNA polymerase (EC 2.7.7.6) chain ABC10 alpha - yeast (Saccharomyces cerevisiae) ; (U23378) RNA polymerase I, II and III subunit ABC10 alpha [Saccharomyces cerevisiae] ; (U10397) Rpb12p: RNA polymerase II subunit [Saccharomyces cerevisiae] " (AC000133) pyrC [Emeticella nidulans]
18341	ENU02135	ANI61C7399: 23-42 82..293	23-42	172-192	NAP		g1903364		44	0.0002			
18342	ENU02136	ANI61C8581: 70-89 4554..4777	70-89	232-251	NAP		g102033	98	42	0.0007			
18343	ENU02137	ANI61C3361: 24-43 1117..893	24-43	187-206	NAP		g1789035	162	62	4.00E-10	46	84	
18344	ENU02138	ANI61C5161: 51-70 5997..5772	51-70	215-235	NAP		g1710603	169	62	6.00E-10	38	87	
18345	ENU02139	ANI61C3149: 31-49 77..306	31-49	197-218	NAP		g2507327	156	51	0.000001	44	86	
18346	ENU02140	ANI61C7173: 71-90 1312..1550	71-90	241-267	NAP		g3395591	176	70	2.00E-12			
18347	ENU02141	ANI61C4095: 53-72 457..696	53-72	231-250	NAP		g3647370	210	80	3.00E-15	50	84	
18348	ENU02142	ANI61C8881: 59-79 2362..2604	59-79	240-259	NAP		g730606	134	56	0.000000	45	88	
18349	ENU02143	ANI61C1355: 59-78 1288..1532	59-78	230-261	NAP		g1870226	531	187	2.00E-47	98	86	

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18350	ENU02144	ANI61S4306: 22-55 291..46	22-55	190-225	NAP		g2315135	415	166	3.00E-41	100	100	beta subunit of coupling factor one [Arabidopsis thaliana]
18351	ENU02145	ANI61S3217: 35-56 14..263	35-56	215-242	NAP								
18352	ENU02146	ANI61C1479: 22-50 2010..2265	22-50	215-235	NAP		g4586031	147	56	0.000000	59	94	(AC007109) unknown protein [Arabidopsis thaliana]
18353	ENU02147	ANI61C7312: 53-76 3506..3246	53-76	252-271	NAP		g1352897	133	56	0.000000			hypothetical 11.3 KD protein in MIR1-STE18 intergenic region ; probable membrane protein YJR085c - yeast (Saccharomyces cerevisiae) ; (Z49585) ORF YJR085c [Saccharomyces cerevisiae] ; (L47993) ORF YJR085c [Saccharomyces cerevisiae]
18354	ENU02148	ANI61C9353: 39-62 3290..3021	39-62	247-266	NAP		g4139493	187	87	4.00E-17	64	92	Rub1
18355	ENU02149	ANI61C5287: 31-55 1745..2017	31-55	234-261	NAP		g3978168	135	55	0.000000			(AF047427) unknown [Pasteurella haemolytica]
18356	ENU02150	ANI61C1253: 26-49 6115..5837	26-49	242-261	NAP		g607954	218	66	6.00E-11	62	80	(U12823) hemolysin [Acanthamoeba polyphaga]
18357	ENU02151	ANI61S4051: 22-53 117..395	22-53	223-258	NAP		g1350634	490	195	7.00E-50	100	100	Chloroplast 50S ribosomal protein L23 ; (X65615) ribosomal protein L23 [Sinapis alba]
18358	ENU02152	ANI61C1068 49-68 5:367..649	49-68	270-289	NAP		g2879888	453	155	5.00E-38	75	84	(AJ223315) rAsp f 7 [Aspergillus fumigatus]
18359	ENU02153	ANI61C563:2 53-72 600..2315	53-72	275-296	NAP		g2326720	48	34	0.27	32	12	(X95503) zinc finger protein [Mus musculus] ; (X95504) zinc finger protein [Mus musculus]
18360	ENU02154	ANI61C6455: 23-44 1510..1223	23-44	249-268	NAP		g267125	269	96	8.00E-20	53	87	"Thioredoxin ; thioredoxin - Emericella nidulans ; thioredoxin [Aspergillus nidulans, Peptide, 109 aa] "
18361	ENU02155	ANI61C3233: 48-69 630..331	48-69	284-305	NAP		g1346341		32	1.5			"Keratin, type I cytoskeletal 47 KD ; (X04805) keratin B1 [Xenopus laevis] "
18362	ENU02156	ANI61C1135 26-45 8:3396..3096	26-45	253-284	NAP		g3420051	477	189	5.00E-48	74	91	(AC004680) unknown protein [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18363	ENU02157	ANI61C4231: 31-51 689..386	31-51	264-292	NAP		g3334316	170	59	0.000000			"DNA-directed RNA polymerase I, II, and III 8.3 kD polypeptide (ABC10-beta) ; (D89596) RNA polymerase II subunit Rpb10 [Schizosaccharomyces pombe] ; (U80219) RNA polymerases I-III common subunit Rpb10 [Schizosaccharomyces pombe] ; (AF027818) RNA polymerases I, II and III subunit Rpb10 [Schizosaccharomyces pombe] ; (Z98598) dna-directed rna polymerases i, ii, and iii 8.3 kD polypeptide(abc10-beta).dna-directed rna polymerases i, ii, and iii 8.3 kD polypeptide(abc10-beta). [Schizosaccharomyces pombe] "
18364	ENU02158	ANI61C5142: 47-66 39..343	47-66	289-309	NAP		g1870220	97	41	0.002			(AC000133) ORF [Emericella nidulans]
18365	ENU02159	ANI61C2477: 22-57 4094..3787	22-57	262-287	NAP		g4507311		92	1.00E-18			suppressor of Ty (S.cerevisiae) 4 homolog 1 ; transcription initiation protein SPT4 homolog 1 ; (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] ; (U38818) SUPT4H [Homo sapiens] ; (U38817) SUPT4H [Homo sapiens] ; (U43154) Supt4h [Mus musculus] ; (U96809) chromatin structural protein homolog [Mus musculus]
18366	ENU02160	ANI61C5703: 61-80 440..747	61-80	307-326	NAP		g4506645	167	61	0.000000	64	72	ribosomal protein L38 ; 60S ribosomal protein L38 ; ribosomal protein L38 - rat ; ribosomal protein L38 - human ; (X57007) ribosomal protein L38 [Rattus rattus] ; (Z26876) ribosomal protein [Homo sapiens]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18367	ENU02161	ANI61C914:1 532..1221	22-55	272-291	NAP		g731363	131	57	0.000000 03			PET100 protein precursor ; probable membrane protein YDR079w - yeast (Saccharomyces cerevisiae) ; (X82086) 1 putative transmembrane spans [Saccharomyces cerevisiae] ; (Z46796) unknown [Saccharomyces cerevisiae] ; (Z74375) ORF YDR079w [Saccharomyces cerevisiae] ; (U91943) cytochrome c oxidase-specific assembly factor [Saccharomyces cerevisiae] (Z99165) hypothetical protein [Schizosaccharomyces pombe] (AC007195) putative blue copper- binding protein II [Arabidopsis thaliana] "Histone H3.2, minor; histone H3.3- like protein - Arabidopsis thaliana ; (X60429) histone H3.3 like protein [Arabidopsis thaliana] ; (X60429) histone H3.3 like protein [Arabidopsis thaliana] ; (U09458) histone H3.2 [Medicago sativa] ; (U09460) histone H3.2 [Medicago sativa] ; (U09461) histone H3.2 [Medicago sativa] ; (U09464) histone H3.2 [Medicago sativa] ; (U09465) histone H3.2 [Medicago sativa] ; (X79714) histone H3 [Lolium temulentum] ; (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] ; (AF024716) histone 3 [Gossypium hirsutum] ; (AB015760) histone H3 [Nicotiana tabacum] ; (AF093633) histone H3 [Oryza sativa] ; (AF109910) histone H3 [Porteresia coarctata] ; (AL035708) histone H3.3 [Arabidopsis thaliana] ; (AL035708) Histon H3 [Arabidopsis thaliana] " (AC000133) mt2 [Emericella nidulans]
18368	ENU02162	ANI61C1597: 24-50 238..550	24-50	271-294	NAP		g2656010	201	76	5.00E-14	29	71	
18369	ENU02163	ANI61C4533: 24-52 799..857	24-52	267-295	NAP		g4589971	572	221	1.00E-57	97	98	
18370	ENU02164	ANI61C466:4 65-84 309..3995	65-84	318-337	NAP		g417103	338	141	1.00E-33			
18371	ENU02165	ANI61C5625: 23-50 900..586	23-50	270-295	NAP		g1870224	569	224	2.00E-58	98	99	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18372	ENU02166	ANI61C1062 2:5429..5743	31-50	282-303	NAP		g465533	166	46	0.00008	32	87	hypothetical 11.5 KD protein in HTB2- NTH2 intergenic region ; hypothetical protein YBL001c - yeast (Saccharomyces cerevisiae) ; (Z26494) unknown [Saccharomyces cerevisiae] ; (Z35762) ORF YBL001c [Saccharomyces cerevisiae] ; ORF YBL0105 [Saccharomyces cerevisiae] (U12823) hemolysin [Acanthamoeba polyphaga] Conidiation-specific protein 6 ; (L26036) conidiation protein [Neurospora crassa] (U12823) hemolysin [Acanthamoeba polyphaga] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L- lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L- lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] hypothetical protein YDR286c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr286cp [Saccharomyces cerevisiae] "(S53434) L46=ribosomal protein [Kluyveromyces marxianus, Peptide, 51 aa] [Kluyveromyces marxianus] " epoxide hydrolase [Rattus norvegicus]
18373	ENU02167	ANI61C1253: 29-53 6112..5796	29-53	273-303	NAP		g607954	218	57	2.00E-11	57	91	
18374	ENU02168	ANI61C5247: 22-50 3049..2733	22-50	276-296	NAP		g461773	98	46	0.00006	34	91	
18375	ENU02169	ANI61C1253: 29-53 6112..5796	29-53	273-303	NAP		g607954	218	57	2.00E-11	57	91	
18376	ENU02170	ANI61C3429: 22-50 379..62	22-50	278-297	NAP		g117803	132	78	2.00E-14	44	15	
18377	ENU02171	ANI61C592:9 22-53 05..1225	22-53	279-300	NAP		g2131413	70	49	0.000009	23	92	
18378	ENU02172	ANI61C7935: 22-54 802..902	22-54	282-302	NAP		g263485	139	33	0.6			
18379	ENU02173	ANI61C1965: 62-86 393..70	62-86	323-343	NAP		g228278	148	56	0.000000	31	95	
18380	ENU02174	ANI61C8199: 24-49 2534..2210	24-49	287-306	NAP		g3850571	286	100	5.00E-21	57	95	
18381	ENU02175	ANI61C7018: 24-43 469..141	24-43	288-310	NAP		g4581479	335	104	2.00E-22	60	74	
													(AC005278) Similar to gb U85207 snRNP core Sm protein homolog Sm- X5 from Mus musculus. EST gb AA612141 comes from this gene. [Arabidopsis thaliana] (Z98595) 60s ribosomal protein l22 [Schizosaccharomyces pombe]

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18382	ENU02176	ANI61C107:1 553..1225	22-54	286-308	NAP		g1723740	99	50	0.000004	31	82	hypothetical 12.4 KD protein in NAB1A-GPI1 intergenic region ; hypothetical protein YGR215w - yeast (Saccharomyces cerevisiae) ; (Z73000) ORF YGR215w [Saccharomyces cerevisiae]
18383	ENU02177	ANI61C1034 4-4492..4822	27-46	292-315	NAP		g586501	138	64	4.00E-10	35	92	hypothetical 13.2 KD protein in ORC2-TTP1 intergenic region ; hypothetical protein YBR062c - yeast (Saccharomyces cerevisiae) ; (Z35931) ORF YBR062c [Saccharomyces cerevisiae]
18384	ENU02178	ANI61C2076: 1448..1116	37-56	295-327	NAP		g3850102	437	161	1.00E-39	67	77	(AL033388) putative golgi membrane protein-sorting protein [Schizosaccharomyces pombe]
18385	ENU02179	ANI61C4334: 606..943	22-51	297-317	NAP		g2132826	91	56	0.000000	34	93	probable membrane protein YOL026c - yeast (Saccharomyces cerevisiae) ; (Z74768) ORF YOL026c [Saccharomyces cerevisiae]
18386	ENU02180	ANI61C6137: 3737..4075	35-53	312-331	NAP		g2131721	217	64	1.00E-17	52	91	hypothetical protein YHR004c-a - yeast (Saccharomyces cerevisiae) ; (Z80875) Mrs1 lp [Saccharomyces cerevisiae] ; (U10555) Mrs1 lp [Saccharomyces cerevisiae]
18387	ENU02181	ANI61C4486: 475..137	72-92	350-369	NAP		g1175403	164	60	0.000000	36	54	hypothetical 19.0 KD protein C31A2.08 in chromosome I ; hypothetical protein SPAC31A2.08 - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe]
18388	ENU02182	ANI61C5870: 684..1024	60-79	334-358	NAP		g2281089	152	74	3.00E-13	54	81	(AC002333) Sm protein F isolog [Arabidopsis thaliana]
18389	ENU02183	ANI61C3916: 2424..2765	61-88	339-360	NAP		g3183357		41	0.002			hypothetical 13.4 KD protein C17H9.07 in chromosome I ; (Z98597) hypothetical protein [Schizosaccharomyces pombe]
18390	ENU02184	ANI61C3209: 50..393	70-89	351-371	NAP		g2498272	267	98	2.00E-20	46	77	Cyanate lyase (cyanate hydrolase) (cyanase) ; (U59481) cyanate lyase [Synechococcus PCC7942] ; (AB000100) cyanase [Synechococcus sp.]

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18391	ENU02185	ANI61C8982: 33-51 7793..7448	33-51	317-336	NAP		g2983605	238	100	4.00E-21	46	72	ribose 5-phosphate (AE000725) isomerase B [Aquifex aeolicus]
18392	ENU02186	ANI61C1601: 56-77 115..462	56-77	341-361	NAP		g1351714	52	52	0.000002			putative transporter C11D3.18C; (Z68166) unknown
18393	ENU02187	ANI61C5803: 22-43 2298..1951	22-43	309-327	NAP		g3183399	125	55	0.000000 2	28	91	[Schizosaccharomyces pombe] hypothetical 13.9 KD protein C2E11.03C in chromosome I; (AL031181) very hypothetical protein [Schizosaccharomyces pombe]; (AL035064) very hypothetical protein [Schizosaccharomyces pombe]
18394	ENU02188	ANI61C1064 29-54 1:1334..986	29-54	314-335	NAP		g731777	149	61	1.00E-10	38	97	"hypothetical 11.0 KD protein in FAA3-MAS3 intergenic region; hypothetical protein YIL008w - yeast (Saccharomyces cerevisiae); (Z38113) orf, len: 99, CAl=0.21 [Saccharomyces cerevisiae]"
18395	ENU02189	ANI61C4009: 52-71 872..523	52-71	342-359	NAP		g2276355	328	101	2.00E-21	60	80	(Z97992) putative small ribonuclear protein [Schizosaccharomyces pombe]
18396	ENU02190	ANI61C6138: 35-68 562..657	35-68	322-343	NAP		g1363744	260	41	0.004	38	45	hypothetical protein YLR435w - yeast (Saccharomyces cerevisiae); (U21094) Ylr435wp [Saccharomyces cerevisiae] (AC000133) ORF [Emmericella nidulans]
18397	ENU02191	ANI61C1127 42-62 4:431..79	42-62	329-352	NAP		g1870220	685	234	2.00E-61	98	87	hypothetical 10.7 KD protein C17C9.09C in chromosome I; (Z73099) hypothetical protein [Schizosaccharomyces pombe]
18398	ENU02192	ANI61C9645: 54-74 1347..993	54-74	347-366	NAP		g1723568		48	0.00002			small nuclear ribonucleoprotein polypeptide E; U1 and U2 small nuclear ribonucleoprotein E (SNRNP-E); small nuclear ribonucleoprotein E - human; (X12466) snRNP E protein (AA 1-92) [Homo sapiens]; (L19064) small nuclear ribonucleoprotein E [Gallus gallus]; (X65702) SmE protein [Gallus gallus]; (M37716) small nuclear RNA protein (snRNP E) [Homo sapiens]
18399	ENU02193	ANI61C1000 26-45 4:3168..3523	26-45	307-339	NAP		g4507129	169	68	2.00E-11			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18400	ENU02194	ANI61C9311: 44-63 3740..3382	44-63	341-360	NAP		g1175442	759	138	1.00E-32	58	39	hypothetical protein C22F3.01 in chromosome I; hypothetical protein SPAC22F3.01 - fission yeast (Schizosaccharomyces pombe) (fragment); (Z54285) unknown [Schizosaccharomyces pombe] Lectin precursor (agglutinin); lectin precursor - rice; (M24504) lectin [Oryza sativa]
18401	ENU02195	ANI61C8065: 65-84 714..354	65-84	364-383	NAP		g113509	78	68	2.00E-11	35	45	
18402	ENU02196	ANI61C5436: 34-59 564..925	34-59	334-353	NAP		g2833359	268	45	0.0002	57	73	60S ribosomal protein L35
18403	ENU02197	ANI61C4673: 28-57 38..402	28-57	329-350	NAP		g464706	506	108	1.00E-37	78	76	"40S ribosomal protein S15 (S12); ribosomal protein S12, cytosolic - Podospora anserina; (Z23267) cytoplasmic ribosomal protein S12 [Podospora anserina]"
18404	ENU02198	ANI61C7221: 50-72 1542..1906	50-72	353-372	NAP		g4176531	1107	89	1.00E-17	34	18	(AL035263) weak similarity to chick phosphatidylcholine-ste rol acetyltransferase
18405	ENU02199	ANI61C9819: 31-56 4967..4600	31-56	337-356	NAP		g1351034	167	47	0.000000	52	95	[Schizosaccharomyces pombe] putative protein transport protein SEC61 gamma subunit; hypothetical protein SPA C4G8.02c - fission yeast (Schizosaccharomyces pombe); (Z56276) putative protein transport protein sec61-gamma subunit
18406	ENU02200	ANI61C3164: 69-88 630..263	69-88	368-394	NAP		g731437	244	53	2.00E-15	44	81	[Schizosaccharomyces pombe] nuclear transport factor 2 (NTF-2) (nuclear transport factor P10); hypothetical protein YER009w - yeast (Saccharomyces cerevisiae); (U18778) Ntf2p: Nuclear Transport Factor 2
18407	ENU02201	ANI61C4957: 60-79 460..85	60-79	368-393	NAP		g3810851	851	96	1.00E-19	33	15	[Saccharomyces cerevisiae] (AL032684) putative ubiquitin-protein ligase [Schizosaccharomyces pombe]
18408	ENU02202	ANI61C6549: 63-84 905..529	63-84	378-397	NAP		g3183481	299	92	1.00E-18	51	56	hypothetical 23.0 KD protein in SNF2-CPA1 intergenic region; hypothetical protein YOR294w - yeast (Saccharomyces cerevisiae); (Z75202) ORF YOR294w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18409	ENU02203	ANI61C1235: 24-43 5312..4932	24-43	341-362	NAP		g114663	685	167	4.00E-41	97	88	"ATP synthase protein 9, mitochondrial precursor (LIPID-binding protein) ; (M30144) mitochondrial ATP synthase precursor [Emicella nidulans]"
18410	ENU02204	ANI61C2997: 61-89 203..584	61-89	381-400	NAP		g1362228	448	161	2.00E-39	60	54	pac2 protein - fission yeast (Schizosaccharomyces pombe) ; (D43748) Pac2p [Schizosaccharomyces pombe] ; (Z98979) camp independent regulatory protein [Schizosaccharomyces pombe] (AJ002026) rAsp f 13 [Aspergillus fumigatus] (AL031349) 4-nitrophenylphosphatase [Schizosaccharomyces pombe] hypothetical ZINC-type alcohol dehydrogenase-like protein in pre-5-FET4 intergenic region ; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae) ; (Z54141) unknown [Saccharomyces cerevisiae] (Z97050) hypothetical protein Rv0163 [Mycobacterium tuberculosis] (X99300) unknown epidymal protein [Mus musculus] (Z99259) small nuclear ribonucleoprotein [Schizosaccharomyces pombe] ubiquitin-like protein SMT3 ; SMT3 protein - yeast (Saccharomyces cerevisiae) ; (U27233) Smt3p [Saccharomyces cerevisiae] ; (U33057) suppressor of MIF2 mutations; CAI: 0.31 [Saccharomyces cerevisiae] hypothetical 14.1 KD protein C31A2.02 in chromosome I ; hypothetical protein SPAC31A2.02 - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe] (AC000133) ORF [Emicella nidulans]
18411	ENU02205	ANI61C7253: 51-70 458..73	51-70	375-394	NAP		g3005841	341	143	7.00E-34	54	80	
18412	ENU02206	ANI61C8384: 67-86 1877..1491	67-86	392-411	NAP		g3451473	587	121	2.00E-27	50	41	
18413	ENU02207	ANI61C6419: 69-88 1328..941	69-88	389-414	NAP		g2492777	314	99	9.00E-21	40	35	
18414	ENU02208	ANI61C1015: 63-91 1142..753	63-91	390-410	NAP		g2213500	173	85	3.00E-16	39	76	
18415	ENU02209	ANI61C2495: 24-55 1465..1076	24-55	343-371	NAP		g1430862	90	61	0.000000	26	91	
18416	ENU02210	ANI61C9745: 30-56 4615..4226	30-56	358-377	NAP		g2414614	177	43	0.000000	50	60	
18417	ENU02211	ANI61C2576: 22-53 433..823	22-53	351-370	NAP		g2501450	201	76	7.00E-17	46	94	
18418	ENU02212	ANI61C1557: 55-75 227..620	55-75	386-406	NAP		g1175395	290	80	5.00E-15	43	84	
18419	ENU02213	ANI61C1098 22-54 1..605..998	22-54	349-373	NAP		g1870220	169	81	3.00E-15	39	97	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18420	ENU02214	ANI61C727:1 776..1382	45-64	362-397	NAP		g1708982	550	129	1.00E-29	52	23	Ammonium transporter MEP3 ; ammonium transport protein MEP3 - yeast (Saccharomyces cerevisiae) ; (U40829) Similar to B. subtilis membrane protein NrgA (Swiss Prot. accession number Q07429) [Saccharomyces cerevisiae] "(AB007633) Myo3 [Schizosaccharomyces pombe] ; (Z98762) SPAC4A8.05c, myosin heavy chain, len:2104aa, similar eg. to MYS2_DICDI, P08799, myosin ii heavy chain; non musc le, (2116aa),fasta scores, opt: 2488, E0:0, (29.5% identit y in 2167 aa overlap), PS00017 ATP/GTP-bindi..." "ATP synthase D chain, mitochondrial ; (AF019223) F1Fo-ATP synthase subunit 7 [Kluveromyces lactis] " DNA-directed RNA polymerase II 13.3 KD polypeptide (RPB1) (RPB14) ; (D85818) RNA polymerase II subunit RPB14 [Mus musculus] (AF099136) vacuolar ATP synthase subunit F [Neurospora crassa] (X89714) rhamnogalacturonan acetyltransferase [Aspergillus aculeatus] (Z28052) ORF YKL053c-a [Saccharomyces cerevisiae] ; (Z28054) ORF YKL053c-a [Saccharomyces cerevisiae] (AL031326) putative protein [Arabidopsis thaliana] "ribosomal protein L11.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z72870) ORF YGR085c [Saccharomyces cerevisiae] " (AC007196) unknown protein [Arabidopsis thaliana] (AB011378) MAT-2 protein [Fusarium oxysporum]
18421	ENU02215	ANI61C7854: 785..1181	45-72	376-399	NAP		g2828348	362	64	5.00E-10			
18422	ENU02216	ANI61C5660: 1057..1454	68-88	396-423	NAP		g3023324	414	133	5.00E-31	48	76	
18423	ENU02217	ANI61C9131: 580..181	54-73	389-411	NAP		g2500634	198	56	3.00E-12	52	70	
18424	ENU02218	ANI61C6203: 9440..9041	52-73	381-409	NAP		g4426615	398	73	2.00E-15	57	75	
18425	ENU02219	ANI61C5382: 1245..845	22-50	356-379	NAP		g1004217	840	127	6.00E-31	64	47	
18426	ENU02220	ANI61C1044 2:1486..1886	36-58	374-394	NAP		g2980812	86	37	0.003			
18427	ENU02221	ANI61C4350: 2224..1823	69-89	408-428	NAP		g3451060		34	0.38			
18428	ENU02222	ANI61C9613: 1012..610	55-77	390-415	NAP		g71107	635	154	2.00E-42	76	63	
18429	ENU02223	ANI61C1800: 1807..2209	31-50	372-391	NAP		g4582434	207	36	1.00E-11	54	87	
18430	ENU02224	ANI61C7401: 1335..930	46-65	389-409	NAP		g3168589	206	59	4.00E-19	38	93	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18431	ENU02225	ANI61C6584; 35-56 1988..2396			NAP		g4322266	1653	245	1.00E-64	82	28	(AF077355) protein phosphatase 2A regulatory B subunit [Neurospora crassa]
18432	ENU02226	ANI61C5101; 27-51 3160..3569		377-394	NAP		g3676762	443	105	7.00E-32	71	90	(AF087136) RS6/L7A ribosomal protein homolog [Schizosaccharomyces pombe]
18433	ENU02227	ANI61C4456; 43-62 102..512		388-411	NAP		g1082211	148	57	1.00E-10	31	3	"ankyrin 3, long form - human ; (U13616) ankyrin G [Homo sapiens] "
18434	ENU02228	ANI61C5487; 52-71 414..3		400-421	NAP		g131668	218	59	0.000000	49	85	Oleate-induced peroxisomal protein POX18 (lipid-transfer protein) (PXP-18); POX18 protein - yeast (Candida tropicalis); lipid transfer protein - imperfect fungus (Candida tropicalis); (X53633) POX18 [Candida tropicalis]; (M24440) peroxisomal protein [Candida tropicalis]
18435	ENU02229	ANI61C1012 57-76 1:661..1075		407-429	NAP		g730548	446	112	1.00E-24	76	55	"probable 60S ribosomal protein L27; ribosomal protein L27.e.A, cytosolic - yeast (Saccharomyces cerevisiae); (U10400) Rpl27p: Probable 60S ribosomal protein L27 [Saccharomyces cerevisiae] "
18436	ENU02230	ANI61C7031; 49-68 561..145		404-423	NAP		g113701	702	99	1.00E-20			Acetamidase; amdS protein - Emericella nidulans; (M16371) acetamidase enzyme [Emericella nidulans]
18437	ENU02231	ANI61C1047 39-61 0:6088..5671		395-414	NAP		g3915963	1420	152	9.00E-37	60	8	ATP-dependent bile acid permease; probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae); (Z73153) ORF YLL048c [Saccharomyces cerevisiae]
18438	ENU02232	ANI61C3552; 25-44 725..306		383-402	NAP		g3249567	200	52	4.00E-14	50	87	[Saccharomyces cerevisiae] (AF047694) glutaredoxin [Vernicia fordii]
18439	ENU02233	ANI61C8615; 22-40 3216..2797		379-399	NAP		g2833220	579	101	1.00E-32	68	33	hypothetical 35.7 KD protein in DNL4-SLG1 intergenic region; hypothetical protein YOR006c - yeast (Saccharomyces cerevisiae); (U43491) hypothetical protein UND313 [Saccharomyces cerevisiae]; (Z74914) ORF YOR006c [Saccharomyces cerevisiae]

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18440	ENU02234	ANI61C1677: 4351..4771	47-67	396-425	NAP		g418574	520	106	8.00E-23	38	45	mitochondrial carrier protein YMC1 precursor ; (X67122) mitochondrial carrier protein [Saccharomyces cerevisiae]
18441	ENU02235	ANI61C662:8 26-47	26-47	382-406	NAP		g3850125	193	94	6.00E-19	35	27	(AL033391) hypothetical membrane protein [Candida albicans]
18442	ENU02236	ANI61C1479: 45-64	45-64	405-425	NAP		g627570	180	68	3.00E-11			phosphorylation regulatory protein HP-10 - human
18443	ENU02237	ANI61C3138: 24-52	24-52	386-405	NAP		g2493096	103	57	0.000000	30	96	"putative ATP synthase G chain, mitochondrial ; hypothetical protein YPR020w - yeast (Saccharomyces cerevisiae) ; (Z49919) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]"
18444	ENU02238	ANI61C7858: 4680..4257	60-79	414-441	NAP		g2293314		69	2.00E-11			(AF008220) putative cysteine synthase [Bacillus subtilis] ; (Z99119) similar to cysteine synthase [Bacillus subtilis]
18445	ENU02239	ANI61C394:1 71-91	71-91	434-453	NAP		g3006160	456	165	2.00E-40	51	33	(AL022305) mitochondrial import inner membrane translocase subunit precursor [Schizosaccharomyces pombe]
18446	ENU02240	ANI61C1107 33-53	33-53	397-415	NAP		g1926396		33	1.2			(Y08703) SlyA protein [Simorhizobium meliloti]
18447	ENU02241	ANI61C506:1 28-48	28-48	391-411	NAP		g2950478	276	79	1.00E-14	39	82	(AL022070) hypothetical protein [Schizosaccharomyces pombe]
18448	ENU02242	ANI61C3144: 22-43	22-43	385-406	NAP		g140479	260	102	1.00E-21	39	27	"probable transporter FEN2 ; probable membrane protein YCR028c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR028c, len:512 [Saccharomyces cerevisiae]"
18449	ENU02243	ANI61S1388: 58-78	58-78	425-444	NAP		g2244709	136	46	0.0001	33	78	(AB005295) HY5 [Arabidopsis thaliana] ; (AB005456) HY5 [Arabidopsis thaliana]
18450	ENU02244	ANI61C7468: 39-58	39-58	405-426	NAP		g730733	368	83	9.00E-16	50	15	protein transport protein SEC9 ; SEC9 protein - yeast (Saccharomyces cerevisiae) ; (L34336) Sec9 [Saccharomyces cerevisiae] ; (Z72794) ORF YGR009c [Saccharomyces cerevisiae]

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18451	ENU02245	ANI61C9311:	38-57	398-425	NAP			g731668	517	74	6.00E-13	31	31	SSF1 protein; SSF1 protein - yeast (Saccharomyces cerevisiae); (U00061) Ssf1p [Saccharomyces cerevisiae]; (U18113) Ssf1p [Saccharomyces cerevisiae]
18452	ENU02246	ANI61C8081:	67-86	436-455	NAP			g1710760	218	56	4.00E-10	84	73	probable 40S ribosomal protein S28 (S33); (Z70691) ribosomal protein S28 [Schizosaccharomyces pombe]; (AL031545) probable 40S ribosomal protein 28s [Schizosaccharomyces pombe]
18453	ENU02247	ANI61C6597:	72-94	434-461	NAP			g1923256	980	169	1.00E-41	53	46	pad1 homolog [Homo sapiens]
18454	ENU02248	ANI61C1463:	50-69	420-440	NAP			g1073534	224	72	8.00E-14	37	40	iucB protein - Escherichia coli; (X76100) iucB [Escherichia coli]
18455	ENU02249	ANI61C1898:	37-64	409-428	NAP			g2271497	316	84	4.00E-16	45	39	(AF009672) unknown [Acinetobacter sp. ADP1]
18456	ENU02250	ANI61C7592:	25-44	394-416	NAP			g1176485	251	101	3.00E-21	42	96	hypothetical 16.2 KD protein in IME2-MEF2 intergenic region; probable membrane protein YJL104w - yeast (Saccharomyces cerevisiae); (X85021) orf 8 [Saccharomyces cerevisiae]; (Z49379) ORF YJL104w [Saccharomyces cerevisiae]
18457	ENU02251	ANI61C5414:	24-43	381-416	NAP			g731459	168	73	1.00E-12	38	84	hypothetical 17.1 KD protein in SAH1-MEI4 intergenic region; hypothetical protein YER044c - yeast (Saccharomyces cerevisiae); (U18796) Yer044cp [Saccharomyces cerevisiae]
18458	ENU02252	ANI61C9241:	67-88	430-460	NAP			g4538668	98	45	0.0002	32	73	(AL049474) similar to glycosylphosphatidylinositol anchor [Schizosaccharomyces pombe]
18459	ENU02253	ANI61C1281:	60-79	434-453	NAP			g417254	1206	211	2.00E-54	69	35	Lipoic acid synthetase precursor (LIP-SYN) (lipoate synthase); lipoic acid synthase (EC 2.8.1.-) precursor - yeast (Saccharomyces cerevisiae); (Z75104) ORF YOR196c [Saccharomyces cerevisiae]
18460	ENU02254	ANI61C1100	51-74	410-444	NAP			g1871596	180	78	2.00E-14	29	29	(Z92669) hypothetical protein Rv0223c [Mycobacterium tuberculosis]

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18461	ENU02255	ANI61C3253: 72-92 92..527	72-92	444-465	NAP		g1703247	561	221	2.00E-57	70	39	"fructose-bisphosphate aldolase ; (L42380) fructose 1,6 biphosphate-aldolase [Neurospora crassa] "
18462	ENU02256	ANI61C426:5 72-91 40..103	72-91	441-467	NAP		g729580	697	200	5.00E-51	61	20	"1,4-alpha-glucan branching enzyme (glycogen branching enzyme) ; 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) - yeast (Saccharomyces cerevisiae) ; (U18530) 1,4-alpha-glucan branching enzyme [Saccharomyces cerevisiae] "
18463	ENU02257	ANI61C9851: 59-80 1250..813	59-80	435-454	NAP		g3128287	134	63	9.00E-10	33	86	[AF010496] hypothetical protein [Rhodobacter capsulatus]
18464	ENU02258	ANI61C2552: 63-82 1180..1618	63-82	440-459	NAP		g2131439	192	83	9.00E-16	34	28	hypothetical protein YDR348c - yeast (Saccharomyces cerevisiae) ; (U51032) Ydr348cp [Saccharomyces cerevisiae] thrombospondin 1 ; (X14787)
18465	ENU02259	ANI61C8575: 23-46 5652..6090	23-46	400-419	NAP		g4507485		38	0.05			precursor polypeptide (AA -31 to 1139) [Homo sapiens]
18466	ENU02260	ANI61C9787: 53-75 994..555	53-75	427-449	NAP		g1175439	258	55	3.00E-14	38	15	hypothetical 107.1 KD protein C24H6.11C in chromosome I ; hypothetical protein SPAC24H6.11c - fission yeast (Schizosaccharomyces pombe) ; (Z54142) hypothetical protein [Schizosaccharomyces pombe]
18467	ENU02261	ANI61C1796: 38-58 784..345	38-58	415-435	NAP		g118513	517	155	1.00E-37	54	39	Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASA DH) ; aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) - yeast (Saccharomyces cerevisiae) ; (X15649) aspartic semi-aldehyde dehydrogenase (AA 1-365) [Saccharomyces cerevisiae] ; (Z50046)
18468	ENU02262	ANI61C9323: 62-81 667..1106	62-81	425-459	NAP		g793875	274	111	3.00E-24	42	98	Hom2p [Saccharomyces cerevisiae] (Z49149) 100% identity in 135 aa ov with the CSE1 protein from S. cerevisiae. This ORF is incomplete. [Saccharomyces cerevisiae] ; HRC135 gene [Saccharomyces cerevisiae]
18469	ENU02263	ANI61C1144 69-97 8:84..524	69-97	434-467	NAP		g1805251	235	87	8.00E-17	36	26	(U58946) transposase [Aspergillus awamori]

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18470	ENU02264	ANI61C1465: 3404..2964	22-50	399-420	NAP		g133131	116	48	0.00004	37	79	"mitochondrial 60S ribosomal protein L31 precursor (YML31) ; ribosomal protein Yml31 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X15099) precursor rpL31 protein [Saccharomyces cerevisiae] ; (Z28138) ORF YKL138c [Saccharomyces cerevisiae] "
18471	ENU02265	ANI61C6213: 60-81 3568..3128	60-81	438-458	NAP		g1723832	368	72	3.00E-17	58	62	hypothetical 15.9 KD protein in OLE1-DUP1 intergenic region ; probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae) ; (Z72576) ORF YGL054c [Saccharomyces cerevisiae]
18472	ENU02266	ANI61C3405: 35-59 14..456	35-59	415-434	NAP		g1170186	200	54	0.000000	34	19	probable ATP-dependent RNA helicase DBP4 (helicase CA4) (helicase UF1) ; probable RNA helicase CA4 - yeast (Saccharomyces cerevisiae) ; (Z49308) ORF YJL033w [Saccharomyces cerevisiae]
18473	ENU02267	ANI61C3640: 71-91 929..486	71-91	451-472	NAP		g1805251	1188	93	8.00E-19	37	26	(U58946) transposase [Aspergillus awamori]
18474	ENU02268	ANI61C7618: 63-84 4854..5297	63-84	444-464	NAP		g1710803	714	92	1.00E-18	31	23	Retrograde regulation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRP588; EMBL:SCRTG2X;M97691; PIR:B44344;B44344 [Saccharomyces cerevisiae] ; (M97691) Rtg2p [Saccharomyces cerevisiae] ; (Z72774) ORF YGL252c [Saccharomyces cerevisiae]
18475	ENU02269	ANI61C2182: 38-57 949..505	38-57	418-440	NAP		g731298	256	105	2.00E-22	37	24	probable transporter SEO1 ; probable membrane protein YAL067c - yeast (Saccharomyces cerevisiae) ; (U12980) Seo1p; putative membrane protein [Saccharomyces cerevisiae]
18476	ENU02270	ANI61C6415: 65-84 7368..7813	65-84	449-468	NAP		g3873405		43	0.002			(U17129) unknown [Rhodococcus erythropolis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18477	ENU02271	ANI61C9683: 199..645	71-92	452-475	NAP		g465011	1037	261	1.00E-69	97	43	Uricase (urate oxidase) ; urate oxidase (EC 1.7.3.3) - Emericella nidulans ; (X72210) urate oxidase [Emericella nidulans]
18478	ENU02272	ANI61C3079: 27-53		413-432	NAP		g171183	383	129	1.00E-29	45	34	(M61194) CDC14 [Saccharomyces cerevisiae]
18479	ENU02273	ANI61C7257: 30-49		407-436	NAP		g1723218	294	107	2.00E-23	51	83	hypothetical 19.5 KD protein C3H8.07C in chromosome I ; (Z69086) unknown [Schizosaccharomyces pombe]
18480	ENU02274	ANI61C6494: 22-50		409-428	NAP		g1850768	177	88	4.00E-17	47	89	(AB001289) YNL157W homolog [Schizosaccharomyces pombe]
18481	ENU02275	ANI61C497: 31-49		414-438	NAP		g3023637	2950	213	4.00E-55	68	12	probable ATP-dependent RNA helicase HRH1 (DEAH box protein 8) ; probable RNA helicase 1 - human ; (D50487) RNA helicase (HRH1) [Homo sapiens]
18482	ENU02276	ANI61C1049: 39-69		428-447	NAP		g3024439	1855	234	2.00E-61	84	35	26S PROTEASE regulatory subunit 6B homolog ; (U15601) 26S proteasome subunit [Aspergillus niger]
18483	ENU02277	ANI61C3576: 26-54		416-435	NAP		g3169068	276	56	5.00E-18	67	84	(AL023704) putative transcription factor iia small subunit [Schizosaccharomyces pombe]
18484	ENU02278	ANI61C2679: 64-84		443-473	NAP		g2132651	286	127	3.00E-29	42	25	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) ; (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
18485	ENU02279	ANI61C1083: 24-48		403-435	NAP		g3265058	703	165	2.00E-40	91	84	(AF060232) monoubiquitin/carboxy extension protein fusion [Botryotinia fuckeliana]
18486	ENU02280	ANI61C3200: 70-91		462-481	NAP		g1078650	546	136	9.00E-42	81	61	"peptidylprolyl isomerase (EC 5.2.1.8) a, cytosolic - fungus (Fusarium sporotrichioides)"
18487	ENU02281	ANI61C5329: 61-80		451-472	NAP		g131768	605	68	3.00E-11			quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans]

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18488	ENU02282	ANI61C7023; 22-49 2151..1697	22-49	414-434	NAP		g465702	221	83	2.00E-20	42	64	probable ribosomal protein B0303.15 in chromosome III ; ribosomal protein L11 homolog - Caenorhabditis elegans ; (M77697) ribosomal protein L11 [Caenorhabditis elegans] (AC000133) G4P04 [Emmericella nidulans]
18489	ENU02283	ANI61C1355; 60-79 3033..2578	60-79	451-473	NAP		g1870214	839	267	4.00E-74	98	68	hypothetical protein YPR100w - yeast (Saccharomyces cerevisiae) ; (U32445) Note that there is a 357 codon ORF contained within this ORF on the other strand [Saccharomyces cerevisiae]
18490	ENU02284	ANI61C1024; 26-47 1606..1150	26-47	420-440	NAP		g2132281	217	76	2.00E-20	41	94	"Lysyl-TRNA synthetase, cytoplasmic (lysine--TRNA ligase) (LYSRS) ; lysine--TRNA ligase (EC 6.1.1.6) - yeast (Saccharomyces cerevisiae) ; (J04186) lysyl-TRNA synthetase [Saccharomyces cerevisiae] ; (Z68196) Krs1p [Saccharomyces cerevisiae] ; (Z74333) ORF YDR037w [Saccharomyces cerevisiae] "
18491	ENU02285	ANI61C2432; 25-44 2470..2013	25-44	421-440	NAP		g135139	698	241	3.00E-63	75	25	3-Isopropylmalate dehydratase (isopropylmalate isomerase) (alpha-IPM isomerase) (IPMI) ; (D63833) 3-isopropylmalate dehydratase [Rhizopus niveus] ; alpha-isopropylmalate isomerase [Rhizopus niveus] (AJ001732) rAsp f 4 [Aspergillus fumigatus]
18492	ENU02286	ANI61C1783; 52-72 465..7	52-72	445-467	NAP		g2492643	621	195	1.00E-49	66	19	(AC004077) putative urease accessory protein [Arabidopsis thaliana] ; protein [Arabidopsis thaliana] (AC004481) putative urease accessory protein [Arabidopsis thaliana] (Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E (SW:P08578); cDNA EST yk375g7.3 comes from this gene; cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gene; ...
18493	ENU02287	ANI61C4724; 56-78 272..729	56-78	451-471	NAP		g3005839	485	125	2.00E-28	53	52	
18494	ENU02288	ANI61C7180; 51-70 3401..2941	51-70	450-469	NAP		g3128220	721	195	2.00E-49	62	55	
18495	ENU02289	ANI61C9804; 71-95 2148..2608	71-95	470-489	NAP		g3876465	129	39	0.0005	63	80	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18496	ENU02290	ANI61C5930: 6899..6438	24-59	424-443	NAP		g3646479	526	70	1.00E-11	37	91	(AJ010981) putative transposase [Talaromyces stipitatus]
18497	ENU02291	ANI61C7029: 64-84 3128..2975	64-84	464-483	NAP		g1169238	935	169	1.00E-41	56	30	"glutamate decarboxylase (GAD) ; glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia ; (L16797) glutamate decarboxylase [Petunia hybrida] ; (L16977) glutamate decarboxylase [Petunia hybrida] " (AF079317) unknown [Sphingomonas aromaticivorans]
18498	ENU02292	ANI61C8332: 33-52 1002..541	33-52	432-452	NAP		g3378330	347	131	4.00E-30	40	79	hypothetical 29.7 KD protein in RSP5-PAK1 intergenic region ; hypothetical protein YER126c - yeast (Saccharomyces cerevisiae) ; (U18916) Yer126cp [Saccharomyces cerevisiae]
18499	ENU02293	ANI61C9046: 46-66 928..466	46-66	441-466	NAP		g731511	805	189	1.00E-47	63	58	(AL035656) hypothetical protein [Arabidopsis thaliana]
18500	ENU02294	ANI61C1064 22-46 8-96..558	22-46	417-442	NAP		g4490325	104	58	0.000000	25	70	Prohibitin ; prohibitin - yeast (Saccharomyces cerevisiae) ; (Z72917) ORF YGR132c [Saccharomyces cerevisiae]
18501	ENU02295	ANI61C7541: 42-61 993..531	42-61	443-462	NAP		g1730544	909	163	3.00E-53	73	53	"2,2-dialkylglycine decarboxylase (DGD) ; (J05282) 2,2-dialkylglycine decarboxylase structural protein [Pseudomonas cepacia] "
18502	ENU02296	ANI61C3317: 32-51 409..870	32-51	433-452	NAP		g729318	784	106	1.00E-28	49	35	(AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis]
18503	ENU02297	ANI61C5842: 68-99 889..427	68-99	463-488	NAP		g2909465	226	78	3.00E-14			(AF093540) ribosomal protein L26 [Zea mays]
18504	ENU02298	ANI61C1473: 72-91 3926..4389	72-91	471-493	NAP		g3747050	380	115	1.00E-25	68	85	Mannose-6-phosphate isomerase (phosphomannose isomerase) (PMI) (phosphohexomutase) ; mannose-6-phosphate isomerase (EC 5.3.1.8) - yeast (Candida albicans) ; (X82024) mannose-6-phosphate isomerase [Candida albicans]
18505	ENU02299	ANI61C2300: 64-83 2249..2713	64-83	464-486	NAP		g462565	294	71	3.00E-12	32	31	hypothetical protein YPR040w - yeast (Saccharomyces cerevisiae) ; (Z68111) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
18506	ENU02300	ANI61C5903: 33-54 2023..1559	33-54	433-455	NAP		g2132260	318	86	2.00E-16	46	37	

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18507	ENU02301	ANI61C7819: 2..466	23-42	425-445	NAP		g4235093	357	118	2.00E-27	43	19	(AF108944) beta-xylosidase [Aspergillus niger]
18508	ENU02302	ANI61C4975: 68-88	68-88	473-492	NAP		g1749584	415	157	6.00E-38	45	74	(D89188) unnamed protein product [Schizosaccharomyces pombe]
18509	ENU02303	ANI61C2732: 72-94	72-94	461-496	NAP		g1722894	465	187	3.00E-47	56	47	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-L-arabinofuranosidase (arabinosidase) ; xylosidase/arabinosidase - Bacteroides ovatus (strain V975) ; (U04957) xylosidase/arabinosidase [Bacteroides ovatus] ; xylosidase-arabinosidase [Bacteroides ovatus]"
18510	ENU02304	ANI61C1138: 22-41	22-41	428-447	NAP		g1931638	414	145	2.00E-34	42	12	(U95973) transcription factor rush-1 alpha isolog [Arabidopsis thaliana]
18511	ENU02305	ANI61C2853: 34-53	34-53	436-459	NAP		g731448	70	43	0.001	31	62	hypothetical 18.3 KD protein in GAL83-YPT8 intergenic region ; hypothetical protein YER030w - yeast (Saccharomyces cerevisiae) ; (U18778) Yer030wp [Saccharomyces cerevisiae] probable sterigmatoctysin biosynthesis p450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emmericella nidulans]
18512	ENU02306	ANI61C3640: 67-87	67-87	459-493	NAP		g2493387	267	96	1.00E-19	38	27	(AL034353) putative acetyltransferase [Schizosaccharomyces pombe]
18513	ENU02307	ANI61C1140: 48-67	48-67	452-474	NAP		g3925776	258	108	3.00E-23	39	94	(AF047464) Tpr1 [Schizosaccharomyces pombe]
18514	ENU02308	ANI61C1115: 62-81	62-81	470-489	NAP		g2896142	984	85	2.00E-16	40	15	[Schizosaccharomyces pombe]
18515	ENU02309	ANI61C2532: 24-46	24-46	432-451	NAP		g3006140	622	220	6.00E-57	68	60	(AL022299) ribosomal protein [Schizosaccharomyces pombe] ; (AJ001133) ribosomal protein L7 [Schizosaccharomyces pombe]
18516	ENU02310	ANI61C8155: 64-84	64-84	468-492	NAP		g1572791	63	42	0.003			(U70852) weak similarity to neutral endopeptidases [Caenorhabditis elegans]
18517	ENU02311	ANI61C5147: 69-100	69-100	477-498	NAP		g4580321		36	0.12			(AF095903) unknown [Sinorhizobium meliloti]

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18518	ENU02312	ANI61C8277; 1289..818	68-87	478-497	NAP		g134975	495	101	3.00E-31	52	23	Heat shock protein STI1 ; stress-induced protein STI1 - yeast (Saccharomyces cerevisiae) ; (M28486) heat shock protein STI1 [Saccharomyces cerevisiae] ; (X87331) STI1 heat shock protein [Saccharomyces cerevisiae] ; (Z74935) ORF YOR027w [Saccharomyces cerevisiae]
18519	ENU02313	ANI61C4165; 5..478	22-55	432-452	NAP		g548437	364	146	7.00E-35	47	18	OSH1 protein ; SWH1 protein (version 1) - yeast (Saccharomyces cerevisiae) ; (L28920) Osh1p [Saccharomyces cerevisiae] (AF039376) polyprotein [Arabidopsis arenosa] hypothetical 34.1 KD protein C11D3.03C in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe] CUT8 protein ; (D31772) ORF [Schizosaccharomyces pombe] ; (Z73099) protein kinase [Schizosaccharomyces pombe] (AC005397) putative 3-methyl-2-oxobutanoate hydroxy-methyl-transferase [Arabidopsis thaliana] hypothetical zinc finger protein ZK686.4 in chromosome III ; ZK686.4 protein - Caenorhabditis elegans ; (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]
18520	ENU02314	ANI61C102;1 28-46 415..1889	28-46	435-460	NAP		g2865437	214	83	1.00E-15			
18521	ENU02315	ANI61C1075 23-44 2:1531..1057	23-44	435-455	NAP		g1351700	696	137	7.00E-42	57	46	
18522	ENU02316	ANI61C8453; 59-81 1035..561	59-81	464-491	NAP		g729231	249	108	2.00E-23	33	60	
18523	ENU02317	ANI61C2468; 54-74 374..848	54-74	461-486	NAP		g3702336	566	134	4.00E-31	46	45	
18524	ENU02318	ANI61C2736; 35-60 518..44	35-60	448-467	NAP		g466044	150	72	2.00E-12	28	37	
18525	ENU02319	ANI61C9206; 22-43 3099..3574	22-43	436-455	NAP		g2213500	133	66	2.00E-10	35	91	(Z97050) hypothetical protein Rv0163 [Mycobacterium tuberculosis] (AL023859) putative tRNA splicing endonuclease gamma subunit [Schizosaccharomyces pombe] (AF079317) unknown [Sphingomonas aromaticivorans]
18526	ENU02320	ANI61C1049 25-47 4:875..1350	25-47	439-458	NAP		g3218411	386	98	4.00E-20	31	55	
18527	ENU02321	ANI61C7100; 59-78 517..41	59-78	472-493	NAP		g3378265	1233	150	3.00E-45	67	35	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18528	ENU02322	ANI61C1087 0:2456..1980	63-85	475-497	NAP		g1934614	269	109	1.00E-23	36	14	(U93874) cytochrome P450 102 [Bacillus subtilis] ; (Z99117) similar to cytochrome P450 / NADPH-cytochrome P450 reductase [Bacillus subtilis]
18529	ENU02323	ANI61C35:18 1..657	41-60	456-475	NAP		g2498971	502	66	2.00E-10			putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emericella nidulans] "(U40939) Similar to dihydroflavonol-4-reductase (maize, petunia, tomato). [Caenorhabditis elegans] "
18530	ENU02324	ANI61C8224: 1960..1483	66-84	467-501	NAP		g1072179	109	40	0.009			(U61841) cutinase G-box binding protein [Fusarium solani f. sp. pisi] "(AF125459) contains similarity to enoyl-CoA hydratases/isomerases (Pfam:PF00378, Score=59.1, E=3.3e-16, N=1) [Caenorhabditis elegans] "
18531	ENU02325	ANI61C2974: 648..169	51-70	464-486	NAP		g1438949	424	69	1.00E-18	42	28	(Z95556) fadD35 [Mycobacterium tuberculosis]
18532	ENU02326	ANI61C3312: 1079..601	30-49	447-466	NAP		g4226133		34	0.00006			(AE001038) enoyl-CoA hydratase (fad-3) [Archaeoglobus fulgidus]
18533	ENU02327	ANI61C7634: 551..72	40-68	458-477	NAP		g2113938	551	105	2.00E-30	51	25	probable serine/threonine-protein kinase YOL045W ; hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae) ; (Z74788)
18534	ENU02328	ANI61C2961: 41..520	62-81	480-499	NAP		g2649635	292	124	4.00E-28	40	61	ORF YOL045w [Saccharomyces cerevisiae]
18535	ENU02329	ANI61C9447: 1448..1928	63-82	481-501	NAP		g2499624	662	187	4.00E-47	68	12	hypothetical 16.9 KD protein in ALD6-PDR12 intergenic region ; hypothetical protein YPL059w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe13p [Saccharomyces cerevisiae]
18536	ENU02330	ANI61C7555: 3253..3734	46-66	455-485	NAP		g3025275	375	102	2.00E-38	59	94	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18537	ENU02331	ANI61C465:6 444..6926	51-70	467-491	NAP		g4557817	1328	187	5.00E-47	57	30	3-oxoacid CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor; succinyl-CoA:3-ketoacid-COenzyme A transferase precursor (succinyl CoA:3-oxoacid COA-transferase) (OXCCT); (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens]
18538	ENU02332	ANI61C1508: 42-62 698..216	42-62	458-482	NAP		g1363392	267	113	8.00E-25	36	24	beta-glucosidase/xylosidase - Erwinia chrysanthemi
18539	ENU02333	ANI61C4557: 57-84 485..3	57-84	474-497	NAP		g3451474	563	224	3.00E-58	63	25	(AL031349) conserved hypothetical protein [Schizosaccharomyces pombe]
18540	ENU02334	ANI61C2769: 44-63 109..591	44-63	465-484	NAP		g729079	644	134	4.00E-31	61	41	"Carboxy-cis,cis-muconate cyclase (3-carboxy-cis,cis-muconate lactonizing enzyme) (CMLE); carboxy-cis,cis-muconate cyclase (EC 5.5.1.5) - Neurospora crassa; (L27538) 3-carboxy-cis,cis-muconate cyclase [Neurospora crassa]"
18541	ENU02335	ANI61C323:4 22-41 833..5316	22-41	444-463	NAP		g549686	238	119	1.00E-26	39	16	Manganese resistance protein; hypothetical protein YKL064w - yeast (Saccharomyces cerevisiae); (X75781) B969 [Saccharomyces cerevisiae]; (Z28064) ORF YKL064w [Saccharomyces cerevisiae]; ORF [Saccharomyces cerevisiae] (AB025252) reverse transcriptase [Magnaporthe grisea] (D87924) ORF 6 [Actinomyadura hibisca]
18542	ENU02336	ANI61C1029 60-79 8:4168..3685	60-79	482-501	NAP		g4586458	163	85	2.00E-16	35	55	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe]
18543	ENU02337	ANI61C1099 25-42 3:1728..1245	25-42	446-466	NAP		g2580447		86	2.00E-16			tuberos scleros protein 2 - human
18544	ENU02338	ANI61C2925: 70-89 666..183	70-89	492-511	NAP		g3650394	157	75	2.00E-13	33	80	(AL031540) uroporphyrin methyltransferase
18545	ENU02339	ANI61C349:7 23-53 145..6662	23-53	445-464	NAP		g631482	273	68	4.00E-11			[Schizosaccharomyces pombe]
18546	ENU02340	ANI61S1334: 61-82 492..8	61-82	484-503	NAP		g3581882	492	197	5.00E-50	59	32	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
18547	ENU02341	ANI61C9558: 65-84 6029..6513	65-84	488-507	NAP		g3395556	695	156	8.00E-38	50	48	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18548	ENU02342	ANI61C1812: 519..35	46-67	468-488	NAP		g2440206	412	122	2.00E-27	42	20	putative integral membrane protein [Schizosaccharomyces pombe]
18549	ENU02343	ANI61C5509: 27-46 817..332	27-46	451-470	NAP		g140400	1065	201	3.00E-51	65	50	"hypothetical 37.2 KD protein in CHA1-PRD1 intergenic region ; hypothetical protein YCL059c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL059c, len:316 [Saccharomyces cerevisiae]"
18550	ENU02344	ANI61C6930: 26-46 2648..2163	26-46	450-469	NAP		g2160183	316	47	0.000000	47	42	"(AC000132) Identical to A. thaliana U2 SnRNP-specific A' protein (gb X69137). ESTs gb ATTS0705, gb ATTS0339 come from this gene. [Arabidopsis thaliana]"
18551	ENU02345	ANI61C9624: 22-57 43..530	22-57	446-466	NAP		g2842472	174	83	1.00E-15	31	65	[Schizosaccharomyces pombe] "probable 60S ribosomal protein YIL052C ; ribosomal protein L34.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z38060) spliced ribosomal protein, len: 121, CAI: 0.77, RL34_RAT P11250 60S ribosomal protein L34 [Saccharomyces cerevisiae]"
18552	ENU02346	ANI61C1031 22-56 8:1335..1135	22-56	445-466	NAP		g731810	335	92	2.00E-18	65	94	"(D89220) similar to Saccharomyces cerevisiae glutathion-dependent formaldehyde dehydrogenase, SWISS-PROT Accession Number P32771 [Schizosaccharomyces pombe]"
18553	ENU02347	ANI61C6624: 68-87 815..1301	68-87	491-512	NAP		g1749648		32	2.5			hypothetical 66.4 KD protein in SMC3-MRPL8 intergenic region ; hypothetical protein YJL069c - yeast (Saccharomyces cerevisiae) ; (Z34288) HRE594 [Saccharomyces cerevisiae] ; (X88851) hypothetical protein [Saccharomyces cerevisiae] ; (Z49344) ORF YJL069c [Saccharomyces cerevisiae]
18554	ENU02348	ANI61C2275: 69-88 87..573	69-88	493-513	NAP		g731935	374	138	2.00E-32	52	24	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18555	ENU02349	ANI61C1036 2:4828..4341	50-69	462-495	NAP		g128478	171	93	1.00E-18	38	75	Modulation protein L ; nodulation protein nodL - Rhizobium leguminosarum bv. viciae plasmid pRL1J1 ; (Y00548) nodL [Rhizobium leguminosarum] ; (X17557) nodL [Rhizobium leguminosarum] (Z99295) hypothetical protein [Schizosaccharomyces pombe] "splicing factor, arginine/serine-rich 2 ; splicing factor, arginine/serine-rich 2 (splicing factor SC35) (SC-35) (splicing component, 35 KD) (PR264 protein) ; splicing factor SC35 - human ; (M90104) splicing factor [Homo sapiens] "
18556	ENU02350	ANI61C7084: 30-53 437..924	30-53	455-475	NAP		g2414606	252	81	4.00E-15			hypothetical 27.7 KD protein in UME3-HDA1 intergenic region ; probable membrane protein YNL024c - yeast (Saccharomyces cerevisiae) ; (Z71300) ORF YNL024c [Saccharomyces cerevisiae] (U94183) unknown [Glomerella cingulata]
18557	ENU02351	ANI61C4309: 43-63 4625..4138	43-63	469-488	NAP		g4506899	173	53	0.000001	42	68	(Z28283) ORF YKR057w [Saccharomyces cerevisiae] hypothetical 48.0 KD protein in MRPL37-RIF1 intergenic region ; probable membrane protein YBR271w - yeast (Saccharomyces cerevisiae) ; (Z36140) ORF YBR271w [Saccharomyces cerevisiae] (U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]
18558	ENU02352	ANI61C9255: 57-86 158..645	57-86	472-502	NAP		g1730714	220	86	1.00E-16	37	66	
18559	ENU02353	ANI61C4912: 50-70 2125..2612	50-70	473-495	NAP		g2707187	301	116	1.00E-25	67	96	
18560	ENU02354	ANI61C9554: 23-46 3070..3558	23-46	450-469	NAP		g2131127	277	102	2.00E-21	71	57	
18561	ENU02355	ANI61C6119: 25-46 961..473	25-46	450-471	NAP		g586387	199	87	8.00E-17	46	31	
18562	ENU02356	ANI61C1090 35-54 7:626..137	35-54	463-482	NAP		g2673951	1172	247	3.00E-65	89	10	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18563	ENU02357	ANI50C1.11 18:883..1373	66-86	484-514	NAP		g2493561		117	2.00E-33			Cytosine deaminase (cytosine aminohydrolase) ; hypothetical protein YPR062w - yeast (Saccharomyces cerevisiae) ; (Z49219) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] ; (U55193) cytosine deaminase [Saccharomyces cerevisiae] ; [Saccharomyces cerevisiae] ; (AF005261) cytosine deaminase [Saccharomyces cerevisiae] ; catalase B ; (U80672) catalase [Emicella nidulans] "hypothetical 22.0 KD protein in FOX3-UBP7 intergenic region ; probable membrane protein YIL157c - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len 197, CAI: 0.19 [Saccharomyces cerevisiae] "
18564	ENU02358	ANI61C2752: 664..174	40-59	469-488	NAP		g2493540	965	314	3.00E-85	99	22	ketol-L-acid reductoisomerase precursor (acetohydroxy-acid reductoisomerase) (alpha-keto-beta-hydroxylacil reductoisomerase) ; alpha-keto-beta-hydroxylacil reductoisomerase - Neurospora crassa ; (M84189) alpha-keto-beta-hydroxylacil reductoisomerase [Neurospora crassa] (AF035619) pyridoxine biosynthesis protein [Cercospora nicotianae] (AL031540) short chain dehydrogenase [Schizosaccharomyces pombe]
18565	ENU02359	ANI61C6673: 529..38	27-49	447-476	NAP		g731886	189	88	3.00E-17	32	83	Probable nicotinate phosphoribosyltransferase (NAPRTASE) ; probable nicotinate phosphoribosyltransferase (EC 2.4.2.11) - yeast (Saccharomyces cerevisiae) ; (Z75117) ORF YOR209c [Saccharomyces cerevisiae]
18566	ENU02360	ANI61C1188: 10464..9973	42-63	471-491	NAP		g729839	985	240	4.00E-79	89	41	Coatmer beta subunit (beta-coat protein) (beta-COP) ; beta-COP protein - rat ; (X57228) beta COP [Rattus norvegicus]
18567	ENU02361	ANI61C9579: 2085..2576	45-65	473-494	NAP		g2979688	923	169	1.00E-41	73	46	
18568	ENU02362	ANI61C6739: 1038..547	37-56	467-486	NAP		g3581884	362	58	3.00E-17	46	50	
18569	ENU02363	ANI61C8503: 556..65	71-90	500-520	NAP		g2507262	786	64	4.00E-21	42	33	
18570	ENU02364	ANI61C5428: 2..495	23-42	446-474	NAP		g116923	715	222	9.00E-58	62	17	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18571	ENU02365	ANI61C4891: 22-47 93..587		455-474	NAP		g2132942	275	110	7.00E-24	36	31	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
18572	ENU02366	ANI61C8291: 70-89 1757..2252		500-523	NAP		g548818	283	85	1.00E-25	57	85	"DNA-directed RNA polymerase I, II, and III 15 KD polypeptide (RPABC6) ; (L00597) RNA polymerase small common phosphorylated subunit [Schizosaccharomyces pombe] ; (L25592) RNA polymerase [Schizosaccharomyces pombe] ; (AL023518) dna-directed RNA polymerase [Schizosaccharomyces pombe] "
18573	ENU02367	ANI61C2932: 64-83 65..562		499-518	NAP		g3850092	819	149	9.00E-50	72	32	(AL033389) argininosuccinate lyase [Schizosaccharomyces pombe]
18574	ENU02368	ANI61C8403: 48-69 873..1369		483-502	NAP		g1353060	439	185	1.00E-46	58	89	"3-hydroxyanthranilate 3,4-dioxygenase (3-HAO) (3-hydroxyanthranilic acid dioxygenase) ; (3-hydroxyanthranilate oxygenase) ; hypothetical protein YJR025c - yeast (Saccharomyces cerevisiae) ; (Z49525) ORF YJR025c [Saccharomyces cerevisiae] ; (X87297) J1550 [Saccharomyces cerevisiae] "
18575	ENU02369	ANI61C171:1 24-54 451..955		452-478	NAP		g1408257	305	117	6.00E-26	35	29	(U60989) putative transposase [Magnaporthe grisea]
18576	ENU02370	ANI61C7500: 54-73 1600..1103		489-509	NAP		g1706568	140	85	3.00E-16	34	64	putative enoyl-CoA hydratase ; (Z73101) echA6 [Mycobacterium tuberculosis]
18577	ENU02371	ANI61C6450: 57-77 567..1064		492-512	NAP		g1351658	351	131	4.00E-30	54	79	Adaptin complex small chain homolog C30D11.05 ; hypothetical protein SPAC30D11.05 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) adaptin complex small chain homolog [Schizosaccharomyces pombe]
18578	ENU02372	ANI61C7324: 28-48 3468..3965		455-483	NAP		g1763539	77	55	0.000000	32	67	(U77369) transcription factor dMax [Drosophila melanogaster]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18579	ENU02373	ANI61C5863: 29-51 862..1360		466-485	NAP		g1169869	267	50	0.00001			"eukaryotic translation initiation factor 3 gamma subunit (EIF-3 gamma) (EIF3 P62) (translation initiation factor EIF3, P62 subunit) (GCD10 protein) ; GCD10 protein - yeast (Saccharomyces cerevisiae) ; (X83511) Gcd10p [Saccharomyces cerevisiae] ; (Z71338) ORF YNL062c [Saccharomyces cerevisiae] ; (U12141) Gcd10p [Saccharomyces cerevisiae] "
18580	ENU02374	ANI61C3397: 27-47 1034..1532		453-483	NAP		g4206286	1929	173	5.00E-43	52	16	H(+)-ATPase [Emericella nidulans] (AL022103) hypothetical protein [Schizosaccharomyces pombe] cyclin-dependent kinaseS regulatory subunit (cell division control protein CKS1) ; protein kinase CDC28 complex subunit CKS1 - yeast (Saccharomyces cerevisiae) ; (M26033) protein kinase [Saccharomyces cerevisiae] ; (X75891) CKS1 [Saccharomyces cerevisiae] ; (Z36004) ORF YBR135w [Saccharomyces cerevisiae] ; CKS1 gene [Saccharomyces cerevisiae]
18583	ENU02377	ANI61C1300: 23-44 1684..1185		459-480	NAP		g2501011	453	77	9.00E-14	28	16	Isoleucyl-TRNA synthetase (isoleucine--TRNA ligase) (ILERS) ; (D90907) isoleucyl-tRNA synthetase [Synecocystis sp.]
18584	ENU02378	ANI61C6297: 58-77 1764..1264		497-516	NAP		g465677	196	109	1.00E-23	37	60	hypothetical 30.5 KD protein C30A5.3 in chromosome III ; C30A5 protein - Caenorhabditis elegans ; (L10990) putative [Caenorhabditis elegans] (AL023794) putative proline oxidase precursor [Schizosaccharomyces pombe]
18585	ENU02379	ANI61C298:3 65-85 165..2664		504-523	NAP		g3192023	220	79	2.00E-14	32	33	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18586	ENU02380	ANI61C462:6 88..188	39-58	478-497	NAP		g4504799	837	127	2.00E-34	63	32	isovaleryl Coenzyme A dehydrogenase ; isovaleryl-CoA dehydrogenase precursor (IVD) ; isovaleryl-CoA dehydrogenase (EC 1.3.99.10) precursor - human ; (M34192) isovaleryl-coA dehydrogenase (IVD) [Homo sapiens]
18587	ENU02381	ANI61C9323: 38-59 4590..4089	38-59	477-497	NAP		g1077341	137	50	0.000000	40	88	"hypothetical protein YLR281c - yeast (Saccharomyces cerevisiae) ; (U17243) This gene is in the -2 reading frame. There are also overlapping ORFs in the -3 reading frame, and in the +1 reading (on the other strand). The longest ORF was arbitrarily chosen as L8003.11 [Saccharomyces cerevisiae] "
18588	ENU02382	ANI61C1396: 52-74 31..532	52-74	492-511	NAP		g2873363	212	108	4.00E-23	37	23	(U89492) arylsulfatase [Neurospora crassa]
18589	ENU02383	ANI61C9179: 56-75 9190..9691	56-75	494-515	NAP		g731012	1431	217	5.00E-56	74	31	Anthranilate synthase component I ; anthranilate synthase (EC 4.1.3.27) component I - yeast (Saccharomyces cerevisiae) ; (X68327) anthranilate synthase (component I) [Saccharomyces cerevisiae] ; (U18839) Trp2p: anthranilate synthase component I [Saccharomyces cerevisiae]
18590	ENU02384	ANI61C6172: 70-89 146..648	70-89	511-530	NAP		g3169083	279	81	6.00E-15	36	49	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18591	ENU02385	ANI61C3386: 65-86 625..124	65-86	506-525	NAP		g2495634		69	3.00E-11			hypothetical 43.3 KD protein in EVGS-GLK intergenic region ; (AE000325) putative enzyme [Escherichia coli]
18592	ENU02386	ANI61C6376: 46-65 4221..4723	46-65	486-506	NAP		g3219935	546	215	6.00E-56	70	92	probable peptidyl-prolyl cis-trans isomerase C57A10.03 ; (Z94864) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18593	ENU02387	ANI61C2093: 42-62 101..604	42-62	484-503	NAP		g1711596	231	91	5.00E-18	40	16	putative sulfate transporter YPR003C; probable membrane protein YPR003c-yeast (Saccharomyces cerevisiae); (Z48951) unknown [Saccharomyces cerevisiae]; (U31900) Lpz3p [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae] "mitochondrial 60S ribosomal protein L30 precursor (YML30); ribosomal protein Yml30 precursor, mitochondrial - yeast (Saccharomyces cerevisiae); (X96722) ORF N0864 [Saccharomyces cerevisiae]; (Z71528) ORF YNL252c [Saccharomyces cerevisiae] "
18594	ENU02388	ANI61C2410: 22-43 3097..3601	22-43	462-484	NAP		g1710602	192	73	9.00E-13	30	57	
18595	ENU02389	ANI61C6738: 27-55 8..512	27-55	458-489	NAP		g1723485	364	152	2.00E-36	43	41	hypothetical 47.3 KD protein C17G8.13C in chromosome I; (Z69795) unknown [Schizosaccharomyces pombe] alpha-glucosidase (EC 3.2.1.20) MAL62 - yeast (Candida albicans); (M94674) alpha-glucosidase [Candida albicans] (AL023777) rna binding protein [Schizosaccharomyces pombe]
18596	ENU02390	ANI61C8016: 59-78 5896..6401	59-78	488-522	NAP		g323015	1408	118	3.00E-26	37	29	40S ribosomal protein S17; (M13933) ribosomal protein S17 [Cricetulus griseus]; (D25213) ribosomal protein S17 [Mus musculus]
18597	ENU02391	ANI61C7458: 22-45 1..506	22-45	462-485	NAP		g3184100	327	145	2.00E-34	43	61	sorbitol dehydrogenase (L-idoitol 2-dehydrogenase); L-idoitol 2-dehydrogenase (EC 1.1.1.14) precursor - mouse; (U27014) sorbitol dehydrogenase precursor [Mus musculus domesticus]
18598	ENU02392	ANI61C1126: 66-89 149..655	66-89	511-530	NAP		g133820	334	92	1.00E-31	62	91	hypothetical 45.7 KD protein in RPS3-PSD1 intergenic region; hypothetical protein YNL175c - yeast (Saccharomyces cerevisiae); (Z71451) ORF YNL175c [Saccharomyces cerevisiae]
18599	ENU02393	ANI61C4302: 34-63 950..1456	34-63	477-498	NAP		g2492773	574	96	1.00E-19	37	41	
18600	ENU02394	ANI61C879:5 46-68 66..1072	46-68	491-510	NAP		g1730806	196	87	6.00E-17	31	36	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18601	ENU02395	ANI61C631:1 24..617	53-73	489-517	NAP		g2497216	123	62	0.000000 003	28	22	hypothetical 83.4 KD protein in DSK2-CAT8 intergenic region ; hypothetical protein YMR277w - yeast (Saccharomyces cerevisiae) ; (Z49704) unknown [Saccharomyces cerevisiae] (U34346) unknown [Paracoccus denitrificans] (AB001288) ribosomal protein S23 homolog [Schizosaccharomyces pombe] (AB023235) KIAA1018 protein [Homo sapiens] hypothetical 21.6 KD protein F37A4.2 in chromosome III ; F37A4.2 protein - Caenorhabditis elegans ; (U00032) F37A4.2 gene product [Caenorhabditis elegans] Aspergillopepsin II precursor (acid protease A) (proctase A) ; aspergillopepsin II (EC 3.4.23.19) precursor - Aspergillus niger (var. macrosporus) ; (M68871) acid proteinase A [Aspergillus niger] ; acid protease A [Aspergillus niger macrosporus] hypothetical 65.3 KD protein in pre3-SAG1 intergenic region ; hypothetical protein YJR001w - yeast (Saccharomyces cerevisiae) ; (X87611) ORF YJR83.4 [Saccharomyces cerevisiae] ; (Z49501) ORF YJR001w [Saccharomyces cerevisiae] "(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]"
18602	ENU02396	ANI61C8419: 34-54 3562..3056	34-54	470-498	NAP		g1002864	555	198	2.00E-50	53	85	
18603	ENU02397	ANI61C2838: 45-64 298..805	45-64	488-510	NAP		g1850766	614	144	1.00E-56	86	86	
18604	ENU02398	ANI61C4555: 47-79 28..535	47-79	491-512	NAP		g4589686	210	100	1.00E-20	33	16	
18605	ENU02399	ANI61C7287: 45-66 842..750	45-66	492-511	NAP		g1176711	137	59	0.000000 03	22	89	
18606	ENU02400	ANI50C1_10 35:32..540	40-59	480-506	NAP		g131056		237	4.00E-62	69	60	
18607	ENU02401	ANI61C5560: 53-73 638..129	53-73	501-520	NAP		g1353046	190	45	0.0003	37	22	
18608	ENU02402	ANI61C9150: 26-50 217..726	26-50	464-493	NAP		g1911486	388	90	4.00E-34	51	52	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18609	ENU02403	ANI61C8849: 225..734	72-93	520-539	NAP		g2497193	499	152	2.00E-36	44	33	hypothetical 56.2 KD protein in ERG8-UBP8 intergenic region ; probable membrane protein YMR221c - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae] (AL031349) N-acetyltransferase [Schizosaccharomyces pombe] (Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi] sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
18610	ENU02404	ANI61C6707: 62-81	62-81	508-530	NAP		g3451464	370	111	1.00E-35	59	88	
18611	ENU02405	ANI61C5252: 65-90	65-90	505-533	NAP		g3549891	562	102	2.00E-21	46	28	
18612	ENU02406	ANI61C4094: 22-47	22-47	472-491	NAP		g1711561	283	110	6.00E-24	34	29	
18613	ENU02407	ANI61C3490: 22-45	22-45	472-491	NAP		g3851164	163	62	0.000000	23	32	(AF097181) tuftelin-interacting protein 10 [Mus musculus]
18614	ENU02408	ANI61C7357: 70-96	70-96	521-540	NAP		g4204901	215	71	7.00E-12	38	66	(U57100) orf256; putative triose phosphate isomerase [Brucella abortus]
18615	ENU02409	ANI61C5347: 46-65	46-65	495-516	NAP		g3929399		96	1.00E-19			proline-specific permease (proline transport protein) ; (X79797) proline permease [Emmericella nidulans]
18616	ENU02410	ANI61C6339: 34-54	34-54	480-506	NAP		g1352881	180	66	2.00E-10	37	94	hypothetical 15.7 KD protein in NUP85-SSC1 intergenic region ; probable membrane protein YJR044c - yeast (Saccharomyces cerevisiae) ; (Z49544) ORF YJR044c [Saccharomyces cerevisiae] ; (L36344) ORF; putative [Saccharomyces cerevisiae]
18617	ENU02411	ANI61C6057: 60-79	60-79	512-533	NAP		g4150918	288	113	7.00E-28	50	70	(Z50728) putative acetyltransferase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18618	ENU02412	ANI61C3771: 875..359	22-41	470-496	NAP		g417274	407	181	3.00E-45			mitochondrial import inner membrane translocase subunit TIM23
													3) (mitochondrial protein import protein MAS6) (membrane import machinery protein MIM23) ; mitochondrial inner membrane protein MIM23 - yeast (Saccharomyces cerevisiae) ; (X71633) MAS6 [Saccharomyces cerevisiae] ; (X74161) MIM23 [Saccharomyces cerevisiae] ; (Z71632) ORF YNR017w [Saccharomyces cerevisiae] (AF048992) ribonuclease H1 [Schizosaccharomyces pombe] (AL031535) transcription initiation factor tfiid 60 kd subu nit [Schizosaccharomyces pombe] (X96943) Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi] (AL033391) hypothetical membrane protein [Candida albicans] (Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi] hypothetical 63.0 KD protein in PYC2-PDB1 intergenic region ; probable membrane protein YBR220c - yeast (Saccharomyces cerevisiae) ; (Z36088) ORF YBR220c [Saccharomyces cerevisiae]
18619	ENU02413	ANI61C9517: 44-63	44-63	500-519	NAP		g2911504	332	94	4.00E-25	44	55	
18620	ENU02414	ANI61C1044 1144..627 0:584..1101	44-63	500-519	NAP		g3560272	594	84	7.00E-16	38	36	
18621	ENU02415	ANI61C1050 36-55 5:5005..5523	36-55	491-512	NAP		g1524045	459	132	1.00E-30	42	38	
18622	ENU02416	ANI61C3996: 23-44 6129..5611	23-44	480-499	NAP		g3850125	542	115	2.00E-25	41	32	
18623	ENU02417	ANI61C8551: 32-54 3297..2779	32-54	489-508	NAP		g3549879	436	88	1.00E-22	40	28	
18624	ENU02418	ANI61C1086 60-79 9:3385..3906	60-79	520-539	NAP		g586338	913	126	9.00E-29	43	26	
18625	ENU02419	ANI61C4950: 27-58 575..54	27-58	486-506	NAP		g3850144	198	75	1.00E-17	36	60	
18626	ENU02420	ANI61C9832: 22-57 82..604	22-57	483-502	NAP		g1706102	133	77	7.00E-14	32	11	
													"Cleavage and polyadenylation specificity factor, 160 KD subunit (CPSF 160 KD subunit) ; (U37012) cleavage and polyadenylation specificity factor [Homo sapiens] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18627	ENU02421	ANI61C6709: 1093..571	23-46	472-503	NAP		g2500360	157	64	6.00E-15	38	60	60S ribosomal protein L14; ribosomal protein L14 - rat; (X94242) ribosomal protein L14 [Rattus norvegicus]
18628	ENU02422	ANI61C5035: 40-60	23-46	499-521	NAP		g1723738	548	164	4.00E-40	43	34	hypothetical 55.1 KD protein in TRX1-RTA1 intergenic region; hypothetical protein YGR211w - yeast (Saccharomyces cerevisiae); (Z72996) ORF YGR211w [Saccharomyces cerevisiae]; (AF019769) zinc finger protein [Saccharomyces cerevisiae] (U81509) urease [Coccidioides immitis] (U68040) polyketide synthase [Cochliobolus heterostrophus] (U61840) sodium transport ATPase FST [Fusarium solani f. sp. pisi] (X96943)
18629	ENU02423	ANI61C1400: 36-55	36-55	497-517	NAP		g2580518	3042	136	5.00E-39	66	15	Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi] "(AE000952) methylmalonyl-CoA decarboxylase, biotin carboxyl carrier subunit (mmdC) [Archaeoglobus fulgidus]" (AE000855) endonuclease III [Methanobacterium thermoautotrophicum]
18630	ENU02424	ANI61C1002: 29-48	29-48	489-510	NAP		g1546072	1185	68	5.00E-11	29	6	"CAT5 protein (ubiquinone biosynthesis protein COQ7); CAT5 protein - yeast (Saccharomyces cerevisiae); (X82930) CAT5 [Saccharomyces cerevisiae]; (X90518) putative [Saccharomyces cerevisiae]; (X94335) YOR3284c [Saccharomyces cerevisiae]; (Z75033) ORF YOR125c [Saccharomyces cerevisiae]; (S81938) COQ7 [Saccharomyces cerevisiae, Peptide, 272 aa] [Saccharomyces cerevisiae]" (AE000352) putative transport protein [Escherichia coli]
18631	ENU02425	ANI61C1767: 53-74	53-74	510-534	NAP		g1438947	697	272	1.00E-72	67	35	
18632	ENU02426	ANI61C1570: 22-53	22-53	484-503	NAP		g1524045	385	66	8.00E-17	42	33	
18633	ENU02427	ANI61C2430: 22-53	22-53	474-504	NAP		g2648307	127	59	0.000000	32	99	
18634	ENU02428	ANI61C8832: 54-73	54-73	516-536	NAP		g2621854	84	52	0.000002	29	52	
18635	ENU02429	ANI61C303:9 28-48	28-48	491-510	NAP		g1168783	381	118	1.00E-34			
18636	ENU02430	ANI61C3361: 34-53	34-53	498-517	NAP		g1789036	257	61	0.000000	33	56	
		637..112							008				

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18637	ENU02431	ANI61C9483: 32-51 965..1490	48-67	484-515	NAP		g133887	234	94	8.00E-19	54	96	"mitochondrial ribosomal protein S24 ; ribosomal protein S16, mitochondrial - Neurospora crassa ; (X06360) cyt-21 [Neurospora crassa] ; (J03533) ribosomal protein S-24 [Neurospora crassa]"
18638	ENU02432	ANI61C2362: 48-67 805..1330	48-67	510-531	NAP		g699196	316	104	4.00E-22			(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]
18639	ENU02433	ANI61C9152: 63-82 6161..6686	63-82	525-546	NAP		g133336	145	53	1.00E-12			DNA-directed RNA polymerase II 32 KD polypeptide (B32) ; DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB4 - yeast (Saccharomyces cerevisiae) ; (X58099) RPB4 cerevisiae] ; (X58099) RPB4 [Saccharomyces cerevisiae] ; (M27253) RNA polymerase II subunit RPB4 [Saccharomyces cerevisiae] ; (X87371) RNA polymerase II subunit 4 [Saccharomyces cerevisiae] ; (Z49415) ORF YJL140w [Saccharomyces cerevisiae]
18640	ENU02434	ANI61C2487: 61-82 2519..1994	61-82	525-544	NAP		g2983039	285	132	2.00E-30	41	30	(AE000686) proline-tRNA synthetase [Aquifex aeolicus]
18641	ENU02435	ANI50C3497 28-47 5_1:867..341	28-47	492-512	NAP		g462739		109	2.00E-23	38	26	NPL4 protein ; NPL4 protein - yeast (Saccharomyces cerevisiae) ; (X72224) NPL4 [Saccharomyces cerevisiae] ; (X74437) open reading frame YBR12.31 [Saccharomyces cerevisiae] ; (Z36039) ORF YBR170c [Saccharomyces cerevisiae]
18642	ENU02436	ANI61C383:5 61-80 5..581	61-80	526-545	NAP		g399112	199	91	6.00E-18	33	16	beta-galactosidase (lactase) ; beta-galactosidase (EC 3.2.1.23) - yeast (Kluyveromyces marxianus var. lactis) ; (M84410) beta-D-galactosidase [Kluyveromyces lactis]
18643	ENU02437	ANI61C6528: 28-49 2573..3100	28-49	488-513	NAP		g3880440	190	69	2.00E-11	32	96	(Z82062) cDNA EST yk415c12.5 comes from this gene [Caenorhabditis elegans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18644	ENU02438	ANI61C6109: 1824..1296	23-43	482-509	NAP		g3123100	351	99	6.00E-33	50	99	"hypothetical 15.9 KD protein C4A8.02C in chromosome I; (Z98762) SPAC4A8.02c, unknown, len:142aa, similar eg. to YJBQ_ECOLI_P32698, hypothetical 15.7 kd protein, (138aa), fast a scores, opt:403, E0: 2.4e-32, (41.0% identity in 134 aa overlap) [Schizosaccharomyces pombe] "
18645	ENU02439	ANI61C5925: 38-57 1611..1083	38-57	504-524	NAP		g543649	245	86	2.00E-21	53	91	hypothetical protein 133 - Rhodococcus erythropolis (fragment); (D14454) P47K protein [Rhodococcus erythropolis]; ORF P47K [Rhodococcus erythropolis] Pyridoxamine 5'-phosphate oxidase (PNP/PMP oxidase); pyridoxamine-phosphate oxidase (EC 1.4.3.5) - yeast (Saccharomyces cerevisiae); (X76992) pyridoxamine-phosphate oxidase [Saccharomyces cerevisiae]; (X76078) YBR0321 [Saccharomyces cerevisiae]; (Z35904) ORF YBR035c [Saccharomyces cerevisiae]; ORF YBR0321 [Saccharomyces cerevisiae] (AL023554) zinc finger protein [Schizosaccharomyces pombe] (AF034090) MAPKK kinase [Neurospora crassa] SAP1 protein; hypothetical protein YER047c - yeast (Saccharomyces cerevisiae); (U18796) Yer047cp [Saccharomyces cerevisiae] (AJ000084) putative acetyl transferase [Proteus mirabilis] sterigmatocystin 7-O-methyltransferase precursor; (L25836) O-methyltransferase [Aspergillus flavus] hypothetical 59.3 KD protein C17C9.16C in chromosome I; (Z73099) hypothetical protein [Schizosaccharomyces pombe]
18646	ENU02440	ANI61C7364: 22-50 2988..3517	22-50	490-509	NAP		g585656	249	86	2.00E-16			
18647	ENU02441	ANI61C137:1 22-42 940..1410	22-42	484-510	NAP		g3133097	114	48	0.00005	30	35	
18648	ENU02442	ANI61C1321: 23-47 82..612	23-47	490-511	NAP		g2654103	751	250	4.00E-66	67	25	
18649	ENU02443	ANI61C7991: 27-55 555..23	27-55	496-516	NAP		g731461	793	138	4.00E-41	57	19	
18650	ENU02444	ANI61C8177: 61-81 4238..3705	61-81	531-550	NAP		g3395518	124	60	0.000000	28	88	
18651	ENU02445	ANI61C3627: 56-77 3038..3570	56-77	525-546	NAP		g2498701	127	63	0.000000	33	37	
18652	ENU02446	ANI61C8243: 41-62 920..388	41-62	507-531	NAP		g1723574	549	74	8.00E-13	33	33	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18653	ENU02447	ANI61C8767: 2767..2233	28-48	501-520	NAP		g3334833		66	2.00E-10			(AJ007932) ketoreductase [Streptomyces argillaceus]
18654	ENU02448	ANI61C4182: 35-54		497-528	NAP		g2330829	826	182	2.00E-45	52	11	(Z98530) hypothetical protein [Schizosaccharomyces pombe]
18655	ENU02449	ANI61C7614: 28-47		502-521	NAP		g118066	259	104	5.00E-22	35	32	cyclohexanone monooxygenase; (M19029) cyclohexanone monooxygenase [Acinetobacter sp.]
18656	ENU02450	ANI61C6208: 32-51		503-525	NAP		g1350839	257	114	5.00E-25	52	60	RIBOSE 5-phosphate isomerase (phosphoRIBOisomerase); (L35034) ribose 5-phosphate isomerase [Mus musculus]
18657	ENU02451	ANI61C8852: 60-79		530-554	NAP		g2832629		60	0.000000			(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]
18658	ENU02452	ANI61C1084: 39-60		513-534	NAP		g2131743	361	129	1.00E-29	52	85	hypothetical protein YLR009w - yeast (Saccharomyces cerevisiae); (Z73181) ORF YLR009w [Saccharomyces cerevisiae]
18659	ENU02453	ANI61C1271: 44-63		517-539	NAP		g1729996	667	228	2.00E-59	62	60	TOXD protein; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]
18660	ENU02454	ANI61C1190: 25-44		502-522	NAP		g999873	616	106	9.00E-23	49	51	Lipase (E.C.3.1.1.3) (Triacylglycerol Acylhydrolase)
18661	ENU02455	ANI61C1070: 29-49		506-526	NAP		g1351617	728	138	4.00E-32	45	31	hypothetical 62.6 KD protein C29E6.02 in chromosome I; (Z66525) unknown [Schizosaccharomyces pombe]
18662	ENU02456	ANI61C2194: 46-72		524-543	NAP		g1705519	153	68	3.00E-12	31	31	Benzaldehyde lyase (benzoic aldolase) (BL) (BZL); (U04048) benzaldehyde lyase [Pseudomonas fluorescens]
18663	ENU02457	ANI61C3754: 24-47		496-521	NAP		g2498971	574	110	8.00E-24	32	36	putative sterigmatocystin biosynthesis monooxygenase STCW; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans]
18664	ENU02458	ANI61C9710: 22-44		487-520	NAP		g3192040	147	48	0.00004	28	98	(AL023796) hypothetical protein [Schizosaccharomyces pombe]

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18665	ENU02459	ANI61C7140: 29-48 54..594	505-527	NAP			g4505495	239	104	6.00E-22			8-oxoguanine DNA glycosylase ; (Y11731) DNA glycosylase/AP lyase [Homo sapiens] ; (Y11838) 8-oxoguanine DNA glycosylase homolog 1 [Homo sapiens] ; (AB000410) hOGG1 [Homo sapiens] ; (AF003595) 8-oxoguanine DNA glycosylase 1 [Homo sapiens] ; (U88527) 8-hydroxyguanine glycosylase/lyase [Homo sapiens]
18666	ENU02460	ANI61C3964: 40-59 3178..2638	515-538	NAP			g2492754	582	76	1.00E-18	42	57	sorbitol utilization protein SOU1 ; (AF002134) Sou1p [Candida albicans]
18667	ENU02461	ANI61C2208: 61-80 1388..848	540-559	NAP			g1730712	372	78	4.00E-14	29	35	hypothetical 56.2 KD protein in UME3-HDA1 intergenic region ; hypothetical protein YNL022c - yeast (Saccharomyces cerevisiae) ; (Z71298) ORF YNL022c [Saccharomyces cerevisiae]
18668	ENU02462	ANI61C6637: 36-57 72..613	512-535	NAP			g172203	276	101	5.00E-21	41	17	(M29688) DNA mismatch repair protein [Saccharomyces cerevisiae]
18669	ENU02463	ANI61C9213: 48-71 1179..638	523-547	NAP			g3642873	690	257	3.00E-68	66	85	(AF026523) manganese superoxide dismutase; Mn-SOD [Penicillium chrysogenum] ; (AF026790) manganese superoxide dismutase [Penicillium chrysogenum]
18670	ENU02464	ANI61C8484: 52-71 726..1267	532-551	NAP			g1470090	92	50	0.00001	27	38	(U62028) negative acting factor [Fusarium solani f. sp. pisi]

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18671	ENU02465	ANI61C1889: 845..304	41-61	516-540	NAP		g1346554	42	0.000000	1			probable myosin regulatory light chain ; (Z46793) similar to myosin regulatory light chain 2; cDNA EST
													EMBL:T01273 comes from this gene; cDNA EST EMBL:C09382 comes from this gene; cDNA EST EMBL:C07858 comes from this gene; cDNA EST yk404h11.3 comes from this gene; cDN... ; (Z34801) similar to myosin regulatory light chain 2; cDNA EST EMBL:T01273 comes from this gene; cDNA EST EMBL:C09382 comes from this gene; cDNA EST EMBL:C07858 comes from this gene; cDNA EST yk404h11.3 comes from this gene; cDN...
18672	ENU02466	ANI61C7908: 1440..1982	50-69	526-550	NAP		g3929362	397	97	3.00E-24	41	29	Pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVI]
18673	ENU02467	ANI61C2918: 161..705	49-68	526-550	NAP		g118572	180	59	0.000000			Granaticin polyketide synthase putative ketoacyl reductase 2 (ORF6) ; granaticin-producing polyketide synthase chain 6 - Streptomyces violaceoruber ; (X16144) ketoacyl reductase (AA 1-289) [Streptomyces violaceoruber] ; (X16300) ORF 6 (AA 1-249) [Streptomyces violaceoruber] ; (AJ011500) gra-orf6 [Streptomyces violaceoruber]
18674	ENU02468	ANI61C6924: 396..939	34-53	516-535	NAP		g4503609	375	50	3.00E-19			"electron-transfer-flavoprotein, beta polypeptide ; electron transfer flavoprotein beta-subunit (beta-ETF) ; electron transfer flavoprotein beta chain - human ; Chain B, Three-Dimensional Structure Of Human Electron Transfer Flavoprotein To 2.1 A Resolution ; (X71129) electron transfer flavoprotein beta subunit [Homo sapiens] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18675	ENU02469	ANI61C1036 7:900..1447	37-56	521-540	NAP		g3560474	209	80	2.00E-19	32	51	(U81312) S-adenosyl-methionine-sterol-C- methyltransferase [Nicotiana tabacum]
18676	ENU02470	ANI61C1112 2:63..608	72-93	556-575	NAP		g450864	536	198	2.00E-50	54	32	(L27993) alkaline phosphatase [Neurospora crassa]
18677	ENU02471	ANI61C4008: 89..634	32-56	512-535	NAP		g731922	414	130	8.00E-30	43	64	"hypothetical oxidoreductase in LYS1-HYR1 intergenic region ; probable membrane protein YIR035c - yeast (Saccharomyces cerevisiae) ; (Z38061)orf, len 254, CAI: 0.24, 52.1% similar to orf complement(33925..34716), similar to DHII_human P28845 corticosteroid 11-beta-dehydrogenase [Saccharomyces cerevisiae] "
18678	ENU02472	ANI61C2566: 547..1	53-77	533-557	NAP		g2497980	772	203	6.00E-75	83	51	"ADP,ATP carrier protein (ADP/ATP translocase) (adenine nucleotide translocator) (ANT) ; (Z49974) adenine nucleotide carrier [Schizosaccharomyces pombe] ; (AL023634) adp/atp translocase [Schizosaccharomyces pombe] "
18679	ENU02473	ANI61C3960: 1663..2211	23-51	503-529	NAP		g1351687	108	49	0.00002	28	98	hypothetical 17.2 KD protein C3H1.03 in chromosome I ; (Z68144) hypothetical protein [Schizosaccharomyces pombe]
18680	ENU02474	ANI61C8321: 87..635	50-76	536-556	NAP		g3023267	658	212	6.00E-65	66	18	alpha-glucosidase precursor (maltase) ; (D45356) alpha-galactosidase [Aspergillus niger]
18681	ENU02475	ANI61C6620: 826..1376	43-64	531-551	NAP		g2916970	194	33	1.3			(AL022002) hypothetical protein Rv1672c [Mycobacterium tuberculosis]
18682	ENU02476	ANI61C3952: 556..331	72-91	560-580	NAP		g124205	193	62	0.000000			eukaryotic translation initiation factor 2 beta subunit (EIF-2-beta) ; translation initiation factor eIF-2 beta chain - yeast (Saccharomyces cerevisiae) ; (M21813) translation initiation factor eIF2 beta-subunit [Saccharomyces cerevisiae] ; (Z67751) SUI3 [Saccharomyces cerevisiae] ; (Z73594) ORF YPL237w [Saccharomyces cerevisiae]
18683	ENU02477	ANI61C5937: 1283..733	31-53	520-539	NAP		g2950465	215	76	3.00E-18	38	39	[Saccharomyces cerevisiae] (AL022071) fructosyl amine [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18684	ENU02478	ANI61C8339: 1637..1087	25-44	512-533	NAP		g1730644	243	100	1.00E-20	28	27	hypothetical 73.4 KD protein in ERG24-MET2 intergenic region ; probable membrane protein YNL279w - yeast (Saccharomyces cerevisiae) ; (Z71555) ORF YNL279w [Saccharomyces cerevisiae] (AL032681) putative hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe] "beta-galactosidase precursor (lactase) ; (L06037) beta-D-galactosidase [Aspergillus niger] ; (S37150) beta-galactosidase [Aspergillus niger, Peptide, 1006 aa] [Aspergillus niger] ; beta galactosidase [Aspergillus niger]" (AL035064) queuine tma-ribosyltransferase [Schizosaccharomyces pombe] Rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans] (AL023590) amino acid permease [Schizosaccharomyces pombe] hypothetical 61.8 KD peptidase in MPR1-GCN20 intergenic region ; probable membrane protein YFR006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFR006W [Saccharomyces cerevisiae] (X76302) nucleic acid binding protein [Homo sapiens] (AF029913) unknown [Cochliobolus heterostrophus] ; (AF027687) unknown [Cochliobolus heterostrophus] hypothetical 27.3 KD protein in REF2-CBS2 intergenic region ; hypothetical protein YDR196c - yeast (Saccharomyces cerevisiae) ; (Z48784) unknown [Saccharomyces cerevisiae]
18685	ENU02479	ANI61C1708: 22-51	2796..3346	509-530	NAP		g3810866		60	0.000000			
18686	ENU02480	ANI61C1532: 39-58	364..915	518-548	NAP		g461623	823	146	1.00E-34	53	17	
18687	ENU02481	ANI61C9801: 23-45	99..650	513-532	NAP		g4106673	413	153	6.00E-37	54	38	
18688	ENU02482	ANI61C1130: 65-84	220..771	555-574	NAP		g133264	313	66	4.00E-14	59	81	
18689	ENU02483	ANI61C1027 69-88	1:1045..1597	560-579	NAP		g3136040	706	142	2.00E-33	39	34	
18690	ENU02484	ANI61C9766: 32..584	47-66	535-557	NAP		g1175977	465	136	1.00E-31	37	34	
18691	ENU02485	ANI61C8436: 37-64	110..662	519-547	NAP		g431953	194	39	0.023	36	80	
18692	ENU02486	ANI61C6527: 24-53	3954..3401	516-535	NAP		g2583216	389	152	1.00E-36	47	82	
18693	ENU02487	ANI61C1190: 47-66	915..361	540-559	NAP		g2833198	332	128	3.00E-29	52	67	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18694	ENU02488	ANI61C3516: 1458..2012	29-48	522-541	NAP		g3687456	303	127	8.00E-30	44	97	(AL031798) hypothetical protein [Schizosaccharomyces pombe]
18695	ENU02489	ANI50C392_2:841..394	22-50	515-535	NAP		g2144770	209	209	1.00E-53	65	59	"acidic ribosomal protein P0.e, cytosolic - yeast (Saccharomyces cerevisiae) ; (M37326) ribosomal protein L10e [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (M26506) L10e protein [Saccharomyces cerevisiae] ; (U19028) Rpl10ep [Saccharomyces cerevisiae] "
18696	ENU02490	ANI61C7084: 24-43	24-43	518-537	NAP		g2414606	252	104	6.00E-22	46	94	(Z99295) hypothetical protein [Schizosaccharomyces pombe]
18697	ENU02491	ANI61C7236: 27-48	27-48	522-541	NAP		g548420	373	84	6.00E-31	54	90	mitochondrial import receptor subunit TOM20 (mitochondrial 20 KD outer membrane protein) (MOM19 protein) (translocase of outer membrane 20 KD subunit) ; (M80528) mitochondrial outer membrane protein 19 [Neurospora crassa]
18698	ENU02492	ANI61C7717: 68-87	68-87	550-583	NAP		g4456822	352	141	5.00E-33	42	100	(AL035548) hypothetical oligoribonuclease [Schizosaccharomyces pombe]
18699	ENU02493	ANI61C4632: 68-87	68-87	564-583	NAP		g2351250	325	89	3.00E-17	43	25	(U23425) ropy-2 [Neurospora crassa]
18700	ENU02494	ANI61C1096 1025..468	71-97	554-587	NAP		g2498530	198	100	9.00E-21	40	56	mitochondrial inheritance component MDM12 ; (U64674) mitochondrial inheritance component Mdm12p [Schizosaccharomyces pombe]
18701	ENU02495	ANI61C1484: 50-83	50-83	546-567	NAP		g2708305	766	154	2.00E-43	47	35	(AF016369) U4/U6 small nuclear ribonucleoprotein hPrp4 [Homo sapiens]
18702	ENU02496	ANI61C3181: 42-65	42-65	537-559	NAP		g1054845	1435	159	2.00E-57	62	39	(X92680) allelic to VPS4 [Saccharomyces cerevisiae]
18703	ENU02497	ANI61C9072: 72-94	72-94	569-589	NAP		g1764098	178	31	0.000003	37	20	(U81794) putative permease [Uromyces fabae]
18704	ENU02498	ANI61C2133: 66-88	66-88	562-584	NAP		g1877327	60	60	0.000000	01		(Z92771) hypothetical protein Rv3272 [Mycobacterium tuberculosis]

Seq num	Seq id	Contig	Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18705	ENU02499	ANI61C884:7	03..143	29-49	528-547	NAP		g2500493	324	98	3.00E-27	66	97	putative 40S ribosomal protein in SNF2-CPA1 intergenic region ; ribosomal protein S10.c.A - yeast (Saccharomyces cerevisiae) ; (Z75201) ORF YOR293w [Saccharomyces cerevisiae]
18706	ENU02500	ANI61C8267: 774..213	45-66	543-564	NAP			g481285	342	130	9.00E-30	38	26	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger ; (Z26938) NADPH cytochrome P450 oxidoreductase [Aspergillus niger] ; NADPH cytochrome P450 reductase [Aspergillus niger] (AJ223998) PCZA361.9 [Amycolatopsis orientalis] (AL023592) putative phosphatidylinositol- glycan-class c protein [Schizosaccharomyces pombe] myoSIN-2 isoform ; myosin myo2 - yeast (Saccharomyces cerevisiae) ; (M35532) myosin 1 isoform (myo2) [Saccharomyces cerevisiae] ; (Z75234) ORF YOR326w [Saccharomyces cerevisiae]
18707	ENU02501	ANI61C8414: 2231..2792	48-67	548-567	NAP			g2894160	229	71	4.00E-18	38	59	Deoxyribose-phosphate aldolase (phosphodeoxyriboaldolase) (deoxyriboaldolase) ; deoxyribose aldolase (deoC) homolog - Haemophilus influenzae (strain Rd KW20) ; (U32791) deoxyribose-phosphate aldolase (deoC) [Haemophilus influenzae Rd]
18708	ENU02502	ANI61C9773: 2244	2245..1683	523-542	NAP			g3136049	270	129	2.00E-29	40	56	hypothetical protein YOR171c - yeast (Saccharomyces cerevisiae) ; (U55021) O3615p [Saccharomyces cerevisiae] ; (Z75078) ORF YOR171c [Saccharomyces cerevisiae] (AF027979) carnitine acetyl transferase [Magnaporthe grisea] (Z97210) hypothetical protein [Schizosaccharomyces pombe]
18709	ENU02503	ANI61C8325: 3431..2869	54-75	553-574	NAP			g127736	322	62	4.00E-18	43	9	
18710	ENU02504	ANI61C3214: 2968..2406	56-76	557-576	NAP			g1169268	326	108	2.00E-23	43	81	
18711	ENU02505	ANI61C1078	44-65	546-565	NAP			g2132075	519	117	5.00E-26	30	30	
18712	ENU02506	ANI61C8080: 10..573	31-59	533-552	NAP			g2688966	991	259	1.00E-68	64	30	
18713	ENU02507	ANI61C1189: 9840..9276	41-60	539-563	NAP			g2239219	194	46	0.000000	34	79	

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18714	ENU02508	ANI61C6833: 52-71 2401..1837	52-71	553-574	NAP		g3041696	845	214	4.00E-55	63	60	"Acetolactate synthase small subunit precursor (AHAS) (acetohydroxy-acid synthase small subunit) (ALS) ; (X59720) YCL009c, len:309 [Saccharomyces cerevisiae] " (AL023518) Tall p transaldolase [Schizosaccharomyces pombe] (U65685) phosphoinositide-specific phospholipase C [Botryotinia fuckeliana] hypothetical 117.8 KD protein in STE2-FRS2 intergenic region ; probable membrane protein YFL025c - yeast (Saccharomyces cerevisiae) ; (D50617) YFL025C [Saccharomyces cerevisiae]
18715	ENU02509	ANI61C7768: 72-91 51..615	72-91	575-594	NAP		g3130049	632	142	4.00E-51	69	52	
18716	ENU02510	ANI61C5105: 70-91 1804..1239	70-91	573-593	NAP		g1762781	477	198	2.00E-50	51	18	
18717	ENU02511	ANI61C6332: 69-96 6021..5456	69-96	573-592	NAP		g1175934	861	61	3.00E-14	34	15	
18718	ENU02512	ANI61C9824: 65-90 3254..3820	65-90	570-589	NAP		g2370595	1364	167	6.00E-41	60	19	(AJ001414) GTPase activating protein [Yarrowia lipolytica]
18719	ENU02513	ANI61C1043 47-67 5:2496..3062	47-67	552-571	NAP		g2492633	987	207	4.00E-53	56	44	probable glutaryl-CoA dehydrogenase precursor (GCD) ; (Z66513) similar to acyl-CoA dehydrogenase; cDNA EST EMBL:D70283 comes from this gene; cDNA EST EMBL:D66714 comes from this gene; cDNA EST EMBL:D70641 comes from this gene; cDNA EST EMBL:D70573 comes from this gene; cDNA EST EM... (AB015054) Alg2 [Rhizomucor pusillus] ; (AB015055) Alg2 [Rhizomucor pusillus]
18720	ENU02514	ANI61C4425: 27-47 625..1191	27-47	532-551	NAP		g3868940	433	84	6.00E-25	42	40	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18721	ENU02515	ANI61C1211: 35-65 2342..1775	541-560	541-560	NAP		g4506439	556	129	4.00E-47			retinoblastoma-binding protein 7 ; histone acetyltransferase type B subunit 2 (retinoblastoma binding protein P46) (retinoblastoma-binding protein 7) ; retinoblastoma-binding protein RbAp46 - human ; (X72841) IEF 7442 [Homo sapiens] ; (U35143) retinoblastoma-binding protein RbAp46 [Homo sapiens] ; (AF090306) retinoblastoma binding protein [Rattus norvegicus] ; retinoblastoma-binding protein [Homo sapiens] glucose 1-dehydrogenase IV (GLCDH-IV) ; glucose 1-dehydrogenase (EC 1.1.1.47) - Bacillus megaterium ; (D10626) glucose dehydrogenase [Bacillus megaterium] "(AC006550) Belongs to PF01121 Uncharacterized protein family UPF0038 containing ATP/GTP binding domain. ESTs gb AA585719, gb AA728503 and gb T22272 come from this gene. [Arabidopsis thaliana] " (U81827) 8 kDa cytoplasmic dynein light chain [Emmericella nidulans] (D85924) myosin [Mus musculus] (AL021748) hypothetical protein [Schizosaccharomyces pombe] casein kinase I homolog HHP1 ; hhp1 protein - fission yeast (Schizosaccharomyces pombe) ; casein kinase-I homolog hhp1 - Yeast (Schizosaccharomyces pombe) ; (X78871) Hhp1 protein kinase [Schizosaccharomyces pombe] ; (U10863) casein kinase-1 [Schizosaccharomyces pombe] ; (AL031261) casein kinase i homologue [Schizosaccharomyces pombe]
18722	ENU02516	ANI61C4036: 50-69 774..204	559-576	559-576	NAP		g729327	166	41	0.0006	25	47	
18723	ENU02517	ANI61C3865: 60-81 560..1128	566-586	566-586	NAP		g4587575	251	109	1.00E-23	39	59	
18724	ENU02518	ANI61C6288: 48-68 2459..3027	551-574	551-574	NAP		g4099025	316	62	2.00E-16	84	97	
18725	ENU02519	ANI61C7365: 46-65 6599..6031	549-572	549-572	NAP		g1945080		48	0.00005			
18726	ENU02520	ANI61C1062 30-51 8:4588..4018	538-558	538-558	NAP		g2842503	301	80	5.00E-27	43	75	
18727	ENU02521	ANI61C6548: 44-63 662..91	553-572	553-572	NAP		g729712	1373	225	2.00E-58			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18728	ENU02522	ANI61C1038 8:11908..1247 9	43-68	553-572	NAP		g2842501		81	7.00E-15			(AL021748) putative quinone oxidoreductase [Schizosaccharomyces pombe]
18729	ENU02523	ANI61C7455: 23-42 5596..6167		533-552	NAP		g4506235	165	69	2.00E-11	36	73	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 9 ; 26S proteasome regulatory subunit P27 ; (AB003177) proteasome subunit p27 [Homo sapiens] "
18730	ENU02524	ANI61C1020 0:931..1503	61-80	561-591	NAP		g3929392	633	201	4.00E-62	82	57	vacuolar ATP synthase subunit D (V-ATPase D subunit) ; (AF032320) vacuolar ATPase subunit D [Neurospora crassa]
18731	ENU02525	ANI50C1_10 10:1592..1019	26-46	538-557	NAP		g416837		84	6.00E-16	34	40	cytochrome P450-TERP (cytochrome P450 108) ; cytochrome P450terp - Pseudomonas sp ; (M91440) P450terp [Pseudomonas sp.]
18732	ENU02526	ANI61C8486: 42-64 319..894		554-574	NAP		g3560214	806	207	5.00E-53	67	30	(AL031536) trna splicing protein [Schizosaccharomyces pombe]
18733	ENU02527	ANI61C9210: 62-83 378..952		572-594	NAP		g126192	739	106	2.00E-22			2-isopropylmalate synthase (alpha-isopropylmalate synthase) (alpha-IPM synthetase) ; 2-isopropylmalate synthase (EC 4.1.3.12) - yeast (Saccharomyces cerevisiae) ; (M12893) alpha-isopropylmalate synthase (EC 4.1.3.12) long form [Saccharomyces cerevisiae] ; (Z50161) 2-isopropylmalate Synthase [Saccharomyces cerevisiae] ; (Z71380) ORF YNL104c [Saccharomyces cerevisiae]
18734	ENU02528	ANI61C6322: 55-73 2524..1949	55-73	569-588	NAP		g3873823	169	59	0.000000	39	72	(Z73422) predicted using Genefinder [Caenorhabditis elegans]
18735	ENU02529	ANI61C5608: 71-91 1306..731	71-91	581-604	NAP		g1173624	114	65	3.00E-10	27	36	(U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid SM9108']
18736	ENU02530	ANI61C8209: 43-62 1438..2014	43-62	557-577	NAP		g3114281	437	186	9.00E-47	46	84	"Chain M, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain 1, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution "

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18737	ENU02531	ANI61C1107 9:1871..1295	22-44	536-556	NAP		g1730718	297	140	8.00E-33	43	31	probable mannosyltransferase KTR5 ; probable membrane protein YNL029c - yeast (Saccharomyces cerevisiae) ; (Z71305) ORF YNL029c [Saccharomyces cerevisiae]
18738	ENU02532	ANI61C1137 9:845..1423	56-75	563-591	NAP		g731738	596	122	3.00E-27	37	12	DNA replication helicase DNA2 ; probable purine nucleotide-binding protein YHR164c - yeast (Saccharomyces cerevisiae) ; (U00027) Dna2p: DNA replication helicase [Saccharomyces cerevisiae]
18739	ENU02533	ANI61C2857: 24-59 3..580	24-59	533-559	NAP		g2130462	205	100	7.00E-21	36	30	poly A polymerase (EC 2.7.7.-) - fission yeast (Schizosaccharomyces pombe) ; (X79705) polymerase [Schizosaccharomyces pombe] ; (AL035216) poly A polymerase [Schizosaccharomyces pombe] DNA-directed RNA polymerase II 14.2 KD polypeptide (B12.6) ; DNA- directed RNA polymerase (EC 2.7.7.6) II chain RPB9 - yeast (Saccharomyces cerevisiae) ; (M73060) RNA polymerase II subunit RPB9 [Saccharomyces cerevisiae] ; (Z72592) ORF YGL070c [Saccharomyces cerevisiae]
18740	ENU02534	ANI61C3020: 34-54 2005..2582	34-54	543-569	NAP		g133341	289	91	6.00E-18	51	96	hypothetical 74.4 KD protein C30D11.09 in chromosome I ; hypothetical protein SPAC30D11.09 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe] (Z99111) similar to glucose 1- dehydrogenase [Bacillus subtilis] (AF008220) yteR [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18741	ENU02535	ANI61C2411: 53-72 4214..3636	53-72	570-589	NAP		g1351662	660	205	2.00E-52	48	30	
18742	ENU02536	ANI61C9242: 36-57 72..651	36-57	553-573	NAP		g2633748	305	94	6.00E-19	38	76	
18743	ENU02537	ANI61C8858: 23-45 580..1	23-45	536-560	NAP		g2293194	303	99	3.00E-20			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18744	ENU02538	ANI61C508:2 051..1472	28-56	545-565	NAP		g1077558		33	0.005			hypothetical protein YDR063w - yeast (Saccharomyces cerevisiae) ; (X84162) unknown [Saccharomyces cerevisiae] ; (Z49209) unknown [Saccharomyces cerevisiae] ; (Z74359) ORF YDR063w [Saccharomyces cerevisiae]
18745	ENU02539	ANI61C7498: 22-52 81..660	22-52	540-559	NAP		g2465148	135	75	4.00E-13	32	45	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
18746	ENU02540	ANI61C464:7 45-73 084..7663	45-73	556-582	NAP		g1708006	215	105	2.00E-22	37	95	probable gluconokinase (gluconate kinase) ; (Z69727) probable glucokinase [Schizosaccharomyces pombe]
18747	ENU02541	ANI61C1052 23-49 9:4702..5282	23-49	534-561	NAP		g3873699	160	94	1.00E-18	44	85	(Z73102) predicted using Genefinder; Similarity to viral non-structural proteins (SW:POLN_EEVV3); cDNA EST EMBL:D65747 comes from this gene; cDNA EST EMBL:D69295 comes from this gene; cDNA EST EMBL:C10380 comes from this gene; ...
18748	ENU02542	ANI61C7840: 38-57 1359..778	38-57	557-577	NAP		g1705999	291	123	1.00E-27	33	37	Coatmer delta subunit (delta-coat protein) (delta-COP) ; (X94265) coat protein delta-cop [Bos primigenius] (Z99168) putative heat shock transcription factor [Schizosaccharomyces pombe]
18749	ENU02543	ANI61C2563: 65-85 2203..1622	65-85	584-604	NAP		g3327019	230	89	1.00E-18	41	28	"fructose-bisphosphate aldolase ; (Y11135) fructose-1,6-bisphosphate aldolase type II [Bacillus stearothermophilus]"
18750	ENU02544	ANI61C9392: 47-66 721..1303	47-66	555-586	NAP		g4033506	206	86	2.00E-16	35	60	probable calcium-binding protein ALG-2 (PMP41) (ALG-257) ; (U49112) ALG-2 [Mus musculus]
18751	ENU02545	ANI61C9841: 37-56 222..803	37-56	544-576	NAP		g2506252	340	145	2.00E-34	39	97	sterigmatocystin biosynthesis regulatory protein ; sterigmatocystin synthesis transcriptional regulator aflR - Emericella nidulans ; (U34740) pathway specific transcription factor [Emericella nidulans]
18752	ENU02546	ANI61C9701: 66-87 52..634	66-87	586-605	NAP		g1703202	228	67	1.00E-10	35	44	(L07492) sugar transport protein [Saccharomyces cerevisiae]
18753	ENU02547	ANI61C537:8 36-55 55..274	36-55	543-575	NAP		g409547	138	45	0.0006	38	24	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18754	ENU02548	ANI61C9833: 2910..3493	27-46	545-567	NAP	ANI61C9833: 27-46	g3877351	308	75	9.00E-18			(Z66520) similar to ERG-3 like protein [Caenorhabditis elegans]
18755	ENU02549	ANI61C215:8 22-41	22-41	543-562	NAP	ANI61C215:8 22-41	g3881138	159	85	5.00E-16	38	96	(AL023846) Y52B11C.1 [Caenorhabditis elegans]
18756	ENU02550	ANI61C1039 72-92	72-92	596-615	NAP	ANI61C1039 72-92	g2804470		64	0.000000			(AF043701) contains similarity to ankyrin repeats and protein kinases [Caenorhabditis elegans]
18757	ENU02551	ANI61C3473: 42-61	42-61	556-585	NAP	ANI61C3473: 42-61	g465713	216	71	9.00E-18	32	67	hypothetical 30.3 KD protein in APE1/LAP4-CWPI intergenic region; hypothetical protein YKL099c - yeast (X71133) [Saccharomyces cerevisiae]; YKL449 [Saccharomyces cerevisiae]; (Z28099) ORF YKL099c [Saccharomyces cerevisiae]
18758	ENU02552	ANI61C1071 27-47	27-47	551-570	NAP	ANI61C1071 27-47	g4506617	391	102	1.00E-27	59	67	ribosomal protein L17; 60S ribosomal protein L17 (L23); ribosomal protein L17 - human; (X53777) putative ribosomal protein (AA 1-184) [Homo sapiens]
18759	ENU02553	ANI61C8712: 58-77	58-77	577-602	NAP	ANI61C8712: 58-77	g2498702	79	48	0.00007	34	38	sterigmatocystin 7-O-methyltransferase precursor; (L25835) O-methyltransferase [Aspergillus flavus]; (L25834) O-methyltransferase [Aspergillus parasiticus]; (L22091) O-methyltransferase [Aspergillus parasiticus]
18760	ENU02554	ANI61C2827: 31-60	31-60	556-575	NAP	ANI61C2827: 31-60	g114988	1001	363	e-100	98	16	Kinesin-like protein BIMC; kinesin-related protein bimC - Emericella nidulans; (M32075) kinesin-like protein (bimC) [Emericella nidulans]
18761	ENU02555	ANI61C9570: 44-63	44-63	568-589	NAP	ANI61C9570: 44-63	g1084581	396	118	4.00E-36	50	89	hypothetical protein YER007c-a - yeast (Saccharomyces cerevisiae); (U18778) Yel007c-ap [Saccharomyces cerevisiae]
18762	ENU02556	ANI61C7729: 31-50	31-50	557-576	NAP	ANI61C7729: 31-50	g2231082	1314	100	8.00E-21	37	19	(Y07891) dynamin-related protein [Schizosaccharomyces pombe]
18763	ENU02557	ANI61C4165: 69-95	69-95	591-614	NAP	ANI61C4165: 69-95	g3264834	1030	187	4.00E-47	50	55	(AF072541) xylitol dehydrogenase; XDH [Galactocandida mastotermitis]

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18764	ENU02558	ANI61C8730: 618..31	71-90	594-616	NAP		g130879	580	131	1.00E-48			Proteasome component PUP1 precursor (macropain subunit PUP1) (proteinase YSCE subunit PUP1) (multicatalytic endopeptidase complex subunit PUP1) ; probable multicatalytic endopeptidase complex (EC 3.4.99.46) chain PUP1 - yeast (Saccharomyces cerevisiae) ; (X61189) PUP1 [Saccharomyces cerevisiae] ; (U55020) Pup1p [Saccharomyces cerevisiae] ; (Z75065) ORF YOR157c [Saccharomyces cerevisiae]
18765	ENU02559	ANI61C1935: 1302..714	52-71	576-598	NAP		g2117760	802	92	1.00E-25	50	33	"aspartate transaminase (EC 2.6.1.1), cytosolic - yeast (Saccharomyces cerevisiae) ; (Z73199) ORF YLR027c [Saccharomyces cerevisiae] "
18766	ENU02560	ANI61C6513: 1..589	22-47	545-568	NAP		g3184113	116	66	2.00E-10	35	30	(AL023780) zinc finger protein [Schizosaccharomyces pombe]
18767	ENU02561	ANI61C886:1 19..708	40-59	565-587	NAP		g1063421	252	84	6.00E-16	28	34	(L48797) toxin pump [Cochliobolus carbonum]
18768	ENU02562	ANI61C5484: 53..640	72-92	590-619	NAP		g1730043	222	77	2.00E-17	39	19	Autophagy serine/threonine-protein kinase APG1 ; probable membrane protein YGL180w - yeast (Saccharomyces cerevisiae) ; (X91489) putative ser/thr protein kinase [Saccharomyces cerevisiae] ; (Z72702) ORF YGL180w [Saccharomyces cerevisiae] ; (D29991) Apg1p [Saccharomyces cerevisiae]
18769	ENU02563	ANI61C4438: 1431..842	68-86	594-615	NAP		g730759	197	49	0.000000	33	71	nuclear protein SNF7 ; SNF7 protein - yeast (Saccharomyces cerevisiae) ; (Z73197) ORF YLR025w [Saccharomyces cerevisiae]
18770	ENU02564	ANI61C7200: 456..1046	48-70	571-596	NAP		g3834684	121	66	2.00E-10	30	86	(AF100925) mating type protein MAT-1-3 [Gibberella fujikuroi]
18771	ENU02565	ANI61C1125 0:3007..3597	59-78	584-607	NAP		g464786	235	94	1.00E-26	34	28	SPT10 protein ; regulatory protein SPT10 - yeast (Saccharomyces cerevisiae) ; (L24435) SPT10 [Saccharomyces cerevisiae] ; (Z49402) ORF YJL127c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18772	ENU02566	ANI61C8336: 59-88 834..243	59-88	589-608	NAP		g3722	816	258	2.00E-68	63	32	(X52633) GAP1 protein (AA 1-601) [Saccharomyces cerevisiae]
18773	ENU02567	ANI61C7975: 36-55 95..687	36-55	566-585	NAP		g4056551	666	154	9.00E-57	62	33	(AL034583) putative elongation initiation factor subunit [Schizosaccharomyces pombe]
18774	ENU02568	ANI61C1803: 65-100 44..636	65-100	582-615	NAP		g1805251	273	101	4.00E-21	35	34	(U58946) transposase [Aspergillus awamori]
18775	ENU02569	ANI61C1115 53-73 6:7336..6744	53-73	584-603	NAP		g1723280	354	106	1.00E-22	43	52	hypothetical 34.8 KD protein C4H3.04C in chromosome I ; (Z69380) unknown [Schizosaccharomyces pombe]
18776	ENU02570	ANI61C8494: 59-80 1066..1659	59-80	589-610	NAP		g3913497	637	84	3.00E-33	54	58	putative carboxymethylglutaminyl dienehydrolase (DLH) ; hypothetical protein YDL086w - yeast (Saccharomyces cerevisiae) ; (Z74134) ORF YDL086w [Saccharomyces cerevisiae]
18777	ENU02571	ANI61C6927: 47-66 114..708	47-66	568-599	NAP		g729230	652	191	1.00E-64	82	12	chromosome segregation protein CUT3 ; cut3 protein - fission yeast (Schizosaccharomyces pombe) ; (D30788) cut3 protein [Schizosaccharomyces pombe]
18778	ENU02572	ANI61C4306: 37-57 960..366	37-57	558-589	NAP		g2132076	302	64	2.00E-18	33	44	hypothetical protein YOR173w - yeast (Saccharomyces cerevisiae) ; (U55021) O3625p [Saccharomyces cerevisiae] ; (Z75081) ORF YOR173w [Saccharomyces cerevisiae]
18779	ENU02573	ANI61C6203: 62-81 7640..8235	62-81	582-615	NAP		g4322563	441	103	3.00E-40	60	91	(AF089838) phosphatidylglycerol/phosphatidylinositol transfer protein [Aspergillus oryzae]
18780	ENU02574	ANI61C1145 71-94 1:2151..1556	71-94	605-624	NAP		g2257524	619	127	2.00E-41	56	62	(AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [Schizosaccharomyces pombe]
18781	ENU02575	ANI61C941:9 28-46 7..692	28-46	560-581	NAP		g539079	440	147	2.00E-37	54	14	peroxisomal assembly protein 5 - yeast (Pichia pastoris)

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18782	ENU02576	ANI61C3194: 726..130	23-43	547-577	NAP		g133371	207	74	7.00E-18			DNA-directed RNA polymerase I and III 16 KD polypeptide (AC19) ; DNA-directed RNA polymerase (EC 2.7.7.6) I/III chain AC19 - yeast (Saccharomyces cerevisiae) ; (M64991) AC19 RNA polymerase subunit [Saccharomyces cerevisiae] ; (Z69382) Subunit of RNA polymerase I and III [Saccharomyces cerevisiae] ; (Z71390) ORF YNL113w [Saccharomyces cerevisiae]
18783	ENU02577	ANI61C8284: 40-59 197..794	40-59	573-595	NAP		g461540	796	171	7.00E-57			"phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (phospho-2-keto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) ; 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae) ; (L20296) homology with DAHP-synthase (ARO4) gene [Saccharomyces cerevisiae] ; (X61107) phospho-2-dehydro-3-deoxyheptonate aldolase [Saccharomyces cerevisiae] ; (Z36118) ORF YBR249c [Saccharomyces cerevisiae] "
18784	ENU02578	ANI61C1878: 45-65 1258..660	45-65	572-601	NAP		g4176538	316	67	1.00E-10	37	51	(AL035260) dna-directed ma polymerase iii subunit [Schizosaccharomyces pombe]
18785	ENU02579	ANI61C3975: 66-86 1819..2417	66-86	587-622	NAP		g1351702	337	76	2.00E-13	31	36	hypothetical 61.1 KD protein C11D3.05 in chromosome I ; (Z68166) unknown [Schizosaccharomyces pombe]
18786	ENU02580	ANI61C9713: 63-86 1295..697	63-86	594-619	NAP		g2995375	924	212	4.00E-59	66	46	(AL022245) ser/thr protein kinase [Schizosaccharomyces pombe] ; (AL031603) protein kinase. [Schizosaccharomyces pombe]
18787	ENU02581	ANI61C3218: 70-89 1079..1677	70-89	606-626	NAP		g3184080	394	68	4.00E-11	60	85	(AL023781) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18788	ENU02582	ANI61C1056 3:567..1165	46-65	578-602	NAP		g1722905	157	66	3.00E-14	34	26	"endo-1,4-beta-xylanase D precursor (xylanase D) (XYLD) ; endo-1,4-beta-xylanase (EC 3.2.1.8) D - Cellulomonas fimi ; (X76729) endo-1,4-beta-xylanase [Cellulomonas fimi]"
18789	ENU02583	ANI61C1120 1:712..113	72-91	610-629	NAP		g3184056		56	0.000000			(AL023776) hypothetical protein [Schizosaccharomyces pombe]
18790	ENU02584	ANI61C8956: 131..730	25-46	555-582	NAP		g2598037	257	60	3.00E-17	31	43	(AJ001272) manganese resistance 1 protein [Saccharomyces cerevisiae]
18791	ENU02585	ANI61C7700: 916..316	22-55	561-580	NAP		g133264	341	73	7.00E-21	52	96	Rodlet protein precursor ; Rodletless protein - Emericella nidulans ; (M61113) rodlet peptide [Emericella nidulans]
18792	ENU02586	ANI61C5260: 2894..2294	44-63	581-602	NAP		g1710503	609	161	3.00E-46	69	85	"probable 60S ribosomal protein L18 (RP28) ; ribosomal protein L18.e, cytosolic - fission yeast (Schizosaccharomyces pombe) ; (AL031528) 60S ribosomal protein l18 [Schizosaccharomyces pombe]"
18793	ENU02587	ANI61C3974: 733..1334	48-79	588-607	NAP		g120609	630	199	4.00E-53			Uracyl phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTASE) ; uracyl phosphoribosyltransferase (EC 2.4.2.9) chain FUR1 - yeast (Saccharomyces cerevisiae) ; (M36485) uracyl phosphoribosyltransferase (FUR1) [Saccharomyces cerevisiae] ; (U10398) Fur1p: Uracyl phosphoribosyltransferase [Saccharomyces cerevisiae] ; (X79811) FUR1 [Saccharomyces cerevisiae]
18794	ENU02588	ANI61C1048 3:6359..6960	27-46	564-586	NAP		g2132237	287	112	2.00E-24	48	93	hypothetical protein YPL225w - yeast (Saccharomyces cerevisiae) ; (Z73581) ORF YPL225w [Saccharomyces cerevisiae]
18795	ENU02589	ANI61C7255: 750..1351	30-49	565-589	NAP		g4007771	210	100	1.00E-20	29	30	(AL034433) hypothetical protein [Schizosaccharomyces pombe]
18796	ENU02590	ANI61C8977: 603..2	33-54	570-592	NAP		g577597	347	138	3.00E-32	49	79	(X78082) NADH:ubiquinone oxidoreductase (complex I) [Neurospora crassa]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18797	ENU02591	ANI61C7354: 69-88 2621..3223		610-629	NAP		g586551	490	87	8.00E-17	35	53	hypothetical 33.5 KD protein in MRPS9-YSW1 intergenic region ; probable membrane protein YBR147w - yeast (Saccharomyces cerevisiae) ; (Z36016) ORF YBR147w [Saccharomyces cerevisiae]
18798	ENU02592	ANI61C8993: 22-53 337..939		564-582	NAP		g1170922	293	101	1.00E-30	39	37	Ammonium transporter MEP2 ; ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae) ; (X83608) ammonium transporter [Saccharomyces cerevisiae] ; (Z46843) NH3 permease [Saccharomyces cerevisiae] ; (Z71418) ORF YNL142w [Saccharomyces cerevisiae]
18799	ENU02593	ANI61C8845: 22-49 1887..1285		563-582	NAP		g388249	198	106	2.00E-22	39	60	[Saccharomyces cerevisiae] (X60381) ORF2 [Saccharomyces cerevisiae]
18800	ENU02594	ANI61C3564: 39-58 1873..1269		578-600	NAP		g1352984	365	114	6.00E-25	42	68	hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YJL055w - yeast (Saccharomyces cerevisiae) ; (Z49330) ORF YJL055w [Saccharomyces cerevisiae]
18801	ENU02595	ANI61C3979: 43-62 4348..3745		585-604	NAP		g1352982		52	0.000004			hypothetical protein in DFR1 3'region
18802	ENU02596	ANI61C1076: 32-51 70..673		574-593	NAP		g1361982	354	167	5.00E-41	44	34	4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis thaliana ; (U18675) 4-coumarate--coenzyme A ligase [Arabidopsis thaliana]
18803	ENU02597	ANI61C3755: 34-53 13..617		577-596	NAP		g3135990	322	97	1.00E-25	45	30	(AL023589) membrane transporter [Schizosaccharomyces pombe]
18804	ENU02598	ANI61C5967: 35-55 2012..1408		576-597	NAP		g2499919	494	134	3.00E-31	45	20	hypothetical zinc metalloproteinase T16A9.4
18805	ENU02599	ANI61C4286: 23-50 389..994		559-587	NAP		g1083278	163	87	1.00E-16	33	27	cytochrome P450 3A13 - mouse ; (X63023) cytochrome P-450IIIa [Mus musculus] ; cytochrome P450 Cyp3a-13 [Mus musculus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvng	Description
18806	ENU02600	ANI61C197:6 97..91	25-46	566-589	NAP		g1911486	466	102	2.00E-21	49	61	"(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger] "
18807	ENU02601	ANI61C9009: 45-64 1291..686	45-64	589-609	NAP		g2619026	435	155	3.00E-37	43	46	(AF027868) YoaN [Bacillus subtilis] ; (Z99114) similar to hypothetical proteins [Bacillus subtilis]
18808	ENU02602	ANI61C6045: 34-53 991..385	34-53	570-598	NAP		g1749484	203	76	1.00E-13	41	47	"(D89138) similar to Saccharomyces cerevisiae ORF YGL208W, EMBL Accession Number Z72730 [Schizosaccharomyces pombe] "
18809	ENU02603	ANI61C1111 28-49 5:817..210	28-49	570-593	NAP		g2498970	485	157	6.00E-38	40	73	putative sterigmatocystin biosynthesis protein STCQ ; (U34740) similar to A. parasiticus putative aflatoxin biosynthesis protein [Emmericella nidulans]
18810	ENU02604	ANI61C1209: 55-78 1557..2165	55-78	600-621	NAP		g2132284	367	91	1.00E-36	39	89	hypothetical protein YPR107c - yeast (Saccharomyces cerevisiae) ; (U32445) P8283.17 gene product [Saccharomyces cerevisiae]
18811	ENU02605	ANI61C4438: 68-86 1431..823	68-86	612-634	NAP		g730759	197	49	0.000000	35	74	nuclear protein SNF7 ; SNF7 protein - yeast (Saccharomyces cerevisiae) ; (Z73197) ORF YLR025w [Saccharomyces cerevisiae]
18812	ENU02606	ANI61C5883: 29-48 1197..1805	29-48	564-595	NAP		g731875	437	148	3.00E-35	39	65	"mitochondrial FAD carrier protein FLX1 ; carrier protein FLX1, inner membrane - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 311, CAI: 0.12, similar to peroxisomal membrane protein and mitochondrial carrier proteins [Saccharomyces cerevisiae] ; (L41168) inner membrane carrier protein [Saccharomyces cerevisiae] "
18813	ENU02607	ANI61C7524: 66-86 1430..821	66-86	614-633	NAP		g128337	1671	324	2.00E-88	98	29	G2-specific protein kinase NIMA (never in mitosis) ; probable protein kinase nimA (EC 2.7.1.-) - Emmericella nidulans ; (M20249) never in mitosis protein [Emmericella nidulans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18814	ENU02608	ANI61C1107	24-42	565-591	NAP		g2879805	600	131	3.00E-30	37	12	(AL021813) hypothetical protein [Schizosaccharomyces pombe]
18815	ENU02609	ANI61C8051: 2:1732..2341	36-55	585-604	NAP		g1706087	910	173	7.00E-43	50	37	cytochrome P450-DIT2 (cytochrome P450 56); cytochrome P450 56 - yeast (Saccharomyces cerevisiae); (U32274) Dit2p: cytochrome P450; CAI: 0.13 [Saccharomyces cerevisiae]
18816	ENU02610	ANI61C757:1 22-46	571-590	571-590	NAP		g126597	577	203	8.00E-59	58	87	"N,O-diacetylneuraminidase (lysozyme CH); lysozyme (EC 3.2.1.17) - fungus (Chalara sp.)"
18817	ENU02611	ANI61C8231: 61-81	594-629	594-629	NAP		g130117	813	110	9.00E-24	49	27	phosphate-repressible phosphate permease; phosphate-repressible phosphate permease - Neurospora crassa; (M31364) phosphate permease [Neurospora crassa]
18818	ENU02612	ANI61C3107: 43-62	591-612	591-612	NAP		g730334	405	108	3.00E-23	32	35	putative polyketide biosynthesis protein PKSJ; (U11039) unknown [Bacillus subtilis]; (Z99112) pksJ [Bacillus subtilis]; (Z99113) pksJ [Bacillus subtilis]
18819	ENU02613	ANI61C7361: 63-82	613-632	613-632	NAP		g3687462	370	100	5.00E-29	45	91	(AL031798) coatmer zeta subunit [Schizosaccharomyces pombe]
18820	ENU02614	ANI61C9833: 42-61	592-611	592-611	NAP		g1723488	87	61	0.000000	42	8	hypothetical 104.0 KD protein C32A11.03C in chromosome I; (Z69796) unknown
18821	ENU02615	ANI61C8431: 72-92	611-641	611-641	NAP		g2914565	413	141	1.00E-36	48	70	[Schizosaccharomyces pombe] "Chain A, Yeast Chorismate Mutase, T226s Mutant, Complex With Trp"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18822	ENU02616	ANI61C3868: 22-45 2458..1845	572-593	NAP			g417817	409	176	1.00E-43			protein-S isoprenylcysteine O-methyltransferase (isoprenylcysteine carboxylmethyltransferase) ; farnesyl cysteine carboxyl-methyltransferase - yeast (Saccharomyces cerevisiae) ; (L07952) farnesyl cysteine carboxyl-methyltransferase [Saccharomyces cerevisiae] ; (L15442) isoprenylcysteine carboxyl methyltransferase [Saccharomyces cerevisiae] ; (U33007) Ste14p: farnesyl cysteine carboxyl-methyltransferase; YDR410C; CAI: 0.12 [Saccharomyces cerevisiae]
18823	ENU02617	ANI61C3365: 53-72 1852..2466	592-624	NAP			g3116144	110	54	0.000001	27	64	(AL023290) hypothetical protein [Schizosaccharomyces pombe]
18824	ENU02618	ANI61C502:6 49-72 62..48	596-621	NAP			g482219	290	113	8.00E-25	38	20	hypothetical protein ZK757.3 - Caenorhabditis elegans
18825	ENU02619	ANI61C1027 72-93 0:3109..2495	620-644	NAP			g2494676	1242	123	7.00E-28	38	36	EPD1 protein precursor ; (AB005130) EPD1 [Candida maltosa]
18826	ENU02620	ANI61C1166: 44-67 133..747	597-616	NAP			g4530327	890	205	2.00E-80	79	30	(AF110494) mitochondrial precursor protein import receptor tom70 [Neurospora crassa]
18827	ENU02621	ANI61C8770: 70-89 1278..664	623-642	NAP			g1710055	788	148	2.00E-35	44	44	RDS1 protein ; rds1 protein - fission yeast (Schizosaccharomyces pombe) ; (X77328) rds1 [Schizosaccharomyces pombe]
18828	ENU02622	ANI61C293:2 30-50 630..2016	583-602	NAP			g1929333	120	61	0.000000	26	97	(Z93767) ywrF [Bacillus subtilis] ; (Z99122) ywrF [Bacillus subtilis]
18829	ENU02623	ANI61C5354: 65-83 2585..3200	619-638	NAP			g464725	689	249	2.00E-65	69	91	"40S ribosomal protein S8 (S14) (YS9) (RP19) ; ribosomal protein S8 c, cytosolic - yeast (Saccharomyces cerevisiae) ; (Z26879) ribosomal protein S8 [Saccharomyces cerevisiae] ; (Z35833) ORF YBL072c [Saccharomyces cerevisiae] ; (U18839) Rps8bp: Ribosome protein, small subunit [Saccharomyces cerevisiae] "
18830	ENU02624	ANI61C3563: 58-77 656..41	611-631	NAP			g1526987	450	183	7.00E-46	54	77	(U13050) pectate lyase D [Fusarium solani f. sp. pisi]

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18831	ENU02625	ANI61C8909: 2964..3579	30-49	582-603	NAP		g2773042	750	105	3.00E-22	41	17	(AF038440) phospholipase D2 [Homo sapiens]
18832	ENU02626	ANI61C1583: 22-45 81..697	22-45	571-596	NAP		g1723912	78	50	0.00002	33	11	hypothetical 73.5 KD protein in SCS3-SUP44 intergenic region ; hypothetical protein YGL124c - yeast (Saccharomyces cerevisiae) ; (Z72646) ORF YGL124c [Saccharomyces cerevisiae] ; (X94106) G2889 [Saccharomyces cerevisiae] dehydroshikimate dehydratase (EC 4.2.1.-) - Emericella nidulans ; (M77665) dehydroshikimate dehydratase [Emericella nidulans] "(U24701) beta-1,2-D-glucosidase [Septoria lycopersici] ; (U35462) tomatinase [Septoria lycopersici] ; beta2 tomatinase [Septoria lycopersici] "
18833	ENU02627	ANI61C1141: 71-97 3:1314..698	71-97	626-645	NAP		g83699	1733	264	5.00E-70	98	57	"signal sequence processing protein SEC11 ; signal peptidase (EC 3.4.99.-) SEC11 - yeast (Saccharomyces cerevisiae) ; (Z38061) sec11, len: 167, CAI: 0.17 SC11_yeast P15367 signal sequence processing protein [Saccharomyces cerevisiae] "
18834	ENU02628	ANI61C915:2 43-62 2..639	43-62	591-617	NAP		g799150	179	98	7.00E-20	40	14	PIM1 protein ; pim1 hypothetical protein - fission yeast (Schizosaccharomyces pombe) hypothetical 24.7 KD protein C3A12.04C in chromosome I ; (Z95395) conserved hypothetical protein [Schizosaccharomyces pombe]
18835	ENU02629	ANI61C5294: 22-45 1984..1366	22-45	576-598	NAP		g730717	400	117	1.00E-31	50	90	hypothetical 98.1 KD TRP-ASP repeats containing protein in PAF1-MRPL27 intergenic region ; hypothetical protein YBR281c - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2018-ORF [Saccharomyces cerevisiae] ; (Z36150) ORF YBR281c [Saccharomyces cerevisiae] ; ORF YBR2018 [Saccharomyces cerevisiae]
18836	ENU02630	ANI61C4039: 60-79 1065..1683	60-79	610-636	NAP		g132172	699	154	5.00E-37	38	38	
18837	ENU02631	ANI61C3092: 22-53 1226..606	22-53	580-599	NAP		g3219941	318	77	5.00E-25	34	94	
18838	ENU02632	ANI61C6403: 52-82 97..716	52-82	609-629	NAP		g586394	356	134	4.00E-31			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18839	ENU02633	ANI61C8982: 52-71	610-630	NAP			g3170178		71	5.00E-12			(AF039689) antigen NY-CO-7 [Homo sapiens]
18840	ENU02634	6024..5404	48-67	605-627	NAP		g3004934	801	189	2.00E-47	46	43	(AF036871) annexin XIV [Neurospora crassa]
18841	ENU02635	ANI61C3314: 1350..1971	38-58	582-617	NAP		g21322293	228	75	3.00E-21	38	53	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae); (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325)
18842	ENU02636	ANI61C7556: 41-62	601-620	NAP			g2624417	384	126	1.00E-28	53	88	[Saccharomyces cerevisiae] (AJ002959) Ubiquitin carrier protein [Zea mays]
18843	ENU02637	2814..3435	23-42	581-603	NAP		g2492754	518	127	5.00E-29	44	63	sorbitol utilization protein SOU1; (AF002134) Sou1p [Candida albicans]
18844	ENU02638	949..327	70-89	630-650	NAP		g3327876	189	87	8.00E-17	35	47	(AB016218) unknown: similar to human GA17 protein
18845	ENU02639	ANI61C8297: 1068..446											[Schizosaccharomyces pombe] (AL031852) u-snmp-associated cyclophilin [Schizosaccharomyces pombe]
18846	ENU02640	ANI61C7885: 22-53	575-602	NAP			g3738142	459	80	1.00E-45	57	99	(U00036) R151.6 gene product [Caenorhabditis elegans]
18847	ENU02641	ANI61C8732: 22-50	573-602	NAP			g459002	392	118	2.00E-32	42	78	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase); (U29581) ORF f253 [Escherichia coli]; (AE000368) 2-deoxy-D-gluconate 3-dehydrogenase [Escherichia coli]
18848	ENU02642	3940..4562	68-87	631-650	NAP		g1730032	250	52	2.00E-14	35	66	(AL022019) conserved hypothetical protein [Schizosaccharomyces pombe]
18849	ENU02643	ANI61C1042 3:907..1529	47-71	610-630	NAP		g2924501	390	43	0.001	30	23	Acetamidase; amdS protein - Emericella nidulans; (M16371) acetamidase enzyme [Emericella nidulans]

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18850	ENU02644	ANI61C9290: 49-68 1992..1366	49-68	611-633	NAP		g549626	261	102	2.00E-21	36	92	hypothetical 22.0 KD protein in LAS1-hypothetical intergenic region ; hypothetical CCP1 intergenic region ; hypothetical protein YKR065c - yeast (Saccharomyces cerevisiae) ; (Z28290) ORF YKR065c [Saccharomyces cerevisiae]
18851	ENU02645	ANI61C5915: 33-53 732..106	33-53	598-617	NAP		g586521	369	153	9.00E-37	43	26	hypothetical 86.4 KD protein in PHO5-VPS15 intergenic region ; hypothetical protein YBR094w - yeast (Saccharomyces cerevisiae) ; (X78993) hyp. protein [Saccharomyces cerevisiae] ; (Z35963) ORF YBR094w [Saccharomyces cerevisiae]
18852	ENU02646	ANI61C1650: 23-42 1049..423	23-42	588-607	NAP		g4160346	1532	218	3.00E-56	65	38	(AL035216) nucleolar protein involved in pre-rRNA processing [Schizosaccharomyces pombe]
18853	ENU02647	ANI61C995:8 56-75 13..1439	56-75	621-640	NAP		g2495263	743	248	3.00E-65	56	21	3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMG-CoA reductase) ; (X94307) HMG-CoA reductase [Gibberella fujikuroi]
18854	ENU02648	ANI61C3926: 55-74 848..221	55-74	621-640	NAP		g131761	220	112	3.00E-24	30	38	quininate permease (quininate transporter) ; quininate transport protein - Neurospora crassa ; (X14603) quininate transporter [Neurospora crassa]
18855	ENU02649	ANI61C5699: 46-69 712..85	46-69	611-631	NAP		g98747	248	116	2.00E-25	30	78	7alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) - Eubacterium sp. (strain VPI 12708) ; (M58473) 7-alpha-hydroxysteroid dehydrogenase [Eubacterium sp. VPI 12708]
18856	ENU02650	ANI61C2043: 34-53 763..135	34-53	600-620	NAP		g140496	284	136	2.00E-31	36	55	"hypothetical 42.5 KD protein in TSM1-ARE1 intergenic region ; probable membrane protein YCR044c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR044c, len:357 [Saccharomyces cerevisiae] "
18857	ENU02651	ANI61C7025: 28-50 348..977	28-50	596-615	NAP		g1077536	260	109	2.00E-23	40	77	hypothetical protein YDR140w - yeast (Saccharomyces cerevisiae) ; (Z48179) unknown [Saccharomyces cerevisiae]
18858	ENU02652	ANI61C2654: 40-59 467..761	40-59	608-627	NAP		g2281697	434	57	0.000000	28	17	(AF010138) transcription factor [Mus musculus]

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18859	ENU02653	ANI61C6471: 3381..2751	22-55	590-610	NAP		g4538667	391	126	8.00E-29	65	85	(AL049474) clathrin coat assembly protein [Schizosaccharomyces pombe]
18860	ENU02654	ANI61C2906: 22-53	22-53	583-610	NAP		g762850	299	76	2.00E-13	40	100	(L41166) p21 protein [Schizosaccharomyces pombe]; (Z99262) p21 protein; cell cycle regulatory protein; interacts with cdc2 in the control of the M-G1 transition [Schizosaccharomyces pombe]
18861	ENU02655	ANI61C7933: 37-56	37-56	606-625	NAP		g1077514	302	114	5.00E-25	46	76	hypothetical protein YDR013w - yeast (Saccharomyces cerevisiae); (Z48008) unknown [Saccharomyces cerevisiae]; (X95966) orf:PZA208 [Saccharomyces cerevisiae]; (Z74309) ORF YDR013w [Saccharomyces cerevisiae]
18862	ENU02656	ANI61C9492: 46-65	46-65	616-635	NAP		g1723848	277	89	4.00E-17	46	85	"putative mitochondrial 60S ribosomal protein L7/L12 precursor; probable ribosomal protein L12, mitochondrial - yeast (Saccharomyces cerevisiae); (Z72591) ORF YGL068w [Saccharomyces cerevisiae] "
18863	ENU02657	ANI61C6172: 38-57	38-57	608-627	NAP		g3169083	279	111	6.00E-24	37	61	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18864	ENU02658	ANI61C6638: 28-52	28-52	598-617	NAP		g3915558	169	92	3.00E-18	29	62	hypothetical 36.5 KD protein in GBSA-TLPB intergenic region; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
18865	ENU02659	ANI61C1015	56-77	625-645	NAP		g2131385	270	87	1.00E-16	40	33	hypothetical protein YDR145w - yeast (Saccharomyces cerevisiae); (Z50046) unknown [Saccharomyces cerevisiae]
18866	ENU02660	ANI61C1039	44-63	613-634	NAP		g2104422	323	113	1.00E-24	42	26	(Z95395) putative membrane transport protein [Schizosaccharomyces pombe]
18867	ENU02661	ANI61C7015: 22-42	22-42	591-613	NAP		g1078629	1199	309	1.00E-83	97	31	DNA binding protein - Emericella nidulans; (Z47081) DNA binding protein [Emericella nidulans]
18868	ENU02662	ANI61C3159: 25-44	25-44	585-616	NAP		g1749831	731	165	2.00E-40	45	26	(Z56279) beta-xylo-glucosidase [Thermoanaerobacter brockii]
18869	ENU02663	ANI50C7416	23-42	596-615	NAP		g1781180		47	0.0001	32	29	(Z83859) hypothetical protein Rv1867 [Mycobacterium tuberculosis]

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18870	ENU02664	ANI61C3242: 178..812	42-61	604-634	NAP		g1173168	299	139	2.00E-32	40	75	hypothetical 31.5 KD protein ; (U05664) homologous to Swiss-Prot Accession Number P20435: Saccharomyces cerevisiae RNA polymerase subunit RPO26 [Sulfolobus acidocaldarius] (U48234) spU2AF23 [Schizosaccharomyces pombe] choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
18871	ENU02665	ANI61C4376: 45-66	45-66	620-639	NAP		g2347143	660	224	4.00E-58	55	89	"MRNA capping enzyme (MRNA guanylyltransferase) (GTP--RNA guanylyltransferase) ; (U16143) GTP:RNA guanylyltransferase [Schizosaccharomyces pombe] ; (U18811) GTP--RNA guanylyltransferase [Schizosaccharomyces pombe] ; (Z97211) mma capping enzyme, mma guanylyltransferase [Schizosaccharomyces pombe] "
18872	ENU02666	ANI61C9847: 71-96	71-96	646-666	NAP		g117619	704	131	4.00E-30	36	34	eukaryotic initiation factor 4A (EIF-4A) ; (X80796) translation initiation factor eIF-4A [Schizosaccharomyces pombe] ; (L40627) cell cycle control protein eIF-4A [Schizosaccharomyces pombe]
18873	ENU02667	ANI61C6047: 22-45	22-45	598-617	NAP		g729998	505	174	6.00E-43	45	49	[Z66499] T01B7.8 [Caenorhabditis elegans] hypothetical protein YOL071w - yeast (Saccharomyces cerevisiae) ; (Z74813) ORF YOL071w [Saccharomyces cerevisiae]
18874	ENU02668	ANI61C1029 4:6013..6650	60-86	633-655	NAP		g1708418	1571	354	2.00E-97	86	54	
18875	ENU02669	ANI61C8590: 22-41	22-41	593-617	NAP		g3879236		36	0.25			
18876	ENU02670	ANI61C352:9 557..4920	52-75	628-648	NAP		g2132007	181	79	2.00E-14	40	89	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18877	ENU02671	ANI61C1805: 2409..2293	40-64	618-637	NAP		g728904	335	95	5.00E-19	41	15	calcium-transporting ATPase 2 (vacuolar CA2+-ATPase) ; Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae) ; (U03060) calcium ATPase [Saccharomyces cerevisiae] ; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
18878	ENU02672	ANI61C9127: 44-63 1359..1998	44-63	622-641	NAP		g2959364	326	146	1.00E-34	39	78	(AL022117) putative o-methyltransferase [Schizosaccharomyces pombe]
18879	ENU02673	ANI61C3023: 40-63 1260..621	40-63	617-637	NAP		g1083278	114	55	4.00E-11	32	35	cytochrome P450 3A13 - mouse ; (X63023) cytochrome P-450IIIa [Mus musculus] ; cytochrome P450 Cyp3a-13 [Mus musculus]
18880	ENU02674	ANI61C3023: 40-63 1260..621	40-63	617-637	NAP		g1083278	114	55	4.00E-11	32	35	cytochrome P450 3A13 - mouse ; (X63023) cytochrome P-450IIIa [Mus musculus] ; cytochrome P450 Cyp3a-13 [Mus musculus]
18881	ENU02675	ANI61C8458: 63-85 2393..1754	63-85	641-660	NAP		g3885836		51	5.00E-14			(AF091042) putative cercosporin transporter [Cercospora kikuchii]
18882	ENU02676	ANI61C8439: 68-103 103..745	68-103	649-668	NAP		g2133270	576	100	5.00E-53	91	78	HAP3 protein - Emericella nidulans ; (U35341) HapC [Emericella nidulans]
18883	ENU02677	ANI61C9069: 27-46 831..188	27-46	609-628	NAP		g1617552	2322	229	4.00E-78	97	38	(U70043) NsdD [Emericella nidulans] ; (U70044) DNA binding protein NsdD [Emericella nidulans]
18884	ENU02678	ANI61C2652: 66-87 1432..789	66-87	634-667	NAP		g2956779	556	194	4.00E-49	53	38	(AL022103) histidyl-tRNA synthetase [Schizosaccharomyces pombe]
18885	ENU02679	ANI61C2281: 22-41 3007..2364	22-41	604-623	NAP		g127297	124	53	0.000001			MPV17 protein ; mpv17 protein - mouse ; (M36411) Mpv17 [Mus musculus]
18886	ENU02680	ANI61C1422: 22-52 79..722	22-52	604-623	NAP		g1870230	1304	436	e-122	99	81	(AC000133) ORF [Emericella nidulans]
18887	ENU02681	ANI61C1079: 62-83 4:2116..1472	62-83	642-664	NAP		g4033573	239	85	5.00E-23	43	88	(Z99262) hypothetical protein [Schizosaccharomyces pombe]
18888	ENU02682	ANI61C843: 7 34..90	22-52	603-624	NAP		g4106666	421	171	5.00E-42	44	71	(AL035064) putative ubiquinone biosynthesis protein
18889	ENU02683	ANI61C66: 29 64..2320	36-56	611-638	NAP		g2842509	416	101	9.00E-41	44	38	[Schizosaccharomyces pombe] (AL021748) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18890	ENU02684	ANI61C2870: 64-84 840..1485	64-84	648-667	NAP		g1723479	377	164	4.00E-40	43	89	hypothetical 24.9 KD protein C17G8.07 in chromosome I ; (Z69795) unknown [Schizosaccharomyces pombe]
18891	ENU02685	ANI61C7394: 68-87 86..733	68-87	650-673	NAP		g1723879	252	95	5.00E-19	37	73	hypothetical 32.1 KD protein in MAD1-SCY1 intergenic region ; probable membrane protein YGL085w - yeast (Saccharomyces cerevisiae) ; (Z72607) ORF YGL085w [Saccharomyces cerevisiae]
18892	ENU02686	ANI61C7972: 55-75 2692..2045	55-75	628-660	NAP		g1351612	274	113	7.00E-28	40	61	hypothetical oxidoreductase C23D3.11 in chromosome I ; hypothetical protein SPAC23D3.11 - fission yeast (Schizosaccharomyces pombe)
18893	ENU02687	ANI61C1056 22-47 9:1845..1198	22-47	601-627	NAP		g2132491	274	75	1.00E-25	40	61	probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr284cp [Saccharomyces cerevisiae]
18894	ENU02688	ANI61C5718: 51-74 705..1354	51-74	637-657	NAP		g731073	251	48	0.00006			Uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTASE) ; uracil phosphoribosyltransferase - Bacillus subtilis ; (Z38002) uracil phosphoribosyltransferase [Bacillus subtilis] ; (Z99122) uracil phosphoribosyltransferase [Bacillus subtilis] ; uracil phosphoribosyltransferase [Bacillus subtilis]
18895	ENU02689	ANI61C3229: 24-52 1057..1705	24-52	611-630	NAP		g1362010	267	117	3.00E-28	70	30	ubiquitin-like protein 9 - Arabidopsis thaliana
18896	ENU02690	ANI61C1148 69-88 0:1225..576	69-88	652-676	NAP		g4581523	425	178	3.00E-44	53	87	(AL049559) riboflavin synthase alpha chain [Schizosaccharomyces pombe]
18897	ENU02691	ANI61C8540: 71-90 653..1303	71-90	653-679	NAP		g1788580	657	146	9.00E-35	40	52	(AE000314) putative racemase [Escherichia coli] ; (D90856) similar to [SwissProt Accession Number P31458] [Escherichia coli]
18898	ENU02692	ANI61C7170: 42-62 4254..4905	42-62	632-651	NAP		g2865171	478	118	3.00E-38	69	90	(AB010901) ribosomal protein L21 homolog [Schizosaccharomyces pombe]

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18899	ENU02693	ANI50C6324 8_1:125..776	71-95	661-680	NAP		g465873	63	0.000000	002	25	33	hypothetical 59.1 KD protein F22B7.6 in chromosome III ; f22b7.6 protein - Caenorhabditis elegans ; (L12018)
18900	ENU02694	ANI61C5149: 48-67 2171..2823	48-67	639-658	NAP		g3183389	540	153	8.00E-37	39	23	putative [Caenorhabditis elegans] hypothetical 98.3 KD protein C9G1.06C in chromosome I ; (Z98763) hypothetical src homology domain containing protein
18901	ENU02695	ANI61C8056: 50-69 3051..2399	50-69	641-660	NAP		g3688090	189	59	2.00E-13	43	86	[Schizosaccharomyces pombe] (AC005757) R32611_2 [Homo sapiens]
18902	ENU02696	ANI61C5061: 23-42 22..675	23-42	603-634	NAP		g3560144	370	145	3.00E-34	41	38	(AL031534) putative asparagine synthase [Schizosaccharomyces pombe]
18903	ENU02697	ANI61C5317: 29-48 1951..2606	29-48	619-642	NAP		g1346878	585	141	3.00E-33	39	51	PSI protein ; DNAJ-like protein homolog - fission yeast (Schizosaccharomyces pombe) ; (L37753) Psi protein
18904	ENU02698	ANI61C2530: 45-64 87..742	45-64	637-658	NAP		g2492825	298	89	3.00E-17	29	52	[Schizosaccharomyces pombe] ; DnaJ-like protein [Schizosaccharomyces pombe]
18905	ENU02699	ANI61C3258: 38-57 854..198	38-57	633-652	NAP		g3150262	564	146	1.00E-34	38	61	"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus]" (AL023634) hypothetical protein
18906	ENU02700	ANI61C1430: 65-84 1567..911	65-84	660-679	NAP		g2133013	401	93	1.00E-18	34	51	[Schizosaccharomyces pombe] probable membrane protein YPL264c - yeast (Saccharomyces cerevisiae) ; (Z73620) ORF YPL264c
18907	ENU02701	ANI61C6665: 45-67 1866..1209	45-67	634-660	NAP		g1723253	130	61	0.000000			[Saccharomyces cerevisiae] hypothetical 29.3 KD protein C3F10.08C in chromosome I ; (Z69369) hypothetical protein [Schizosaccharomyces pombe]

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18908	ENU02702	ANI61C6366: 25-56 1788..1130			NAP		g1352984	390	132	1.00E-39	46	81	hypothetical 26.9 KD protein in BTN1-PEP8 intergenic region ; hypothetical protein YJL055w - yeast (Saccharomyces cerevisiae) ; (Z49330) ORF YJL055w [Saccharomyces cerevisiae]
18909	ENU02703	ANI61C718:4 33-55 97..1154		618-648	NAP		g3150116	754	191	4.00E-48	45	39	(AL023595) amino acid permease [Schizosaccharomyces pombe]
18910	ENU02704	ANI61C5178: 40-60 1030..373		636-655	NAP		g1730641	299	79	3.00E-14	29	30	hypothetical 65.0 KD protein in MET2-SEC2 intergenic region ; probable membrane protein YNL275w - yeast (Saccharomyces cerevisiae) ; (Z71551) ORF YNL275w [Saccharomyces cerevisiae]
18911	ENU02705	ANI61C6874: 49-69 1681..1024		643-664	NAP		g3043428	670	174	1.00E-66	68	97	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
18912	ENU02706	ANI61C1298: 66-86 688..29		663-682	NAP		g2492997	438	98	2.00E-33	62	68	probable succinyl-COA:3-ketoacid-Coenzyme A transferase subunit B (succinyl COA:3-OXOacid COA-transferase) (OXCT B) ; (Z95556) scoB [Mycobacterium tuberculosis] (L35053) homolog of retroviral gag genes; putative [Magnaporthe grisea] (Z50728) putative acetyltransferase [Schizosaccharomyces pombe]
18913	ENU02707	ANI61C3599: 22-44 9121..8462		620-639	NAP		g522301	535	160	8.00E-39	41	46	"mitochondrial inner membrane protease subunit 2 ; proteinase 2 precursor, mitochondrial inner membrane - yeast (Saccharomyces cerevisiae) ; (Z49213) Imp2p [Saccharomyces cerevisiae] "
18914	ENU02708	ANI61C1083 72-92 5:2451..3110		670-689	NAP		g4150918	302	113	1.00E-24	40	81	(AL033391) conserved hypothetical protein [Candida albicans]
18915	ENU02709	ANI61C8998: 31-51 323..982		627-648	NAP		g1170551	183	88	7.00E-17	37	96	phosphate-repressible phosphate permease ; phosphate-repressible phosphate permease - Neurospora crassa ; (M31364) phosphate permease [Neurospora crassa]
18916	ENU02710	ANI61C6525: 53-72 279..938		651-670	NAP		g3850129	585	166	2.00E-40	56	85	
18917	ENU02711	ANI61C7950: 70-89 6601..5942		668-687	NAP		g130117	1210	96	1.00E-54	58	30	

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18918	ENU02712	ANI61C3150: 59-80 993..1653	59-80	658-677	NAP		g2492777	537	155	7.00E-39	55	52	hypothetical ZINC-type alcohol dehydrogenase-like protein in prc5-FET4 intergenic region ; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae) ; (Z54141) unknown [Saccharomyces cerevisiae] (AB012725) zinc finger protein [Mus musculus]
18919	ENU02713	ANI61C1022 33-53 0:15..675	33-53	629-651	NAP		g3298472		38	0.088			hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae) ; (U11583) YHL031c gene product
18920	ENU02714	ANI61C8624: 23-50 2360..1699	23-50	619-642	NAP		g731611	247	110	1.00E-23	35	89	[Saccharomyces cerevisiae] hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae) ; (U11583) YHL031c gene product
18921	ENU02715	ANI61C8624: 23-50 2360..1699	23-50	619-642	NAP		g731611	247	110	1.00E-23	35	89	[Saccharomyces cerevisiae] hypothetical 25.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL031c - yeast (Saccharomyces cerevisiae) ; (U11583) YHL031c gene product
18922	ENU02716	ANI61C8082: 57-76 2923..2260	57-76	659-678	NAP		g2144564	606	151	9.00E-61	61	61	[Saccharomyces cerevisiae] phosphoribosylaminoimidazolesuccinocarboxamide synthase (EC 6.3.2.6) - yeast (Saccharomyces cerevisiae) ; (M67445) phosphoribosyl-aminoimidazolesuccinocarboxamide synthetase [Saccharomyces cerevisiae] ; (L22015) Adelphi: phosphoribosyl amino imidazolesuccinocarboxamide synthetase [Saccharomyces cerevisiae] ORM1 protein ; probable membrane protein YGR038w - yeast (Saccharomyces cerevisiae) ; (Z72823) ORF YGR038w [Saccharomyces cerevisiae]
18923	ENU02717	ANI61C9181: 28-47 6564..5901	28-47	622-649	NAP		g1723661	472	169	1.00E-49	59	76	

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18924	ENU02718	ANI61C2491: 4228..3564	23-49	624-645	NAP		g130880	799	167	6.00E-41			"Proteasome component Y7 (macropain subunit Y7) (proteinase YSCE subunit 7) (multicatalytic endopeptidase complex subunit Y7) ; multicatalytic endopeptidase complex (EC 3.4.99.46) chain Y7 - yeast (Saccharomyces cerevisiae) ; Chain B, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain P, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; (X56731) proteasome Y7 subunit [Saccharomyces cerevisiae] ; (Z46660) proteasome component Y gene, len: 250, CAI:0.15, PRCX_ yeast P23639 [Saccharomyces cerevisiae] " (AL022244) hypothetical protein [Schizosaccharomyces pombe] L-fucose permease ; fucose permease - Escherichia coli ; (X15025) fucP ORF (AA 1-438) [Escherichia coli] ; (U29581) L-fucose permease [Escherichia coli] ; (AE000364) fucose permease [Escherichia coli] (Z98601) mitochondrial 40s ribosomal protein mrp4. [Schizosaccharomyces pombe] Elongation factor 2 (EF-2) ; (D83975) elongation factor 2 [Schizosaccharomyces pombe] ; (D83976) elongation factor 2 [Schizosaccharomyces pombe] (AC000133) ORF [Emicella nidulans] (AL035065) protein translation factor sui1. [Schizosaccharomyces pombe]
18925	ENU02719	ANI50C3665 47-66 0_1:1418..754	47-66	649-669	NAP		g2995341		121	5.00E-27	41	39	
18926	ENU02720	ANI61C3667: 33-56 646..1311	33-56	632-656	NAP		g120593	319	74	8.00E-13			
18927	ENU02721	ANI61C1677: 22-49 5888..5223	22-49	626-645	NAP		g4038620	521	186	1.00E-46	51	83	
18928	ENU02722	ANI61C5936: 72-92 693..27	72-92	677-696	NAP		g3122054	1121	364	e-100	77	26	
18929	ENU02723	ANI61C5502: 27-47 520..1187	27-47	617-652	NAP		g1870209	961	265	e-104	86	40	
18930	ENU02724	ANI61C6250: 54-74 1768..1100	54-74	655-679	NAP		g4106682	245	59	7.00E-11	59	82	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18931	ENU02725	ANI61C9933: 144..812	61-80	666-687	NAP		g1175363	535	198	3.00E-50	44	70	hypothetical protein HI1014 ; hypothetical protein HI1014 - Haemophilus influenzae (strain Rd KW20) ; (U32782) conserved hypothetical protein [Haemophilus influenzae Rd] (AL034353) putative 60s ribosomal protein [Schizosaccharomyces pombe] (AF120278) proline dehydrogenase; PRODH [Homo sapiens] (U82513) random slug cDNA25 protein [Dictyostelium discoideum] (U00063) weakly similar to R. rickettsii protein P34 [Caenorhabditis elegans] (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] RAS-like GTP-binding protein RYL2 ; (L06970) ras-like protein [Yarrowia lipolytica] (Z97204) hypothetical protein [Schizosaccharomyces pombe] Cutinase precursor (L1) ; (D38311) Cutinase [Aspergillus oryzae] "NADH-ubiquinone oxidoreductase 21 KD subunit (complex I-21KD) (CI- 21KD) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 20.9K chain - Neurospora crassa ; (X60829) NADH dehydrogenase, 21 kDa subunit [Neurospora crassa]" putative 40S ribosomal protein YHR148W ; hypothetical protein YHR148w - yeast (Saccharomyces cerevisiae) ; (X69480) uORF1 [Saccharomyces cerevisiae] ; (U10397) Yhr148wp [Saccharomyces cerevisiae] (AE000955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus]
18932	ENU02726	ANI61C8405: 22-43	22-43	623-649	NAP		g3925782	333	146	1.00E-34	48	91	
18933	ENU02727	ANI61C205:1 45-66	45-66	653-672	NAP		g4581877	144	92	3.00E-18	30	40	
18934	ENU02728	ANI61C3750: 33-54	33-54	640-660	NAP		g2367392	873	118	4.00E-26	34	30	
18935	ENU02729	ANI61C1118 32-52	32-52	641-660	NAP		g488189	367	87	7.00E-22	29	51	
18936	ENU02730	ANI61C4356: 23-42	23-42	632-651	NAP		g1020413	319	145	4.00E-34	34	41	
18937	ENU02731	ANI61C8178: 66-85	66-85	676-695	NAP		g1173334	401	157	9.00E-38	52	82	
18938	ENU02732	ANI61C9465: 22-52	22-52	631-651	NAP		g2226413	148	41	0.00002	43	65	
18939	ENU02733	ANI61C1088 57-77	57-77	667-687	NAP		g1706202	656	152	1.00E-61	70	87	
18940	ENU02734	ANI61C9472: 44-64	44-64	646-674	NAP		g464287	410	145	2.00E-34	56	82	
18941	ENU02735	ANI61C4807: 25-47	25-47	631-655	NAP		g418596	431	91	3.00E-19	56	93	
18942	ENU02736	ANI61C11:25 22-53	22-53	632-652	NAP		g2648355	318	73	3.00E-17	34	72	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18943	ENU02737	ANI61C5118; 756..83	71-91	675-702	NAP		g2492756	213	47	0.0001			putative sterigmatocystin biosynthesis ketoreductase STCE ; (U34740)
18944	ENU02738	ANI61C1354; 23-53	23-53	635-654	NAP		g729965	467	124	9.00E-39	66	44	putative ketoreductase [Emericella nidulans]
18945	ENU02739	ANI61C3530; 26-45	26-45	638-657	NAP		g3420982	502	112	2.00E-24	57	52	"saccharopine dehydrogenase [NAD ⁺ , L-lysine forming] (lysine--2-oxoglutarate reductase) (SDH) ; saccharopine dehydrogenase (NAD ⁺ , L-lysine-forming) - yeast (Yarrowia lipolytica) (strain W29) ; (M34929)
18946	ENU02740	ANI61C5321; 57-76	57-76	663-689	NAP		g3947880	533	120	4.00E-49	62	98	saccharopine dehydrogenase [Yarrowia lipolytica]" (Z97628) Similarity to Brugia peptidylprolyl isomerase (TR:G984562) [Caenorhabditis elegans] ; (Z81080) Similarity to Brugia peptidylprolyl isomerase (TR:G984562) [Caenorhabditis elegans]
18947	ENU02741	ANI61C566;1 22-40	22-40	629-654	NAP		g1077519	163	85	4.00E-16	36	98	(AL034382) putative ras-related GTP-binding protein [Schizosaccharomyces pombe]
18948	ENU02742	ANI61C7088; 22-57	22-57	636-655	NAP		g626443	140	68	5.00E-11	32	96	hypothetical protein YDR071c - yeast (Saccharomyces cerevisiae) ; (Z46796) unknown [Saccharomyces cerevisiae] ; (Z74367) ORF YDR071c [Saccharomyces cerevisiae]
18949	ENU02743	ANI61C1134 54-73	54-73	668-687	NAP		g3876766	272	104	2.00E-23	45	86	hypothetical protein YLR193c - yeast (Saccharomyces cerevisiae) ; (U14913) Ylr193cp [Saccharomyces cerevisiae] (Z69637) predicted using Genefinder; Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]
18950	ENU02744	ANI61C1253; 25-44	25-44	637-659	NAP		g2995384	706	242	2.00E-71	83	82	(AJ004810) cytochrome P450 monooxygenase [Zea mays]
18951	ENU02745	ANI61C7538; 22-56	22-56	638-657	NAP		g4007800	323	61	3.00E-15	43	92	(AL034463) hypothetical protein [Schizosaccharomyces pombe]
18952	ENU02746	ANI61C9073; 30-49	30-49	634-665	NAP		g171567	338	131	7.00E-34	35	42	(K01609) gal1 [Saccharomyces carlsbergensis]

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18953	ENU02747	ANI61C7240: 3297..2620	70-92	686-705	NAP		g3006178	279	89	3.00E-17	32	32	(AL02304) putative rRNA transport regulator [Schizosaccharomyces pombe]
18954	ENU02748	ANI61C3687: 61-80	61-80	670-697	NAP		g3169083	261	108	4.00E-23	36	66	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
18955	ENU02749	ANI61C1049 7:1379..702	31-51	648-667	NAP		g3041738	1512	81	2.00E-51	61	35	"T-complex protein 1, ETA subunit (TCP-1-ETA) (CCT-ETA) (HIV-1 NEF interacting protein) ; (AF026292) chaperonin containing t-complex polypeptide 1, eta subunit; CCT-eta [Homo sapiens]"
18956	ENU02750	ANI61C5629: 40-59 4616..5294	40-59	643-676	NAP		g100489	133	72	3.00E-12			transposase Tam3 - garden snapdragon transposon Tam3 ; (X55078) Tam3-transposase [Antirrhinum majus] ; (AB013982) transposase [Antirrhinum majus] ; (AB013983) transposase [Antirrhinum majus] ; (AB013984) transposase [Antirrhinum majus] ; (AB013986) transposase [Antirrhinum majus] ; (AB013990) transposase [Antirrhinum majus] ; (AB013991) transposase [Antirrhinum majus] ; (AB013995) transposase [Antirrhinum majus] ; (AB013997) transposase [Antirrhinum majus]
18957	ENU02751	ANI61C7852: 57-88 1392..714	57-88	664-693	NAP		g3650378	1057	154	5.00E-37	51	10	(AL031740) putative rRNA biogenesis protein; rps5 homolog; multiple S1 rna binding domain protein
18958	ENU02752	ANI61C5415: 49-70 698..1378	49-70	668-687	NAP		g2414668	256	86	3.00E-16	39	85	[Schizosaccharomyces pombe] protein complex subunit
18959	ENU02753	ANI61C7921: 69-88 2564..1883	69-88	678-708	NAP		g2501555	296	100	3.00E-24	38	62	[Schizosaccharomyces pombe] possible apospory-associated protein C ; (U13148) possible apospory-associated protein [Pennisetum ciliare] (AJ131733) ubiquitin-conjugating enzyme E2 [Pseudotsuga menziesii]
18960	ENU02754	ANI61C7147: 33-53 5245..5927	33-53	639-673	NAP		g4090259	218	83	2.00E-15	37	85	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18961	ENU02755	ANI61C7273: 22-47 3619..2937	22-47	642-662	NAP		g1723256	227	84	2.00E-19	34	93	"hypothetical 23.0 KD protein C3F10.12C in chromosome I ; (Z69369) SPAC3F10.12c, unknown, 201, similar to transcription factors and SW:CBF1_yeast P17106 centromere-binding protei n 1 (39.8% identity in 113 aa) overlap), contains PS00038 Myc-type, 'helix-loop-helix' dimerization dom..."
18962	ENU02756	ANI61C7786: 25-47 2199..1516	25-47	647-666	NAP		g1363314	213	53	2.00E-11	36	19	probable cell division control protein p5CDC - rat ; (U05341) p55CDC [Rattus norvegicus]
18963	ENU02757	ANI61C1129 54-75 2:688..5	54-75	674-695	NAP		g549750	253	67	1.00E-10	39	71	hypothetical 29.4 KD protein in STE6-LOS1 intergenic region ; hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) ; (Z28207) ORF YKL207w [Saccharomyces cerevisiae]
18964	ENU02758	ANI61C566:5 22-50 915..6599	22-50	645-664	NAP		g1679882	1002	279	2.00E-74	61	31	(L35484) acetylglutamate synthase [Neurospora crassa]
18965	ENU02759	ANI61C6119: 23-44 2350..1665	23-44	647-666	NAP		g3123033	365	90	3.00E-31	37	86	vacuolar protein sorting-associated protein VPS28 ; hypothetical protein YPL065w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe5p [Saccharomyces cerevisiae] ; (U50630) Vps28p [Saccharomyces cerevisiae]
18966	ENU02760	ANI61C8915: 46-79 1782..1096	46-79	664-690	NAP		g1633466	111	56	0.000000	27	79	"Crystal Structure Of Bacteriorhodopsin In Purple Membrane ; Structure Of Bacteriorhodopsin At 3.0 Angstrom Determined By Electron Crystallography ; Chain A, X-Ray Structure Of The Bacteriorhodopsin Trimerlipid Complex ; Bacteriorhodopsinlipid complex " (AL031743) phosphatidylethanolamine methyltransferase.
18967	ENU02761	ANI61C6486: 22-51 1931..2617	22-51	638-666	NAP		g3650386	1486	102	3.00E-21	38	20	[Schizosaccharomyces pombe]
18968	ENU02762	ANI61C6019: 35-59 1760..1071	35-59	662-682	NAP		g3023397	320	160	8.00E-39	41	54	putative oxidoreductase precursor BLI-4 ; (X89499) bli-4 protein [Neurospora crassa]

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18969	ENU02763	ANI61C1042 7:1698..2387	32-51	660-679	NAP		g1730832	258	111	6.00E-24	37	61	hypothetical 31.6 KD protein in SIN4-URE2 intergenic region ; hypothetical protein YNL232w - yeast (Saccharomyces cerevisiae) ; (Z69381) N1154 [Saccharomyces cerevisiae] ; (Z71508) ORF YNL232w [Saccharomyces cerevisiae] (AB010439) steroid monooxygenase [Rhodococcus rhodochrous] ubiquitin carboxyl-terminal hydrolase 5 (ubiquitin thiolesterase 5) (ubiquitin-specific protease 5) ; (DEubiquitinating enzyme 5) ; ubiquitin-specific proteinase UBP5 (EC 3.4.-.-) - yeast (Saccharomyces cerevisiae) ; (U10082) ubiquitin-specific protease [Saccharomyces cerevisiae] ; (U18917) Ubp5p: ubiquitin-specific protease [Saccharomyces cerevisiae] (AE000848) ribonuclease PH [Methanobacterium thermoautotrophicum] (Z99165) dehydrogenase [Schizosaccharomyces pombe] (Z99118) similar to opine catabolism [Bacillus subtilis] "Phenylalanyl-tRNA synthetase beta chain cytoplasmic (phenylalanine--TRNA ligase beta chain) ; phenylalanine--tRNA ligase (EC 6.1.1.20) beta chain, cytosolic - yeast (Saccharomyces cerevisiae) ; (D50617) cytoplasmic phenylalanyl-tRNA synthetase beta chain [Saccharomyces cerevisiae]"
18970	ENU02764	ANI61C191:1 251..561	22-52	647-670	NAP		g2804298	89	68	5.00E-11	26	40	
18971	ENU02765	ANI61C8095: 52..743	72-92	702-721	NAP		g731042	398	118	1.00E-32			
18972	ENU02766	ANI61C6486: 5121..5812	55-74	675-704	NAP		g2621768	73	40	0.0003	31	72	
18973	ENU02767	ANI61C9140: 81..773	22-55	651-672	NAP		g2408060	306	133	1.00E-30	44	66	
18974	ENU02768	ANI61C1828: 2180..1488	56-76	687-706	NAP		g2635242	347	102	3.00E-21	28	65	
18975	ENU02769	ANI61C8024: 152..844	58-77	680-708	NAP		g1174509	898	315	2.00E-85	71	41	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18976	ENU02770	ANI61C4361: 67-86 890..197			NAP		g586321	47	0.000002				hypothetical 25.3 KD protein in RIM2-MS11 intergenic region; hypothetical protein YBR193c - yeast (Saccharomyces cerevisiae); (Z21487) unknown product [Saccharomyces cerevisiae]; (Z36062) ORF YBR193c [Saccharomyces cerevisiae] Potential proteasome component C5 (multicatalytic endopeptidase complex subunit C5); multicatalytic endopeptidase complex (EC 3.4.99.46) chain PRS3 - yeast (Saccharomyces cerevisiae); (M34777) proteasome subunit [Saccharomyces cerevisiae]; (D00845) proteasome subunit [Saccharomyces cerevisiae]; (X78214) PRS3 [Saccharomyces cerevisiae]; (Z35802) ORF YBL041w [Saccharomyces cerevisiae] (Y15013) copalyl diphosphate synthase [Gibberella fujikuroi] (AB024617) isotrichodermin C-15 hydroxylase [Gibberella zeae] (Z81110) predicted using GeneFinder; cDNA EST EMBL:D76086 comes from this gene; cDNA EST EMBL:T00045 comes from this gene; cDNA EST EMBL:T00046 comes from this gene; cDNA EST EMBL:D73101 comes from this gene; cDNA EST EMBL:C077... (AF063095) SELIL [Mus musculus] (AJ005963) 100 kDa protein [Ajellomyces capsulatus] "hypothetical 21.1 KD protein in FUS1-AGPI intergenic region; hypothetical protein YCL026c-a - yeast (Saccharomyces cerevisiae); (X59720) YCL026c-a, len:192 [Saccharomyces cerevisiae] "
18977	ENU02771	ANI61C3960: 23-58 920..226		646-675	NAP		g130882	593	259	2.00E-68			
18978	ENU02772	ANI61C7782: 60-79 719..25		690-712	NAP		g3549899	1287	146	1.00E-34	32	23	
18979	ENU02773	ANI61C548:7 69-88 87..93		698-721	NAP		g4589927	232	52	3.00E-13	32	39	
18980	ENU02774	ANI61C5279: 28-47 94..789		662-681	NAP		g3879255	261	117	7.00E-26	34	56	
18981	ENU02775	ANI61C6626: 69-88 4422..5118		704-723	NAP		g4159995	577	93	2.00E-18			
18982	ENU02776	ANI61C4759: 46-65 28..724		680-700	NAP		g3135013	808	323	1.00E-87	66	25	
18983	ENU02777	ANI61C322:5 52-71 962..5264		688-707	NAP		g586554	160	56	0.000000	32	92	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
18984	ENU02778	ANI61C8274: 1073..376	72-93	708-727	NAP		g1171666	303	70	3.00E-16	51	87	NADH-ubiquinone oxidoreductase 14.8 KD subunit (complex I-14.8KD) (CI-14.8KD) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) - Neurospora crassa ; (X76344) NADH dehydrogenase (ubiquinone) [Neurospora crassa]
18985	ENU02779	ANI61C7893: 87..787	43-62	679-701	NAP		g1708501	245	73	8.00E-22	36	11	Integrin alpha chain-like protein (alpha-INT1) ; (U35070) integrin-like protein alpha Int1p [Candida albicans]
18986	ENU02780	ANI61C301:5 9..761	24-43	650-684	NAP		g1064798	256	83	6.00E-20	40	47	(D78193) homologous to gp:PSEFD_1 (formaldehyde dehydrogenase) [Bacillus subtilis] ; (Z99124) similar to formaldehyde dehydrogenase [Bacillus subtilis]
18987	ENU02781	ANI61C1078 9:1345..643	57-82	697-717	NAP		g3152652	365	155	4.00E-37	38	49	"(AF064870) endo-1,3(4)-beta-glucanase [Xanthophyllomyces dendrorhous]"
18988	ENU02782	ANI61C3321: 1870..2572	57-77	698-717	NAP		g1723660	211	76	6.00E-20	33	89	hypothetical 27.6 KD protein in RPL26B-ACB1 intergenic region ; probable membrane protein YGR036c - yeast (Saccharomyces cerevisiae) ; (Z72821) ORF YGR036c [Saccharomyces cerevisiae]
18989	ENU02783	ANI61C301:5 9..761	24-43	650-684	NAP		g1064798	256	83	6.00E-20	40	47	(D78193) homologous to gp:PSEFD_1 (formaldehyde dehydrogenase) [Bacillus subtilis] ; (Z99124) similar to formaldehyde dehydrogenase [Bacillus subtilis]
18990	ENU02784	ANI61C3956: 704..1	42-74	677-703	NAP		g3702646	401	66	3.00E-10			(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
18991	ENU02785	ANI61C6073: 648..705	23-42	659-684	NAP		g2132916	448	136	2.00E-31	43	32	probable membrane protein YOR206w - yeast (Saccharomyces cerevisiae) ; (Z75114) ORF YOR206w [Saccharomyces cerevisiae]
18992	ENU02786	ANI61C2284: 5724..6427	70-90	707-731	NAP		g3766371	328	152	2.00E-36	40	90	(AL031907) hypothetical protein [Schizosaccharomyces pombe]
18993	ENU02787	ANI61C7986: 1000..898	63-82	705-724	NAP		g3006189	646	81	4.00E-32	63	62	(AL022304) 60s ribosomal protein l7-c. [Schizosaccharomyces pombe]

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18994	ENU02788	ANI61C7899: 40-59 4999..4295	40-59	680-702	NAP		g417305	788	113	2.00E-30	42	35	"mannosyl-oligosaccharide alpha-1,2-mannosidase (MAN(9)-alpha-mannosidase) ; alpha-mannosidase MNS1 (EC 3.2.1.-) - yeast (Saccharomyces cerevisiae) ; (M63598) alpha-mannosidase [Saccharomyces cerevisiae] ; (Z49631) ORF YJR131w [Saccharomyces cerevisiae] "
18995	ENU02789	ANI61C6615: 72-96 2346..1642	72-96	715-734	NAP		g1363710	345	90	2.00E-17	27	54	probable membrane protein YLR130c - yeast (Saccharomyces cerevisiae) ; (X91258) L3120 [Saccharomyces cerevisiae] ; (U53881) Ylr130cp [Saccharomyces cerevisiae] ; (Z73302) ORF YLR130c [Saccharomyces cerevisiae]
18996	ENU02790	ANI61C8963: 62-81 3632..4337	62-81	706-725	NAP		g1507666	100	38	0.073			(D84656) ORF N118 [Schizosaccharomyces pombe]
18997	ENU02791	ANI61C7925: 59-82 1866..2573	59-82	699-723	NAP		g1703215	374	77	2.00E-16	31	37	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
18998	ENU02792	ANI61C1046 24-46 1:848..1554	24-46	662-688	NAP		g4028590	625	144	3.00E-54	89	99	[AF104986] calmodulin [Magnaporthe grisea]
18999	ENU02793	ANI61C1518: 34-63 2666..1960	34-63	668-698	NAP		g117619		80	2.00E-17			choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19000	ENU02794	ANI61C7112: 66-85 2765..3471	66-85	710-730	NAP		g1175951	328	114	1.00E-25	40	91	hypothetical 24.0 KD protein in EMP47-SEC53 intergenic region ; probable membrane protein YFL046w - yeast (Saccharomyces cerevisiae) ; (D50617) YFL046W [Saccharomyces cerevisiae]
19001	ENU02795	ANI61C9541: 61-92 60..767	61-92	700-726	NAP		g4160573	199	86	3.00E-16	33	24	(AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]

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19002	ENU02796	ANI61C7325: 24-43	3090..2383	670-689	NAP		g3417433	411	117	9.00E-26	46	57	(AL031262) putative transcription factor [Schizosaccharomyces pombe]
19003	ENU02797	ANI61C3136: 22-52	1862..1155	668-687	NAP		g3914054	783	256	1.00E-67	53	30	MUTS protein homolog 1 ; (Z98559) dna mismatch repair muts family [Schizosaccharomyces pombe]
19004	ENU02798	ANI61C7529: 22-53	1958..1251	663-687	NAP		g4160343	482	102	8.00E-28	37	69	(AL035216) similar to rat synaptic glycoprotein sc2 [Schizosaccharomyces pombe]
19005	ENU02799	ANI61C7521: 40-59	949..241	687-706	NAP		g117093	285	69	4.00E-13	50	86	cytochrome C oxidase polypeptide VI precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain VI precursor - yeast (Saccharomyces cerevisiae) ; (M10138) cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] ; (U00062) Cox6p: cytochrome c oxidase subunit VI [Saccharomyces cerevisiae] (U16782) chlorophenol monooxygenase [Ralstonia eutropha] (U33115) high copy suppressor of polymerase alpha mutations [Saccharomyces cerevisiae] "lysozyme M1 precursor (1,4-beta-N-acetylmuramidase M1) ; lysozyme (EC 3.2.1.17) M1 precursor - Streptomyces globisporus ; (M30645) N-acetylmuramidase M1 precursor [Streptomyces globisporus] " (U85498) glutamate-cysteine ligase catalytic subunit [Mus musculus] hypothetical protein YOR252w - yeast (Saccharomyces cerevisiae) ; (Z75160) ORF YOR252w [Saccharomyces cerevisiae]
19006	ENU02800	ANI61C1008 34-53	814..556	680-700	NAP		g1764155	252	134	5.00E-31	42	39	mitochondrial carrier protein PMT ; mitochondrial uncoupling protein homolog YKL120w - yeast (Saccharomyces cerevisiae) ; (L04948) mitochondrial transporter protein [Saccharomyces cerevisiae] ; (Z28120) ORF YKL120w [Saccharomyces cerevisiae]
19007	ENU02801	ANI61C4037: 67-87	898..187	701-736	NAP		g992654	72	46	9.00E-10	45	8	
19008	ENU02802	ANI61C8195: 22-39	1171..1882	668-691	NAP		g126652	315	144	9.00E-35	38	71	
19009	ENU02803	ANI61C2626: 23-45	82..793	670-692	NAP		g1945070	727	223	9.00E-58	51	34	
19010	ENU02804	ANI61C3329: 71-91	2735..2631	714-741	NAP		g2132100		75	4.00E-13	30	87	
19011	ENU02805	ANI61C8183: 34-53	108..820	684-704	NAP		g417500	568	127	6.00E-44	55	62	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19012	ENU02806	ANI61C1120 5:6686..5974	55-78	704-725	NAP		g2833337	103	73	2.00E-12	30	36	Dihydrofolate reductase / thymidylate synthase (DHFR-TS) ; (U20781) dihydrofolate reductase-thymidylate synthase [Trypanosoma brucei] (AJ009973) hexokinase [Aspergillus niger] choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19013	ENU02807	ANI61C2275: 65-86 1667..955	65-86	716-735	NAP		g4140255	2000	401	e-111	83	48	
19014	ENU02808	ANI61C559:8 37..124	22-49	664-693	NAP		g117619		37	0.17			
19015	ENU02809	ANI61C7117: 27-46 1674..961	27-46	676-698	NAP		g4249578	892	355	2.00E-97	75	97	(AF022892) orotidine monophosphate pyrophosphorylase [Coccidioides immitis] "(S76267) Snq2 homolog=bfr1 [Schizosaccharomyces pombe=fission yeast, Peptide, 1530 aa] [Schizosaccharomyces pombe]" (U41625) coded for by C. elegans cDNA yk52e10.5; coded for by C. elegans cDNA yk52e10.3; coded for by C. elegans cDNA yk50f4.3; coded for by C. elegans cDNA yk50f4.5; Similar to acetyl-coenzyme A synthetase. [Caenorhabditis elegans] (AF036871) annexin XIV [Neurospora crassa]
19016	ENU02810	ANI61C414:1 4..724	26-51	675-698	NAP		g913016	332	124	3.00E-32	37	14	
19017	ENU02811	ANI61C1124: 22-45 887..1601	22-45	667-694	NAP		g1118129	524	88	4.00E-27	41	25	
19018	ENU02812	ANI61C2113: 71-90 847..132	71-90	725-744	NAP		g3004934	490	144	6.00E-34	35	49	
19019	ENU02813	ANI61C8918: 54-74 643..1358	54-74	697-727	NAP		g2132018	288	96	2.00E-25	36	94	hypothetical protein YOL135c - yeast (Saccharomyces cerevisiae) ; (Z74877) ORF YOL135c [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae] acid proteinase eapC precursor - chestnut blight fungus ; (X83997) acid proteinase [Cryphonectria parasitica]
19020	ENU02814	ANI61C8241: 30-49 1541..2257	30-49	673-704	NAP		g2133287	421	189	2.00E-47	43	85	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19021	ENU02815	ANI61C952:1 569..852	34-68	683-709	NAP		g130582	173	92	4.00E-18	28	17	Retrovirus-related pol polyprotein from transposon TNT 1-94 [contains: protease; reverse transcriptase ; endonuclease] ; hypothetical protein - common tobacco ; (X13777) ORF [Nicotiana tabacum]
19022	ENU02816	ANI61C9559: 23-58 713..1430	23-58	678-698	NAP		g3913768	102	61	0.000000 009	28	98	phosphoglycolate phosphatase (PGP) ; (AE000735) phosphoglycolate phosphatase [Aquifex aeolicus]
19023	ENU02817	ANI61C6527: 66-84 2787..2619	66-84	722-741	NAP		g3122361	271	116	2.00E-25	42	86	putative lipote-protein ligase B (lipote biosynthesis protein B) ; (Z98980) hypothetical protein [Schizosaccharomyces pombe]
19024	ENU02818	ANI50C2369 22-43 01_1:30..748	22-43	672-698	NAP		g118126		59	0.000000 05	36	90	regulatory protein CYS-3 ; regulatory protein cys-3 - Neurospora crassa ; (M26008) cys-3 [Neurospora crassa]
19025	ENU02819	ANI61C1250: 36-55 3498..2780	36-55	693-712	NAP		g2499588	1079	248	e-100	98	62	cell division control protein 2 (cyclin-dependent protein kinase) ; (U07169) protein kinase functional homolog of cdc2 [Emicella nidulans]
19026	ENU02820	ANI61C1099 44-65 9:1170..1888	44-65	689-720	NAP		g2804298	372	85	4.00E-16	32	28	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
19027	ENU02821	ANI61C1040 27-47 9:1373..655	27-47	684-703	NAP		g2132880	284	83	8.00E-23	27	89	probable membrane protein YOR087w - yeast (Saccharomyces cerevisiae) ; (Z74995) ORF YOR087w [Saccharomyces cerevisiae]
19028	ENU02822	ANI61C5788: 22-49 5396..6114	22-49	678-698	NAP		g131031	328	113	1.00E-29	41	96	putative PRT1 protein ; probable PRT1 protein - yeast (Hansenula polymorpha) ; (X15111) put. PRT1 protein (AA 1-221) (1 is 1st base in codon) [Pichia angusta]
19029	ENU02823	ANI61C1758: 72-92 10004..9286	72-92	729-748	NAP		g2497056	214	86	3.00E-16	36	47	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
19030	ENU02824	ANI61C1211: 22-41 821..102	22-41	680-699	NAP		g3183014	706	150	3.00E-65	65	85	GTP cyclohydrolase I (GTP-CH-I) ; (Z98849) gtp cyclohydrolase I [Schizosaccharomyces pombe]

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19031	ENU02825	ANI61C8770: 47-67 4573..3854	47-67	698-724	NAP		g2981719	776	91	1.00E-30	44	30	Crystal Structures Of The Copper-Containing Amine Oxidase From Arthrobacter Globiformis In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone ; Crystal Structures Of The Copper-Containing Amine Oxidase From Arthrobacter Globiformis In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone
19032	ENU02826	ANI61C6467: 22-47 2814..3534	22-47	681-700	NAP		g461926	228	69	5.00E-22	33	95	Haloacetate dehalogenase H-2 ; haloacetate dehalogenase (EC 3.8.1.3) H-2 - Moraxella sp. plasmid pUOI ; (D90423) haloacetate dehalogenase H-2 [Moraxella sp.]
19033	ENU02827	ANI61C9085: 57-76 505..1225	57-76	716-735	NAP		g2506921	158	45	0.0006	37	55	"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613) dioxygenase [Escherichia coli] ; (U73857) dioxygenase [Escherichia coli] ; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli] "
19034	ENU02828	ANI61C3566: 44-65 3337..4058	44-65	697-723	NAP		g731439	132	54	0.000001	28	91	hypothetical 25.6 KD protein in NTF2-SRP1 intergenic region ; hypothetical protein YER010c - yeast (Saccharomyces cerevisiae) ; (U18778) Yer010cp [Saccharomyces cerevisiae] (AF051914) C-4 methyl sterol oxidase [Candida albicans] (AL035521) hypothetical protein [Arabidopsis thaliana] (Z98056) putative glyoxylate pathway regulator [Schizosaccharomyces pombe]
19035	ENU02829	ANI61C353:2 27-56 718..3439	27-56	688-706	NAP		g2970627	908	304	4.00E-82	60	71	
19036	ENU02830	ANI61C8203: 23-44 39..760	23-44	682-702	NAP		g4455171	303	146	1.00E-34	33	27	
19037	ENU02831	ANI61C7700: 57-76 3994..3273	57-76	717-736	NAP		g2281979	362	131	5.00E-30	46	64	
19038	ENU02832	ANI61C9556: 26-45 759..37	26-45	687-706	NAP		g2330757	649	259	4.00E-68	61	86	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19039	ENU02833	ANI61C1110 7:5697..6419	42-66	703-722	NAP		g585896	267	130	1.00E-29	38	94	"probable mitochondrial 60S ribosomal protein L16 precursor ; ribosomal protein L16 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X78214) L16 ribosomal protein [Saccharomyces cerevisiae] ; (Z35799) ORF YBL038w [Saccharomyces cerevisiae] "
19040	ENU02834	ANI61C590:8 40..117	45-65	707-726	NAP		g549607	409	125	2.00E-36	38	35	hypothetical 74.7 KD TRP-ASP repeats containing protein in DAL80-GAP1 intergenic region ; hypothetical protein YKR036c - yeast (Saccharomyces cerevisiae) ; (Z28261) ORF YKR036c [Saccharomyces cerevisiae]
19041	ENU02835	ANI61C6543: 27-52 3639..2915	27-52	690-709	NAP		g2414650	346	93	2.00E-31	69	93	(Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe]
19042	ENU02836	ANI61C7500: 22-51 2405..1681	22-51	684-704	NAP		g3426048	540	167	6.00E-52	51	50	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]
19043	ENU02837	ANI61C4138: 57-76 622..1346	57-76	719-739	NAP		g2496621	310	118	3.00E-26	50	64	hypothetical monooxygenase Y4FC ; (AE000072) Y4fC [Rhizobium sp. NGR234]
19044	ENU02838	ANI61C1289: 23-48 12..737	23-48	685-706	NAP		g3738145	147	90	1.00E-17	31	64	(AL031852) short-chain dehydrogenase [Schizosaccharomyces pombe]
19045	ENU02839	ANI61C5187: 60-80 2678..1953	60-80	721-743	NAP		g1870209	857	132	4.00E-34	38	42	(AC000133) ORF [Emericella nidulans]
19046	ENU02840	ANI61C3158: 50-69 1742..2468	50-69	715-734	NAP		g1723421	318	87	1.00E-16	34	78	ALP11 protein ; (Z69727) homolog of co-factor B [Schizosaccharomyces pombe] ; (AB008750) Alp11 [Schizosaccharomyces pombe]
19047	ENU02841	ANI61C6895: 23-43 1106..1832	23-43	688-707	NAP		g140519	120	74	9.00E-13	29	72	"hypothetical 29.0 KD protein in PWP2-SUP61 intergenic region ; probable membrane protein YCR059c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR059c, len:258 [Saccharomyces cerevisiae] "
19048	ENU02842	ANI61C5862: 25-49 104..830	25-49	684-709	NAP		g3183130	554	200	1.00E-50	52	52	probable glutamate 5-kinase (gamma-glutamyl kinase) (GK) ; (Z98597) hypothetical glutamate 5-kinase [Schizosaccharomyces pombe]

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19049	ENU02843	ANI61C3285: 33-52 2094..1367		700-718	NAP		g3850101	378	137	7.00E-32	47	93	protein [Schizosaccharomyces pombe] (AL033388) putative rna-binding protein [Schizosaccharomyces pombe] (AL023589) membrane transporter [Schizosaccharomyces pombe] hypothetical 77.0 KD protein in HES1-SEC63 intergenic region ; hypothetical protein YOR243c - yeast (Saccharomyces cerevisiae) ; (Z75151) ORF YOR243c [Saccharomyces cerevisiae]
19050	ENU02844	ANI61C459:7 60-79 441..6714		726-745	NAP		g3135988	652	69	3.00E-19	46	37	
19051	ENU02845	ANI61C5557: 56-77 147..875		723-742	NAP		g2501603	311	123	9.00E-28	38	31	
19052	ENU02846	ANI61C1617: 23-41 47..774		688-709	NAP		g1806234		63	1.00E-16			(Z84498) hypothetical protein Rv1928c [Mycobacterium tuberculosis]
19053	ENU02847	ANI61C7616: 64-83 1734..1006		731-750	NAP		g2697132	287	87	3.00E-22	36	84	inducing peptide [Fusarium oxysporum f. sp. erythroxyli] " (U39812) beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus] "
19054	ENU02848	ANI61C990:2 69-88 444..1716		735-755	NAP		g1491795	486	201	6.00E-51	38	26	Pisatin demethylase (cytochrome P450 57A2) ; pisatin demethylase - fungus (Nectria haematococca) ; (X73145) pisatin demethylase [Nectria haematococca]
19055	ENU02849	ANI61C3212: 34-53 197..925		699-720	NAP		g585695	232	120	1.00E-26	32	41	[Schizosaccharomyces pombe] hypothetical 36.3 KD protein C56F8.09 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe] hypothetical 33.7 KD protein in ISC10 3'region ; hypothetical protein YER185w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer185wp [Saccharomyces cerevisiae] (Z83828) AmMst-1 [Amanita muscaria]
19056	ENU02850	ANI61C1640: 34-53 1744..1016		699-720	NAP		g3006187	283	134	5.00E-31	35	74	hypothetical 79.5 KD protein C17A5.12 in chromosome I ; (Z98849) hypothetical protein [Schizosaccharomyces pombe]
19057	ENU02851	ANI61C3047: 56-77 4114..3386		723-742	NAP		g1723441	353	95	6.00E-19	40	51	
19058	ENU02852	ANI61C3602: 47-66 6005..6734		707-733	NAP		g731385	269	63	3.00E-17	39	73	
19059	ENU02853	ANI61C2954: 48-67 27..756		714-735	NAP		g2258125	164	64	0.000000	29	39	
19060	ENU02854	ANI61C8514: 67-87 1538..808		722-755	NAP		g3287949	418	147	3.00E-39	41	30	

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19061	ENU02855	ANI61C943:1 05..835	33-52	700-721	NAP		g140459	61	0.000000	01			"hypothetical 30.7 KD protein in RVS161-ADP1 intergenic region ; hypothetical protein YCR010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR010c, len:283 [Saccharomyces cerevisiae] "
19062	ENU02856	ANI61C7480: 70-88 136..867	70-88	735-759	NAP		g3915154	245	102	3.00E-21	33	39	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
19063	ENU02857	ANI61C6213: 69-100 4926..4195	69-100	740-758	NAP		g113449	552	152	2.00E-36	47	21	"probable ATP-dependent permease precursor ; ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae) ; (X59720) YCR011c, len:1049 [Saccharomyces cerevisiae] "
19064	ENU02858	ANI61C9775: 55-75 4974..4243	55-75	724-744	NAP		g731723	589	178	5.00E-44	46	68	hypothetical 34.9 KD protein in RPL44-DCD1 intergenic region ; hypothetical protein YHR142w - yeast (Saccharomyces cerevisiae) ; (U10397) Yhr142wp [Saccharomyces cerevisiae] (AB013443) cytochrome P450 [Coprinus cinereus]
19065	ENU02859	ANI61C1733: 72-99 1013..279	72-99	742-762	NAP		g3721844	296	73	5.00E-25	36	40	carrier protein [Candida albicans] (AL033503) putative mitochondrial
19066	ENU02860	ANI61C7086: 22-41 1010..278	22-41	693-712	NAP		g3859687	527	150	8.00E-36	53	77	putative para-hydroxybenzoate—polyprenyltransferase precursor (PHB:polyprenyltransferase) ; (Z69728) unknown
19067	ENU02861	ANI61C920:1 46-65 364..631	46-65	717-737	NAP		g1706003	76	3.00E-13				[Schizosaccharomyces pombe]
19068	ENU02862	ANI61C2401: 40-59 1006..273	40-59	711-731	NAP		g136372	2405	310	e-109	80	34	Tryptophan synthase ; tryptophan synthase (EC 4.2.1.20) - Neurospora crassa ; (J04594) tryptophan synthetase [Neurospora crassa]
19069	ENU02863	ANI61C5992: 69-87 8770..8037	69-87	728-760	NAP		g1352065	69	2.00E-11				acetyl-hydrolase ; (M64783) acetyl-hydrolase [Streptomyces hygroscopicus]
19070	ENU02864	ANI61C933:1 25-54 777..1043	25-54	695-717	NAP		g4539598	322	76	9.00E-15	33	62	(AL049522) putative phosphatase component [Schizosaccharomyces pombe]

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19071	ENU02865	ANI61C7676: 68-87 86..820		728-760	NAP		g3123232	643	152	1.00E-58	53	78		general stress protein 39 (GSP39) ; (AB001488) belongs to the insect-type alcohol dehydrogenase / ribitol dehydrogenase family. [Bacillus subtilis] ; (Z99106) similar to alcohol dehydrogenase [Bacillus subtilis] "Chain N, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution ; Chain 2, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution "
19072	ENU02866	ANI61C8467: 23-48 1309..574		694-716	NAP		g3114282	484	163	1.00E-39	47	93		hypothetical 25.2 KD protein in THI5 5'region and in THI12 5'region ; hypothetical protein YFL061w - yeast (Saccharomyces cerevisiae) ; (D50617) YFL061W [Saccharomyces cerevisiae] ; (D44603) unknown [Saccharomyces cerevisiae] ; (Z71611) ORF YNL335w [Saccharomyces cerevisiae] (Y11113) endoglucanase IV [Hypocrea jecorina] (AL034583) hypothetical protein [Schizosaccharomyces pombe] (D85230) hypothetical protein [Plectonema boryanum] hypothetical 69.8 KD protein in BDF1-SFP1 intergenic region ; hypothetical protein YLR401c - yeast (Saccharomyces cerevisiae) ; (U19729) Ylr401cp [Saccharomyces cerevisiae] (U61840) sodium transport ATPase FST [Fusarium solani f. sp. pisi] (Z99759) hypothetical protein [Schizosaccharomyces pombe] glutamate synthase (NADH) precursor (NADH-GOGAT) ; glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa ; (L01660) NADH-glutamate synthase [Medicago sativa]
19073	ENU02867	ANI61C9642: 40-59 5076..4339		706-735	NAP		g1175965	388	171	5.00E-42	41	99		
19074	ENU02868	ANI61C6810: 22-41 3610..4347		692-717	NAP		g2315274	731	297	5.00E-80	56	70		
19075	ENU02869	ANI61C7686: 54-73 1321..584		730-749	NAP		g4056557	266	107	8.00E-23				
19076	ENU02870	ANI61C4371: 33-53 118..858		712-731	NAP		g1339949	174	73	2.00E-12	26	91		
19077	ENU02871	ANI61C1115 24-44 7:847..107		702-722	NAP		g2833203	515	189	1.00E-47	50	35		
19078	ENU02872	ANI61C1748: 64-86 44..784		739-762	NAP		g1438947	932	269	2.00E-94	68	46		
19079	ENU02873	ANI61C1111 42-71 9:21..761		721-740	NAP		g2467272	867	356	9.00E-98	72	31		
19080	ENU02874	ANI61C1719: 40-60 1987..1246		720-739	NAP		g417073	754	302	1.00E-81	58	11		

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19081	ENU02875	ANI61C7336: 6318..7060	72-92	753-772	NAP		g2808725	814	201	0.000000	48	65	(AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis]
19082	ENU02876	ANI61C280-2: 25-45	25-45	706-725	NAP		g113589	814	201	4.00E-51	48	65	Allantoicase ; allantoicase (EC 3.5.3.4) - Neurospora crassa ; (J02927)
19083	ENU02877	ANI61C5029: 33-53	33-53	709-734	NAP		g3183342	248	102	3.00E-21	36	57	allantoicase [Neurospora crassa] hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein
19084	ENU02878	ANI61C5155: 43-62	43-62	717-744	NAP		g2132846	79	4.00E-14				[Schizosaccharomyces pombe] probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]
19085	ENU02879	ANI61C6256: 27-47	27-47	709-728	NAP		g731773	599	105	2.00E-44	59	69	hypothetical 31.9 KD protein in BET1-PAN1 intergenic region ; probable membrane protein YIL003w - yeast (Saccharomyces cerevisiae)
19086	ENU02880	ANI61C4645: 30-61	30-61	713-732	NAP		g2132214	233	98	7.00E-20			hypothetical protein YPL164c - yeast (Saccharomyces cerevisiae) ; (Z73520) ORF YPL164c [Saccharomyces cerevisiae] ; (X96770) P2550 protein [Saccharomyces cerevisiae]
19087	ENU02881	ANI61C6841: 72-96	72-96	741-774	NAP		g1781102	552	185	4.00E-46	38	50	(Z83864) hypothetical protein Rv3854c [Mycobacterium tuberculosis]
19088	ENU02882	ANI61C1062: 54-74	54-74	735-756	NAP		g586554	137	54	0.000001	29	92	"hypothetical 21.1 KD protein in FUS1-AGP1 intergenic region ; hypothetical protein YCL026c-a - yeast (Saccharomyces cerevisiae) ; (X59720) YCL026c-a, len:192 [Saccharomyces cerevisiae]"
19089	ENU02883	ANI61C1146: 54-73	54-73	737-756	NAP		g2950465	544	144	8.00E-34	37	52	(AL022071) fructosyl amine [Schizosaccharomyces pombe]
19090	ENU02884	ANI61C7987: 46-74	46-74	725-748	NAP		g4490679	180	82	6.00E-15	56	43	(AL035635) 60s ribosomal protein l36 [Schizosaccharomyces pombe]

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19091	ENU02885	ANI61C1043 6:2415..3160	44-64	728-747	NAP		g231710	779	256	1.00E-67	86	89	cell division control protein 42 homolog (CDC42SP) ; cell division control protein CDC42 - fission yeast (Schizosaccharomyces pombe) ; (M83650) CDC42sp [Schizosaccharomyces pombe] ; (L25677) Cdc42p [Schizosaccharomyces pombe] hypothetical 22.4 KD protein C6G10.10C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] (AE000853) conserved protein [Methanobacterium thermoautotrophicum] acetyl-CoA hydrolase (acetyl-CoA deacylase) (acetyl-CoA acylase) (acetate utilization protein) ; acu-8 protein - Neurospora crassa ; (M31521) acetate permease (acu-8) [Neurospora crassa]
19092	ENU02886	ANI61C4663: 22-41 4535..5281	22-41	705-725	NAP		g3219969	156	70	2.00E-11	29	96	"phospho-2-dehydro-3-deoxyheptonate aldolase, tyrosine-inhibited (phospho-2-keto-3-deoxyheptonate aldolase) (DAHP synthetase) (3-deoxy-D-arabino-heptulosonate 7-phosphate synthase) ; 2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) ARO4 - yeast (Saccharomyces cerevisiae) ; (L20296) homology with DAHP-synthase (ARO4) gene [Saccharomyces cerevisiae] ; (X61107) phospho-2-dehydro-3-deoxyheptonate aldolase [Saccharomyces cerevisiae] ; (Z36118) ORF YBR249c [Saccharomyces cerevisiae] "
19093	ENU02887	ANI61C7186: 30-52 317..1063	30-52	715-734	NAP		g2621836	150	84	9.00E-16	32	92	(AL031853) putative zinc finger protein [Schizosaccharomyces pombe] (AB014595) KIAA0695 protein [Homo sapiens]
19094	ENU02888	ANI61C8897: 60-81 3183..2437	60-81	741-764	NAP		g113310	1070	193	6.00E-99	79	47	
19095	ENU02889	ANI61C6534: 22-45 3269..2523	22-45	707-726	NAP		g461540	883	336	9.00E-92			
19096	ENU02890	ANI61C3210: 49-68 87..834	49-68	729-754	NAP		g3738206	215	46	0.0003			
19097	ENU02891	ANI61C4686: 30-49 89..838	30-49	715-737	NAP		g3327204	609	125	8.00E-44	44	31	

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19098	ENU02892	ANI61C8599: 47-66 2096..1347	47-66	736-755	NAP		g465105	644	174	1.00E-61	54	31	(U04841) lanosterol synthase [Saccharomyces cerevisiae]
19099	ENU02893	ANI61C4266: 45-64 2651..1899	45-64	725-755	NAP		g731476	201	81	1.00E-14	42	55	hypothetical 14.4 KD protein in RNR1-ALD3 intergenic region ; hypothetical protein YER072w - yeast (Saccharomyces cerevisiae) ; (U18813) Yer072wp [Saccharomyces cerevisiae] (AF008220) yteR [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis] (AF025475) Masc1 [Ascobolus immersus] (AE001036) L-carnitine dehydratase (catB-2) [Archaeoglobus fulgidus] (AL049558) putative phosphatidylinositol-kinase [Schizosaccharomyces pombe] (AL035218) conserved hypothetical protein [Schizosaccharomyces pombe] ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase HUS5) (ubiquitin carrier protein HUS5) ; HUS5 protein - fission yeast (Schizosaccharomyces pombe) ; (X81846) hus5 [Schizosaccharomyces pombe] ; (Z67961) ubiquitin conjugating enzyme [Schizosaccharomyces pombe] ; ubiquitin-conjugating enzyme [Schizosaccharomyces pombe]
19100	ENU02894	ANI61C1600: 43-67 1103..351	43-67	732-753	NAP		g2293194	289	89	4.00E-23			NOT56-like protein ; (Y09022) Not56-like protein [Homo sapiens] ERV25 protein precursor ; probable membrane protein YML012w - yeast (Saccharomyces cerevisiae) ; (Z49810) unknown [Saccharomyces cerevisiae] (Z97336) carnitine racemase homolog [Arabidopsis thaliana] (AL034565) putative abhydrolase [Schizosaccharomyces pombe]
19101	ENU02895	ANI61C9279: 34-53 1147..395	34-53	722-744	NAP		g2558956	343	124	5.00E-34	40	43	
19102	ENU02896	ANI61C9067: 62-86 864..1617	62-86	746-773	NAP		g2649608		60	4.00E-17			
19103	ENU02897	ANI61C8232: 62-82 1133..379	62-82	752-774	NAP		g4581508	727	190	4.00E-69	63	11	
19104	ENU02898	ANI61C8865: 33-52 310..1064	33-52	726-745	NAP		g4160583	699	281	4.00E-75	53	80	
19105	ENU02899	ANI61C1147: 23-48 976..1731	23-48	714-736	NAP		g731040	531	157	6.00E-38			
19106	ENU02900	ANI61C1073: 60-80 6:1321..566	60-80	754-773	NAP		g3024226	547	69	2.00E-23	35	53	
19107	ENU02901	ANI61C352:7 26-46 587..8342	26-46	719-739	NAP		g1730615	390	107	3.00E-36	48	90	
19108	ENU02902	ANI61C7690: 65-84 793..36	65-84	751-780	NAP		g2244799	108	62	0.000000	32	69	
19109	ENU02903	ANI61C1026: 22-49 1372..2129	22-49	709-737	NAP		g4049528	342	82	1.00E-25	39	70	

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19110	ENU02904	ANI61C5273: 22-52 6842..6081	22-52	721-740	NAP		g731758	419	176	1.00E-43	44	37	hypothetical 67.8 KD protein in IKI1-ERG9 intergenic region; hypothetical protein YHR188c - yeast (Saccharomyces cerevisiae) ; (U00030)
19111	ENU02905	ANI61C2115: 63-87 784..23	63-87	750-782	NAP		g1747324	200	68	3.00E-18	47	76	Yhr188cp [Saccharomyces cerevisiae] (D85777) cysteine dioxygenase [Homo sapiens]
19112	ENU02906	ANI61C9458: 48-72 1566..804	48-72	740-767	NAP		g731294	532	108	3.00E-41	39	59	hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN50 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Yal061wp [Saccharomyces cerevisiae]
19113	ENU02907	ANI61C9311: 40-60 2143..2904	40-60	735-759	NAP		g465975	1254	314	4.00E-85			"putative ATP-dependent RNA helicase T26G10.1 in chromosome III ; ATP-dependent RNA helicase homolog T26G10.1 - Caenorhabditis elegans ; (Z29115) similar to RNA helicases, deleted exon 1397-1495 which introduced stop codon at 3' splice; 5' splice looks v. good; ?possible alternate final exon; cDNA EST yk368a4.3 comes from this gene; cDNA EST yk368a4.5 comes fr..."
19114	ENU02908	ANI61C8348: 22-46 1359..596	22-46	723-743	NAP		g549012	512	216	2.00E-55	44	98	matting-type switching protein SWI10 ; SWI10 protein - fission yeast (Schizosaccharomyces pombe) ; (X61926) SWI10 [Schizosaccharomyces pombe] ; (AL031534) mating-type switching protein swi10. [Schizosaccharomyces pombe]
19115	ENU02909	ANI61C3366: 38-57 17..782	38-57	737-761	NAP		g2873363	346	95	8.00E-40	40	35	(U89492) arylsulfatase [Neurospora crassa]
19116	ENU02910	ANI61C3113: 68-99 1253..488	68-99	772-791	NAP		g2507070	429	39	0.027	32	39	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]

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19117	ENU02911	ANI61C8607: 65-84 2162..1397	65-84	768-788	NAP		g549705	61	0.000000	007			36.1 KD protein in BUD2-MIF2 intergenic region ; SEC14 protein homolog YKL091c - yeast (Saccharomyces cerevisiae) ; (Z28091) ORF YKL091c [Saccharomyces cerevisiae]
19118	ENU02912	ANI61C1114 0-928..162	53-72	754-777	NAP		g1175102	266	123	2.00E-27	32	85	hypothetical protein HI0077 ; hypothetical protein HI0077 - Haemophilus influenzae (strain Rd KW20) ; (U32693) H. influenzae predicted coding region HI0077 [Haemophilus influenzae Rd] (Z99113) ymaE [Bacillus subtilis] (D89119) unnamed protein product [Schizosaccharomyces pombe] (U04540) flavocytochrome b5 chimeric protein [synthetic construct] ; (L27087) cytochrome b5 [Artificial gene] pseudouridylylate synthase 3 (pseudouridine synthase 3) (depressed growth-rate protein DEG1) ; depressed growth-rate protein DEG1 - yeast (Saccharomyces cerevisiae) ; (D50617) depressed growth-rate protein [Saccharomyces cerevisiae] ; (D44600) depressed growth-rate protein DEG1 [Saccharomyces cerevisiae]
19119	ENU02913	ANI61C1138 0-1440..2206	40-61	742-764	NAP		g2634109	235	107	8.00E-23	36	93	RTM1 protein ; RTM1 protein - yeast (Saccharomyces cerevisiae) ; (U02618) RTM1 gene product [Saccharomyces cerevisiae]
19120	ENU02914	ANI61C4135: 63-82 42..808	63-82	767-787	NAP		g1749446	399	153	1.00E-36	53	50	quinate permease (quinate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
19121	ENU02915	ANI61C1442: 62-81 992..224	62-81	769-788	NAP		g488428	181	75	6.00E-13	33	33	(AF088907) clock-controlled gene-8 protein [Neurospora crassa]
19122	ENU02916	ANI61C9241: 45-68 2204..1435	45-68	749-772	NAP		g399356	561	171	5.00E-42	49	44	
19123	ENU02917	ANI61C4650: 72-91 3141..3910	72-91	774-799	NAP		g730689	120	50	0.00001	30	64	
19124	ENU02918	ANI61C3926: 55-74 848..78	55-74	759-783	NAP		g131761	220	112	3.00E-24	34	38	
19125	ENU02919	ANI61C5774: 24-43 818..48	24-43	729-752	NAP		g3746897	178	96	3.00E-19	29	85	

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19126	ENU02920	ANI61C3373: 27-60 3533..2763		736-755	NAP		g2133034	475	135	3.00E-31	39	37	probable membrane protein YPR156c - yeast (Saccharomyces cerevisiae) ; (U28371) Similar to S. cerevisiae hypothetical protein Ybr008p (Swiss Prot. accession number P38124) [Saccharomyces cerevisiae] (AL023534) hypothetical protein [Schizosaccharomyces pombe] (AE000202) putative synthetase [Escherichia coli] (AL023534) hypothetical protein [Schizosaccharomyces pombe] ; (AL031534) homology to longevity assurance protein.
19127	ENU02921	ANI61C6835: 42-61 5945..6715		751-770	NAP		g3130039	414	154	7.00E-37	40	95	
19128	ENU02922	ANI61C1057 59-78 3:1358..2128		767-787	NAP		g1787246	178	64	9.00E-10	29	91	
19129	ENU02923	ANI61C5814: 49-68 411..1182		752-778	NAP		g3130041	640	229	2.00E-59	53	64	
19130	ENU02924	ANI61C138:2 25-45 054..1283		732-754	NAP		g1175373	237	80	3.00E-18	31	31	[Schizosaccharomyces pombe] hypothetical 72.5 KD protein C2F7.10 in chromosome I ; hypothetical protein SPAC2F7.10 - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe] (U89985) serine/threonine protein phosphatase PPT1 [Neurospora crassa] (AB004537) hypothetical 47.4KD protein in SHP1-SEC17 intergenic region [Schizosaccharomyces pombe] (AL031798) 40s ribosomal protein s20. [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] het-c4 protein - Podospora anserina ; (L36210) het-c [Podospora anserina] putative mitochondrial carrier YGR257C ; hypothetical protein YGR257c - yeast (Saccharomyces cerevisiae) ; (Z73042) ORF YGR257c [Saccharomyces cerevisiae] ; (X99228) mitochondrial carrier protein [Saccharomyces cerevisiae] (L78243) alternative splice (exon 17) [Homo sapiens]
19131	ENU02925	ANI61C8631: 26-47 5833..5062		731-755	NAP		g2290382	1118	441	e-123	78	53	
19132	ENU02926	ANI61C2278: 44-63 2096..2868		755-774	NAP		g2257524	396	159	2.00E-38	41	92	
19133	ENU02927	ANI61C8986: 43-62 4696..3924		752-773	NAP		g3687464	320	131	6.00E-30	62	65	
19134	ENU02928	ANI61C1011: 53-72 2918..2145		765-784	NAP		g2133323	588	163	1.00E-39	64	94	
19135	ENU02929	ANI61C1071 62-92 5:3566..2793		773-793	NAP		g1723767	361	137	1.00E-31	40	62	
19136	ENU02930	ANI61C8371: 24-59 3..777		736-755	NAP		g1374920	227	86	2.00E-22	33	14	

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19137	ENU02931	ANI61C9255: 23-51 4223..3449	23-51	735-755	NAP		g2764632	796	217	1.00E-67	71	99	(AJ001520) 19.3kD iron-sulfur subunit of mitochondrial complex I [Neurospora crassa]
19138	ENU02932	ANI61C9182: 22-45 4568..5342	22-45	735-754	NAP		g2808634	860	192	2.00E-48	40	29	(AJ001909) transcriptional activator [Aspergillus niger]
19139	ENU02933	ANI61C9243: 25-44 1724..2497	25-44	730-757	NAP		g2493049	303	59	5.00E-19	58	85	"ATP synthase delta chain, mitochondrial precursor"; (Z82020) ATP-synthase delta-subunit [Agaricus bisporus]"
19140	ENU02934	ANI61C9220: 25-58 11..785	25-58	738-757	NAP		g4586458	113	85	7.00E-16	33	60	(AB025252) reverse transcriptase [Magnaporthe grisea]
19141	ENU02935	ANI61C1049 51-72 7:8419..7645	51-72	763-783	NAP		g133892	473	90	2.00E-22	80	82	40S ribosomal protein S26E (CRP5) (13.6 KD ribosomal protein); ribosomal protein S26.e - Neurospora crassa; (X55637) ribosomal protein [Neurospora crassa]
19142	ENU02936	ANI61C1059 24-42 9:3190..2415	24-42	738-757	NAP		g1730831	543	214	5.00E-55	44	68	hypothetical 40.7 KD protein in SIN4-URE2 intergenic region; hypothetical protein YNL231c - yeast (Saccharomyces cerevisiae); (Z69381) Similar to hypothetical yeast protein L3502 [Saccharomyces cerevisiae]; (Z71507) ORF YNL231c [Saccharomyces cerevisiae]
19143	ENU02937	ANI61C6671: 56-76 1311..2086	56-76	763-789	NAP		g2281983	809	252	3.00E-66	59	81	(Z98056) hypothetical protein [Schizosaccharomyces pombe]
19144	ENU02938	ANI61C8852: 34-68 60..836	34-68	734-767	NAP		g2494268	252	64	1.00E-21	37	98	putative sterigmatocystin biosynthesis protein STCT; (U34740) putative translation elongation factor 1 gamma [Emmericella nidulans]
19145	ENU02939	ANI61C7170: 22-43 3870..3094	22-43	737-756	NAP		g1710780	744	225	1.00E-70	84	99	40S ribosomal protein S9 (S7); (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]
19146	ENU02940	ANI61C6870: 24-43 1542..2318	24-43	737-758	NAP		g2494700	514	161	6.00E-39	51	77	hypothetical 31.2 KD protein in CYP5-AMIA intergenic region; (AE000330) putative regulator [Escherichia coli]
19147	ENU02941	ANI61C4612: 70-92 1762..986	70-92	785-804	NAP		g3080524	1235	75	6.00E-13	38	34	(AL022599) hypothetical protein [Schizosaccharomyces pombe]
19148	ENU02942	ANI61C7417: 66-86 2566..1791	66-86	774-800	NAP		g2842510	211	115	5.00E-25	36	26	(AL021748) hypothetical protein [Schizosaccharomyces pombe]

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19149	ENU02943	ANI61C17:10 61-80 67..290	61-80	777-796	NAP		g1723966	355	152	2.00E-36	43	77	hypothetical 32.0 KD protein in GOG5-NIF3 intergenic region ; hypothetical protein YGL224c - yeast (Saccharomyces cerevisiae) ; (Z72746) ORF YGL224c [Saccharomyces cerevisiae]
19150	ENU02944	ANI61C9622: 56-75 1254..477	56-75	769-791	NAP		g2132860	366	107	2.00E-29	41	99	probable membrane protein YOL162w - yeast (Saccharomyces cerevisiae) ; (Z74904) ORF YOL162w [Saccharomyces cerevisiae]
19151	ENU02945	ANI61C8718: 22-44 2042..1265	22-44	737-757	NAP		g2654181	1289	195	1.00E-99	75	55	(AF034963) calmodulin-dependent protein kinase; CgCMK [Glomerella cingulata]
19152	ENU02946	ANI61C8415: 24-52 1102..1880	24-52	741-760	NAP		g2494268	342	123	2.00E-27	38	97	putative sterigmatocystin biosynthesis protein STCT ; (U34740) putative translation elongation factor 1 gamma [Emericella nidulans]
19153	ENU02947	ANI61C1835: 56-75 798..1578	56-75	772-794	NAP		g4140255	1017	153	2.00E-36	43	43	(AJ009973) hexokinase [Aspergillus niger]
19154	ENU02948	ANI61C9772: 24-53 3490..4270	24-53	741-762	NAP		g4586977	2840	272	3.00E-72	47	10	(AB018382) Mok13; Mok13 is homologous to Mok1 which is an alpha-glucan synthase [Schizosaccharomyces pombe]
19155	ENU02949	ANI61C1091 42-65 7:1624..2403	42-65	762-781	NAP		g1346290	1048	216	5.00E-63	49	47	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
19156	ENU02950	ANI61C3316: 70-89 3446..2665	70-89	790-809	NAP		g4106687	480	178	4.00E-44	39	64	(AL035065) putative nadh-dependent flavin oxidoreductase [Schizosaccharomyces pombe]
19157	ENU02951	ANI61C6374: 22-55 5737..4955	22-55	741-762	NAP		g731752	432	178	3.00E-44	46	94	hypothetical 26.3 KD protein in OYE2-GND1 intergenic region ; hypothetical protein YHR181w - yeast (Saccharomyces cerevisiae) ; (U00028) Yhr181wp [Saccharomyces cerevisiae]
19158	ENU02952	ANI61C1159: 61-81 9524..10306	61-81	776-801	NAP		g929862	648	141	7.00E-33	35	51	(X83502) J0916 [Saccharomyces cerevisiae]
19159	ENU02953	ANI61C5218: 47-66 1501..720	47-66	768-787	NAP		g3650379	811	250	1.00E-65	77	95	(AL031740) 60s ribosomal protein 110a. [Schizosaccharomyces pombe]

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19160	ENU02954	ANI61C9551: 3908..4690	22-42	738-762	NAP		g730589	347	153	1.00E-36	41	99	"mitochondrial 60S ribosomal protein L6 precursor (YML6) ; ribosomal protein L6 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (U10397) MRPL6p: Mitochondrial ribosomal protein L6 [Saccharomyces cerevisiae] "
19161	ENU02955	ANI61C1209: 25-46 3642..4425	25-46	740-766	NAP		g1168402	689	273	7.00E-73	69	99	minor allergen ALT A 7 (ALT A VII) ; minor allergen - Alternaria alternata ; (X78225) minor allergen [Alternaria alternata]
19162	ENU02956	ANI61C1656: 42-61 210..993	42-61	764-783	NAP		g3929362	202	53	3.00E-20	34	35	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVI]
19163	ENU02957	ANI61C1095: 61-80 1452..668	61-80	781-803	NAP		g2828147	486	86	4.00E-34	54	88	(AF042384) BC-2 protein [Homo sapiens]
19164	ENU02958	ANI50C6268 55-76 _1:785..6	55-76	762-797	NAP		g586551		76	3.00E-13	27	73	hypothetical 33.5 KD protein in MRPS9-YSW1 intergenic region ; probable membrane protein YBR147w - yeast (Saccharomyces cerevisiae) ; (Z36016) ORF YBR147w
19165	ENU02959	ANI61C1064 22-51 9:1676..891	22-51	745-765	NAP		g1429204	568	208	3.00E-53	56	98	[Saccharomyces cerevisiae] (X99215) leucine zipper [Aspergillus niger]
19166	ENU02960	ANI61C1050 25-44 5:88..873	25-44	747-768	NAP		g114971	456	109	6.00E-45	50	23	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) ; beta-glucosidase (EC 3.2.1.21) precursor - yeast (Kluyveromyces marxianus var. marxianus) ; (X05918) beta-glucosidase (AA 1 - 845)
19167	ENU02961	ANI50C1_19 26-46 01:889..103	26-46	751-770	NAP		g1706333		343	7.00E-94	61	45	[Kluyveromyces marxianus] pyruvate decarboxylase ; (U00967) pyruvate decarboxylase [Aspergillus parasiticus]

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19168	ENU02962	ANI61C7922: 3045..2259	72-91	796-816	NAP		g1176153	290	131	6.00E-30	35	86	"hypothetical 27.4 KD protein in RNPB-SOHA intergenic region (ORF 1) ; (U18997) ORF_f256 [Escherichia coli] ; (AE000394) orf, hypothetical protein [Escherichia coli] "
19169	ENU02963	ANI61C1099 8:8746..7959	42-73	768-787	NAP		g1723499	448	171	7.00E-42	52	47	hypothetical 46.7 KD protein C19G10.05 in chromosome I ; (Z69909) putative proteasome regulatory subunit [Schizosaccharomyces pombe]
19170	ENU02964	ANI61C9746: 1406..2194	72-91	799-818	NAP		g3874345	51	0.00001				[Schizosaccharomyces pombe] (Z81035) predicted using Genefinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes from...
19171	ENU02965	ANI61C7857: 25-44 2128..2917	25-44	753-772	NAP		g3935151	377	133	9.00E-44	43	94	(AC005106) T25N20.15 [Arabidopsis thaliana]
19172	ENU02966	ANI61C8794: 62-81 1258..469	62-81	791-810	NAP		g1705884	725	98	1.00E-57	58	50	"probable citrate synthase, mitochondrial precursor "
19173	ENU02967	ANI61C6439: 54-73 871..81	54-73	783-802	NAP		g2370322	173	55	2.00E-11	32	40	(Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis]
19174	ENU02968	ANI61C1076 5:866..1658	63-82	792-813	NAP		g1709170	263	112	3.00E-24	35	82	26S proteasome regulatory subunit MTS3 ; (X92682) 26S protease regulatory subunit [Schizosaccharomyces pombe]
19175	ENU02969	ANI61C4271: 32-55 2897..2105	32-55	762-782	NAP		g2132860	453	124	7.00E-30	46	93	probable membrane protein YOL162w - yeast (Saccharomyces cerevisiae) ; (Z74904) ORF YOL162w [Saccharomyces cerevisiae]
19176	ENU02970	ANI61C9024: 34-54 4502..5294	34-54	756-784	NAP		g1336011	548	180	1.00E-44	42	47	(U56245) kynurenine 3-monooxygenase [Drosophila melanogaster]

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19177	ENU02971	ANI61C8832: 25-44 5638..6431	25-44	745-776	NAP		g731651	1143	205	2.00E-52	41	38	hypothetical aldehyde-dehydrogenase like protein in PUT2-SRB2 intergenic region ; hypothetical protein YHR039c - yeast (Saccharomyces cerevisiae) ; (U00062) Yhr039cp [Saccharomyces cerevisiae]
19178	ENU02972	ANI61C9335: 23-44 1039..1834	23-44	756-776	NAP		g465506	334	162	3.00E-39	43	97	HTP reductase ; RIB7 protein - yeast (Saccharomyces cerevisiae) ; (X71329) YBR 12.03 [Saccharomyces cerevisiae] ; (Z36022) ORF YBR153w [Saccharomyces cerevisiae] ; (Z21622) HTP reductase [Saccharomyces cerevisiae]
19179	ENU02973	ANI61C8182: 47-67 109..904	47-67	774-800	NAP		g417454	823	309	1.00E-83	63	94	proliferating cell nuclear antigen (PCNA) ; proliferating cell nuclear antigen - fission yeast (Schizosaccharomyces pombe) ; (X54857) proliferating cell nuclear antigen [Schizosaccharomyces pombe] ; (AL035637) proliferating cell nuclear antigen [Schizosaccharomyces pombe] (AL034463) Xenopus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe]
19180	ENU02974	ANI61C3990: 72-91 797..2	72-91	802-825	NAP		g4007792	716	287	6.00E-77	60	20	"40S ribosomal protein S6 ; ribosomal protein S6.e, cytosolic - fission yeast (Schizosaccharomyces pombe) ; (M36382) ribosomal protein S6 (rps6) precursor [Schizosaccharomyces pombe] ; (Z54308) 40S ribosomal protein [Schizosaccharomyces pombe]
19181	ENU02975	ANI61C2420: 44-63 876..81	44-63	778-797	NAP		g133980	591	136	2.00E-31	75	64	(AJ012752) maltose permease [Saccharomyces cerevisiae] (Z83828) AmMst-1 [Amanita muscaria]
19182	ENU02976	ANI61C5533: 64-88 3792..4588	64-88	788-818	NAP		g3901117	570	122	2.00E-27	37	30	
19183	ENU02977	ANI61C3559: 24-47 1207..410	24-47	751-779	NAP		g2258125	526	190	9.00E-51	49	47	

Seq num	Seq id	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19184	ENU02978	ANI61C4093: 56-75 748..1548	792-811	NAP		g3929361	758	167	2.00E-67	75	94	NADH-ubiquinone oxidoreductase 23 KD subunit precursor (complex I-23KD) (Cl-23KD) ; (X95547) ferredoxin-like iron-sulfur subunit of mitochondrial complex I [Neurospora crassa] (Z50095) mannosidase [Agaricus bisporus] lactone hydrolase [Acinetobacter sp. ADP1] ; beta-ketoadipate enol-lactone hydrolase [Acinetobacter calcoaceticus] (U80063) lipase LipA [Streptomyces cinnamomeus] vacuolar ATP synthase 16 KD proteolipid subunit (V-ATPase C-subunit) ; (AF008924) V-ATPase C-subunit [Aedes aegypti] (Y09021) fructosyl amino acid oxidase [Penicillium janthinellum] mucin - rhesus macaque (fragment) ; (U00483) mucin [Macaca mulatta] GCN20 protein ; GCN20 protein - yeast (Saccharomyces cerevisiae) ; (U19971) Gcn20p [Saccharomyces cerevisiae] ; (D50617) YFR009W [Saccharomyces cerevisiae] "(AF069298) similar to ATPases associated with various cellular activities (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana] " "cytochrome P450 52L9 (CYPLIA9) (alkane-inducible P450-ALK5-A) ; cytochrome P450 ALK5-A, alkane-inducible - yeast (Candida maltosa) ; (D12717) n-alkane inducible cytochrome P-450 [Candida maltosa] " (AJ010475) RNA helicase [Arabidopsis thaliana]
19185	ENU02979	ANI61C7409: 55-75 114..913	793-812	NAP		g1679597		37	0.15			
19186	ENU02980	ANI61C3696: 54-73 1569..769	793-812	NAP		g2996620	207	83	2.00E-15	32	91	
19187	ENU02981	ANI61C8073: 22-46 6666..5866	761-780	NAP		g2435400	162	71	9.00E-12	34	55	
19188	ENU02982	ANI50C8867 50-69 _3:902..102	787-808	NAP		g3334403		69	3.00E-11	53	99	
19189	ENU02983	ANI61C8446: 47-68 6996..6195	783-806	NAP		g1654074	217	52	0.000005	35	53	
19190	ENU02984	ANI61C4168: 53-76 1493..234	793-812	NAP		g2134574	200	35	0.74	37	95	
19191	ENU02985	ANI61C1026 56-79 3:1614..811	796-816	NAP		g1169871	956	211	2.00E-81	65	33	
19192	ENU02986	ANI61C7203: 38-57 17..819	779-798	NAP		g3193292	520	116	1.00E-25	42	66	
19193	ENU02987	ANI61C1049 37-58 1:851..48	778-798	NAP		g3913326	467	99	7.00E-22	41	42	
19194	ENU02988	ANI61C6305: 23-42 82..885	766-784	NAP		g3776027	624	107	6.00E-38	45	31	

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19195	ENU02989	ANI61C8325: 23-45 239..1594	766-785	766-785	NAP		g4455301	337	88	7.00E-22	45	87	(AL035528) putative protein [Arabidopsis thaliana]
19196	ENU02990	ANI61C2426: 22-41 1175..371	765-784	765-784	NAP		g1723231	229	114	7.00E-25	36	92	hypothetical 27.1 KD protein C1D4.09C in chromosome I ; (Z69239) unknown [Schizosaccharomyces pombe]
19197	ENU02991	ANI61C1087: 52-71 793..1597	790-814	790-814	NAP		g1764133	346	115	4.00E-25	36	94	(U81790) PIG8 [Uromyces fabae]
19198	ENU02992	ANI61C3686: 64-83 558..848	807-827	807-827	NAP		g126066	230	83	3.00E-15	35	52	L-lactate dehydrogenase (LDH) ; L-lactate dehydrogenase (EC 1.1.1.27) chain Ldh1 - maize ; (Z11754) lactate dehydrogenase [Zea mays]
19199	ENU02993	ANI61C9004: 56-75 1905..2711	798-820	798-820	NAP		g2507431	967	266	2.00E-70	48	55	"phenylalanyl-TRNA synthetase mitochondrial precursor (phenylalanine--TRNA ligase (PHERS) ; phenylalanine--tRNA ligase (EC 6.1.1.20) alpha chain precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49219) Msf1p [Saccharomyces cerevisiae] ; (Z71255) Msf1p [Saccharomyces cerevisiae] " (AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda] "
19200	ENU02994	ANI61C9827: 37-57 104..910	766-801	766-801	NAP		g2245570	205	84	5.00E-16	36	23	(AL022117) hypothetical protein [Schizosaccharomyces pombe]
19201	ENU02995	ANI61C1114: 63-87 686..1493	808-828	808-828	NAP		g2959376	980	203	1.00E-51	56	68	(AC006069) similar to yeast ccc1 protein [Arabidopsis thaliana]
19202	ENU02996	ANI61C8366: 35-54 1075..1883	782-801	782-801	NAP		g4220472	301	73	2.00E-23	34	98	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
19203	ENU02997	ANI61C1234: 49-68 3091..2283	786-815	786-815	NAP		g2497056	586	123	1.00E-27	41	56	"(U52064) Herpesvirus saimiri ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus] ; (U75698) ORF 73; extensive acidic domains, potential leucine zipper; immediate early protein homolog [Kaposi's sarcoma-associated herpesvirus] "
19204	ENU02998	ANI61C5032: 37-58 1371..2180	778-804	778-804	NAP		g1633572	115	47	0.0002			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19205	ENU02999	ANI61C8256: 41-60 855..45	41-60	790-809	NAP		g2497179	145	57	0.000000	28	18	hypothetical 113.2 KD protein in SSO2-HSC82 intergenic region ; hypothetical protein YMR185w - yeast (Saccharomyces cerevisiae) ; (Z49808) unknown [Saccharomyces cerevisiae] lactate 2-monoxygenase (lactate oxidase) ; lactate 2-monoxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monoxygenase [Mycobacterium smegmatis]
19206	ENU03000	ANI61C45:26 33-53 82..3492	33-53	782-801	NAP		g125886	657	181	5.00E-45	41	67	probable oxidoreductase C26F1.07 in chromosome I ; (Z73100) unknown [Schizosaccharomyces pombe] (AE001600) Hypothetical Protein [Chlamydia pneumoniae] "(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus] " 3-oxoacid CoA transferase precursor; succinyl-CoA:3-ketoacid-CoA transferase precursor ; succinyl-CoA:3-ketoacid-coenzyme A transferase precursor (succinyl CoA:3-oxoacid COA-transferase) (OXCT) ; (U62961) succinyl CoA:3-oxoacid CoA transferase precursor [Homo sapiens] (Z98974) hypothetical protein [Schizosaccharomyces pombe] AFG1 protein ; AFG1 protein - yeast (Saccharomyces cerevisiae) ; (U18779) Afg1p [Saccharomyces cerevisiae] (AF003835) isopenentenyl diphosphate:dimethylallyl diphosphate isomerase [Rattus norvegicus] alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) (AL049498) rho1 gdp-gtp exchange protein 1 [Schizosaccharomyces pombe]
19207	ENU03001	ANI61C6754: 22-52 4137..4947	22-52	769-790	NAP		g1723578	652	266	2.00E-70	49	83	
19208	ENU03002	ANI61C6415: 58-77 841..1654	58-77	809-828	NAP		g4376408	384	96	1.00E-30	36	64	
19209	ENU03003	ANI61C1054 29-50 0:6432..6207	29-50	780-799	NAP		g2648302	290	108	4.00E-32	46	79	
19210	ENU03004	ANI61C6496: 24-57 9172..9986	24-57	776-795	NAP		g4557817	1234	250	7.00E-66	54	48	
19211	ENU03005	ANI61C4798: 41-62 1015..1828	41-62	793-812	NAP		g2388907	606	50	0.00002			
19212	ENU03006	ANI61C9801: 59-78 4737..3923	59-78	812-831	NAP		g416589	445	207	7.00E-53	42	49	
19213	ENU03007	ANI61C9149: 42-65 1260..2074	42-65	794-814	NAP		g2253701	524	90	1.00E-45	53	89	
19214	ENU03008	ANI61C7738: 65-91 2704..1890	65-91	810-837	NAP		g2146821	107	48	0.000000	29	32	
19215	ENU03009	ANI61C2364: 23-50 513..1328	23-50	772-796	NAP		g4539279	867	259	2.00E-75	55	18	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19216	ENU03010	ANI61C1752: 55-74 1711..896	55-74	809-828	NAP		g1723371	1081	406	e-113	63	51	hypothetical protein in CRTE 3'region (ORF2) ; (M87280) ORF2 [Erwinia herbicola]
19217	ENU03011	ANI61C3291: 25-55 621..1437	25-55	778-799	NAP		g1514667	331	104	1.00E-26	36	63	(X92509) crg1 [Ustilago maydis]
19218	ENU03012	ANI61C6315: 46-75 1601..785	46-75	801-820	NAP		g3168924		64	9.00E-10			"(AF068712) similar to cytochrome p450 (Pfam: p450.hmm, score: 265.98) [Caenorhabditis elegans]"
19219	ENU03013	ANI61C7472: 55-72 146..965	55-72	813-832	NAP		g1709012	253	59	0.000000	34	55	microfibrillar-associated protein 1 ; microfibrillar protein MFAP1 - human ; (U04209) associated microfibrillar protein [Homo sapiens]
19220	ENU03014	ANI61C9978: 40-59 1088..817	40-59	794-818	NAP		g2645229	488	199	3.00E-50	40	55	(U78597) kinesin light chain [Plectonema boryanum]
19221	ENU03015	ANI61C3973: 51-70 2387..3207	51-70	810-829	NAP		g544370	439	82	1.00E-30			GAR1 protein ; GAR1 protein - fission yeast (Schizosaccharomyces pombe) ; (Z19576) snoRNP protein GAR1 [Schizosaccharomyces pombe] ; (AB000537) snoRNP protein GAR 1 [Schizosaccharomyces pombe] ; (Z95397) Gar1p [Schizosaccharomyces pombe] ; (AL021747) gar1 protein; small nucleolar rnp required for pre-mrna for pre-mrna processing [Schizosaccharomyces pombe]
19222	ENU03016	ANI61C1000 4-4568..3748	22-41	777-800	NAP		g1706921	173	81	1.00E-14	36	99	"5-formyltetrahydrofolate cyclo-ligase (5,10-methenyl-tetrahydrofolate synthetase) (methenyl-THF synthetase) (MTHFS) ; indoleacetate-lysine synthetase (EC 6.3.2.20) - human ; (L38928) 5,10-methenyltetrahydrofolate synthetase [Homo sapiens]"
19223	ENU03017	ANI61C406:9 57..136	39-58	798-818	NAP		g549638	500	171	4.00E-42	38	77	hypothetical 39.6 KD protein in MTD1-NUP133 intergenic region ; hypothetical protein YKR081c - yeast (Saccharomyces cerevisiae) ; (Z27116) ORF YKR401 [Saccharomyces cerevisiae] ; (Z28306) ORF YKR081c [Saccharomyces cerevisiae]

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19224	ENU03018	ANI61C8156: 1457..636	67-86	826-846	NAP		g452120	64	2.00E-15				(L28112) complete cds [Rattus norvegicus]
19225	ENU03019	ANI61C6265: 25-46		785-805	NAP		g2326188	622	182	4.00E-49	43	79	(U81606) mixed-linked glucanase precursor [Cochliobolus carbonum]
19226	ENU03020	ANI61C8257: 40-59		799-820	NAP		g1175386	245	77	2.00E-13	30	78	hypothetical 37.7 KD protein C18B11.06 in chromosome I; hypothetical protein SPAC18B11.06 - fission yeast (Schizosaccharomyces pombe); (Z50728) hypothetical protein [Schizosaccharomyces pombe]
19227	ENU03021	ANI61C8772: 43-62		796-823	NAP		g1208451	347	129	2.00E-29	32	67	(D64004) hypothetical protein [Synecocystis sp.]
19228	ENU03022	ANI61C7523: 22-41		784-803	NAP		g1078634	1309	281	e-130	98	36	sepB protein - Emericella nidulans; sepB protein - Emericella nidulans; (X86399) sepB [Emericella nidulans]
19229	ENU03023	ANI61C5260: 22-50		770-804	NAP		g1362406	531	131	8.00E-30	46	65	probable membrane protein YPR011c - yeast (Saccharomyces cerevisiae); (Z49919) unknown [Saccharomyces cerevisiae]; (U31900) Lpz11p [Saccharomyces cerevisiae]; (Z71255) unknown [Saccharomyces cerevisiae]
19230	ENU03024	ANI61C1027: 22-50		786-805	NAP		g3318617	537	140	3.00E-52	64	71	(AB016066) mitochondrial phosphate transporter [Arabidopsis thaliana]
19231	ENU03025	ANI61C1491: 40-61		806-825	NAP		g516124	1027	109	2.00E-32	43	43	(X78712) glycerol kinase [Homo sapiens]
19232	ENU03026	ANI61C7207: 62-81		828-847	NAP		g4103055	827	146	1.00E-73	59	80	(AF020040) xylose reductase [Pichia guilliermondii]
19233	ENU03027	ANI61C1024: 31-52		798-817	NAP		g2624002	213	101	7.00E-21	31	85	(Z93941) YuxA [Bacillus subtilis]; (Z99120) alternate gene name: yvxA; similar to retinol dehydrogenase [Bacillus subtilis]
19234	ENU03028	ANI61C9660: 67-86		834-853	NAP		g1173139	546	105	1.00E-50	55	86	ribulose-phosphate 3-epimerase (pentose-5-phosphate 3-epimerase) (PPE) (RPE); POS18 protein - yeast (Saccharomyces cerevisiae); (X83571) Ribulose-5-Phosphate-Epimerase [Saccharomyces cerevisiae]; (Z49396) ORF YJL121c [Saccharomyces cerevisiae]
19235	ENU03029	ANI61C286:4 70-89		836-856	NAP		g3355474	359	148	3.00E-35	32	65	(AC004218) unknown protein [Arabidopsis thaliana]

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19236	ENU03030	ANI61C1875: 33..862	54-74	822-841	NAP		g4539944	218	76	1.00E-20	38	61	(AF133841) aldose reductase ALDRXV4 [Xerophyta viscosa]
19237	ENU03031	ANI61C819:2 23-53		790-810	NAP		g1477466	612	128	2.00E-57	50	44	(U35246) vacuolar protein sorting homolog h-vps45 [Homo sapiens]
19238	ENU03032	ANI61C1128 22-51		792-811	NAP		g2047309		71	1.00E-11			(U44750) NAD-dependent 15- hydroxyprostaglandin dehydrogenase [Rattus norvegicus]
19239	ENU03033	ANI61C3329: 27-55		786-816	NAP		g3184115	646	111	5.00E-24	29	52	(AL023780) DNA binding protein [Schizosaccharomyces pombe]
19240	ENU03034	ANI61C3763: 43-62		811-833	NAP		g1351714	297	71	1.00E-11	31	50	putative transporter C11D3.18C; (Z68166) unknown
19241	ENU03035	ANI61C3280: 22-41		786-813	NAP		g603587	1340	404	e-112	70	58	[Schizosaccharomyces pombe] (X83512) Yna1p [Saccharomyces cerevisiae]
19242	ENU03036	ANI61C7044: 64-83		835-855	NAP		g731638	1109	380	e-105	65	50	"asparaginyl-tRNA synthetase, cytoplasmic (asparagine--tRNA ligase) (ASNRS) ; hypothetical protein YHR019c - yeast (Saccharomyces cerevisiae) ; (U10399) Ded81p: Asparaginyl-tRNA synthetase [Saccharomyces cerevisiae] "
19243	ENU03037	ANI61C1058 46-66		818-838	NAP		g1813337	491	159	2.00E-38	82	71	(AB000704) ribosomal protein S11 homolog [Schizosaccharomyces pombe]
19244	ENU03038	ANI61C7997: 22-53		792-815	NAP		g3929362	292	114	7.00E-25	40	36	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976)
19245	ENU03039	ANI61C1048 35-56		808-829	NAP		g3643644	1098	194	9.00E-82	70	59	pisatin demethylase [Nectria haematococca mpVI] (U59215) cyclin-dependent protein kinase PHOA(M1) [Emmericella nidulans]
19246	ENU03040	ANI61C566:1 50-69		823-844	NAP		g731801	269	66	4.00E-25	32	80	36.7 KD protein in CBR5-NOT3 intergenic region ; hypothetical protein YIL041w - yeast (Saccharomyces cerevisiae) ; (Z46861) unknown [Saccharomyces cerevisiae] (AL035539) putative protein [Arabidopsis thaliana] (AC002340) hypothetical protein [Arabidopsis thaliana]
19247	ENU03041	ANI61C6225: 30-49		802-825	NAP		g4539334		36	0.27			
19248	ENU03042	ANI61C2571: 45-64		821-840	NAP		g2880049	251	126	2.00E-28	35	54	

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19249	ENU03043	ANI50C346_1:3130..2293	65-87	835-860	NAP		g731285		66	4.00E-10	35	81	hypothetical 27.1 KD protein in ACS1-GCV3 intergenic region ; hypothetical protein YAL049c - yeast (Saccharomyces cerevisiae) ; (U12980) Yal049cp [Saccharomyces cerevisiae] probable membrane protein YOR378w - yeast (Saccharomyces cerevisiae) ; (Z75286) ORF YOR378w [Saccharomyces cerevisiae] (AL035216) probable involvement in ergosterol biosynthesis [Schizosaccharomyces pombe] DNA-binding protein amdA - Emericella nidulans ; (L28810) regulatory protein [Emericella nidulans]
19250	ENU03044	ANI61C3044: 40-60 852..14	40-60	816-835	NAP		g2132957	310	66	4.00E-10	29	47	hypothetical 35.9 KD protein C56F8.08 in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe] (Z98943) hypothetical protein Rv1533 [Mycobacterium tuberculosis] hypothetical oxidoreductase in PTA-ROCC intergenic region ; hypothetical protein - Bacillus subtilis ; (X73124) ipa-82d [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-82d; similar to glucose 1-dehydrogenase [Bacillus subtilis]
19251	ENU03045	ANI61C8498: 43-62 45..883	43-62	806-839	NAP		g4160344	682	264	5.00E-70	48	54	protein phosphatase 2A (D63916) regulatory subunit (A subunit) [Schizosaccharomyces pombe] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
19252	ENU03046	ANI61C7244: 62-81 133..972	62-81	830-858	NAP		g2133268	575	112	4.00E-49	41	31	putative cytochrome C1 heme lyase (CC1HL) ; (Z98601) cytochrome c1 heme lyase [Schizosaccharomyces pombe]
19253	ENU03047	ANI61C1118 23-58 6:3..842	23-58	801-820	NAP		g1723440	608	204	8.00E-52	50	74	
19254	ENU03048	ANI61C4142: 22-56 923..84	22-56	788-819	NAP		g2370322	220	87	1.00E-16	32	70	
19255	ENU03049	ANI61C9321: 33-52 3703..2864	33-52	811-830	NAP		g732372	202	97	1.00E-19	33	66	
19256	ENU03050	ANI61C1077 48-72 6:2216..3055	48-72	826-845	NAP		g1235752	1535	215	2.00E-69	65	38	
19257	ENU03051	ANI61C4209: 64-83 3767..2927	64-83	842-862	NAP		g3560142	454	160	1.00E-38	32	45	
19258	ENU03052	ANI61C2329: 42-61 3142..2302	42-61	814-840	NAP		g3183375	284	161	8.00E-39	47	95	

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19259	ENU03053	ANI50C1079_1:92..931	32-51	811-830	NAP		g134966	153	1.00E-36	37	27		"STE6 protein ; ste6 protein - fission yeast (Schizosaccharomyces pombe) ; (X53254) ste6 [Schizosaccharomyces pombe] ; (AL049559) guanine-nucleotide releasing factor, Ste6p [Schizosaccharomyces pombe] ; ste6 gene [Schizosaccharomyces pombe]"
19260	ENU03054	ANI61C7943: 2176..1335	28-47	799-827	NAP		g632081	103	1.00E-21				hypothetical protein 4 - Xanthobacter sp ; (X79863) orf4 [Xanthobacter sp. Py2]
19261	ENU03055	ANI61C8446: 47-68	6996..6155	823-846	NAP		g1654074	217	52	0.000005	34	55	(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
19262	ENU03056	ANI61C4954: 39-59	5249..4407	820-839	NAP		g2497056	327	105	8.00E-24	31	60	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
19263	ENU03057	ANI61C2666: 45-64	4935..4092	826-845	NAP		g130971	531	193	1.00E-48	47	93	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) precursor - Pseudomonas aeruginosa (strain PAO) ; (M33557) delta-1-pyrroline-5-carboxylate reductase (EC 1.5.1.2) [Pseudomonas aeruginosa] "(D30688) cytochrome P-450 17 alpha-hydroxylase/C17,20-lyase [Equus caballus]"
19264	ENU03058	ANI50C4625 4_1:1..844	22-53	796-823	NAP		g1132477	50	9.00E-10				fructosyl amino acid oxidase (Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
19265	ENU03059	ANI61C3373: 66-87	1622..2465	848-867	NAP		g1654074	1763	246	e-100	78	54	"(Z99113) endo-1,4-beta-xylanase (xylanase D) [Bacillus subtilis]"
19266	ENU03060	ANI61C9674: 22-49	2561..3405	799-824	NAP		g2634199	426	174	7.00E-43	38	53	lactate 2-monooxygenase (lactate oxidase) ; lactate 2-monooxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monooxygenase [Mycobacterium smegmatis]
19267	ENU03061	ANI61C45:26 48..3492	62-81	845-864	NAP		g125886	657	183	1.00E-45	40	70	(AL023634) cyclin [Schizosaccharomyces pombe]
19268	ENU03062	ANI61C3172: 33-54	1727..881	818-837	NAP		g3150260	169	67	1.00E-10	28	71	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19269	ENU03063	ANI61C2645: 314..1160	22-49	805-826	NAP		g2132011	501	208	5.00E-53	42	94	hypothetical protein YOL080c - yeast (Saccharomyces cerevisiae) ; (Z74822) ORF YOL080c [Saccharomyces cerevisiae]
19270	ENU03064	ANI61C1036 58-80 2:2974..3822	58-80	838-864	NAP		g3334212	1108	235	5.00E-97	65	82	delta-aminolevulinic acid dehydratase (porphobilinogen synthase) (ALADH) ; (AF038566) porphobilinogen synthase [Candida glabrata]
19271	ENU03065	ANI61C6401: 22-54 104..953	22-54	809-829	NAP		g3880867	728	217	1.00E-55	56	56	(AL032639) predicted using Genefinder; similar to Iron-containing alcohol dehydrogenases; cDNA EST yk372c11.5 comes from this gene; cDNA EST yk304d8.3 comes from this gene; cDNA EST yk304d8.5 comes from this gene; cDNA EST yk26... UTR2 protein - yeast (Saccharomyces cerevisiae) ; (U18779) Utr2p [Saccharomyces cerevisiae]
19272	ENU03066	ANI61C5735: 22-46 923..74	22-46	807-829	NAP		g320712	418	159	2.00E-38	31	60	hypothetical 42.4 KD protein in CDC12-ORC6 intergenic region ; hypothetical protein YHR112c - yeast (Saccharomyces cerevisiae) ; (U00059) Yhr112cp [Saccharomyces cerevisiae]
19273	ENU03067	ANI61C8613: 27-47 3511..2662	27-47	800-834	NAP		g731700	817	252	3.00E-66	47	71	"mitogen-activated protein kinase HOG1 (MAP kinase HOG1) (osmosensing protein HOG1) ; protein kinase HOG1 (EC 2.7.1.-), mitogen-activated - yeast (Saccharomyces cerevisiae) ; (X89514) mitogen-activated protein kinase [Saccharomyces cerevisiae] ; (Z73285) ORF YLR113w [Saccharomyces cerevisiae]"
19274	ENU03068	ANI61C8213: 23-54 10..859	23-54	805-830	NAP		g2507192	584	158	5.00E-38	63	47	hypothetical 36.7 KD protein C2F7.14C in chromosome I ; hypothetical protein SPAC2F7.14c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe]
19275	ENU03069	ANI61C8076: 36-55 852..1	36-55	817-845	NAP		g1175376	475	184	6.00E-46	54	67	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19276	ENU03070	ANI61C1075 1:1004..151	59-78	851-870	NAP		g285211	366	128	4.00E-29	40	51	"[3-methyl-2-oxobutanoate dehydrogenase (lipoamide)] kinase (EC 2.7.1.115) - rat ; branched-chain alpha-ketoacid dehydrogenase kinase 44 kda isoform [rats, lung, heart, Peptide Mitochondrial, 412 aa] ; (M93271) branched-chain alpha-ketoacid dehydrogenase kinase [Rattus norvegicus] "
19277	ENU03071	ANI61C1018 5:1671..817	52-71	842-864	NAP		g4007783	320	85	7.00E-26	37	72	"(X72850) hydroxyquinol 1,2-dioxygenase [Sphingomonas sp.] "
19278	ENU03072	ANI61C5164: 40-59 48..903	40-59	834-853	NAP		g1169885	966	314	7.00E-85	65	25	putative glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system P-protein) ; hypothetical protein SPAC13G6.06c - fission yeast (Schizosaccharomyces pombe) ; (Z54308) putative glycine dehydrogenase (decarboxylase) [Schizosaccharomyces pombe]
19279	ENU03073	ANI61C8668: 58-77 2770..3625	58-77	849-871	NAP		g4160354	274	119	3.00E-26	31	93	[Schizosaccharomyces pombe] (Z64354) unknown
19280	ENU03074	ANI61C1132: 24-43 9650..8794	24-43	819-838	NAP		g2190516	224	99	3.00E-20	34	91	[Schizosaccharomyces pombe] (Y13635) Vip1 protein [Schizosaccharomyces pombe] ; (AL009197) hypothetical protein [Schizosaccharomyces pombe]
19281	ENU03075	ANI61C1081 37-56 6:1297..2153	37-56	832-851	NAP		g632081	285	87	2.00E-23	41	84	hypothetical protein 4 - Xanthobacter sp ; (X79863) orf4 [Xanthobacter sp. Py2]
19282	ENU03076	ANI61C3713: 53-72 943..87	53-72	846-867	NAP		g1894771	362	135	3.00E-31	31	57	(Z92954) product highly similar to metabolite transport proteins [Bacillus subtilis] ; (Z99122) similar to metabolite transport protein [Bacillus subtilis]
19283	ENU03077	ANI61C539:2 28-47 464..2568	28-47	823-842	NAP		g3183310	235	112	3.00E-24	46	95	hypothetical 23.2 KD protein C5D6.06C in chromosome I ; (Z98056) putative osmotolerance protein [Schizosaccharomyces pombe]

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19284	ENU03078	ANI61C1029: 51-70 1179..322		838-866	NAP		g1175915	189	64	7.00E-14	44	44	hypothetical 28.8 KD protein in SMC1-SEC4 intergenic region ; probable membrane protein YFL006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFL006W [Saccharomyces cerevisiae] ; (D44604) unknown [Saccharomyces cerevisiae]
19285	ENU03079	ANI61C3377: 22-49 1390..2247		816-837	NAP		g3192044	226	86	3.00E-16	36	80	[AL023796] hypothetical protein [Schizosaccharomyces pombe]
19286	ENU03080	ANI61C683:1 22-51 456..599		814-837	NAP		g134777	248	128	6.00E-29	29	84	stage V sporulation protein K ; spoVJ protein - Bacillus subtilis ; (X59412) spoVJ [Bacillus subtilis]
19287	ENU03081	ANI61C1140 43-63 7:1618..2476		840-859	NAP		g3005897	338	175	4.00E-43	34	38	(Y13623) multifunctional protein2 [Cavia porcellus]
19288	ENU03082	ANI61C7321: 61-80 2751..1892		858-878	NAP		g1654074	240	118	5.00E-26	29	57	(Y09021) fructosyl amino acid oxidase [Penicillium janthinellum]
19289	ENU03083	ANI61C9902: 70-89 639..475		869-888	NAP		g136704	666	162	1.00E-47	66	85	ubiquinol-cytochrome C reductase iron-sulfur subunit precursor (Rieske iron-sulfur protein) (RISP) ; ubiquinol-cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein - Neurospora crassa ; (X02472) cytochrome c reductase iron-sulfur subunit [Neurospora crassa] branched-chain amino acid aminotransferase (BCAT) ; (AE000647) branched-chain-amino-acid aminotransferase (jivE) [Helicobacter pylori 26695]
19290	ENU03084	ANI61C7849: 33-54 1987..1126		819-852	NAP		g3024012	404	184	6.00E-46	36	82	ALDRXV4 [Xerophyta viscosa] probable adenosine deaminase (adenosine aminohydrolase) ; adenosine deaminase homolog YNL141w - yeast (Saccharomyces cerevisiae) ; (Z46843) adenosine deaminase (putative) [Saccharomyces cerevisiae] ; (Z71417) ORF YNL141w [Saccharomyces cerevisiae]
19291	ENU03085	ANI61C1875: 54-74 33..894		854-873	NAP		g4539944	218	76	1.00E-20	37	65	
19292	ENU03086	ANI61C8984: 23-42 1974..1112		821-843	NAP		g1703166	704	218	4.00E-56	45	80	

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19293	ENU03087	ANI61C229:3 436..2573	59-83	857-880	NAP		g549723	738	282	2.00E-75	54	39	hypothetical 75.5 KD protein in SDH1-CIM5/YTA3 intergenic region ; hypothetical protein YKL146w - yeast (Saccharomyces cerevisiae) ; (Z28146) ORF YKL146w [Saccharomyces cerevisiae] (Z95397) unknown [Schizosaccharomyces pombe] (D87681) acetyltransferase [Aspergillus awamori] (U78597) kinesin light chain [Plectonema boryanum] bimD protein - Emericella nidulans ; (L03200) bimD [Emericella nidulans] (Z98979) putative phosphatidylserine decarboxylase proenzyme [Schizosaccharomyces pombe] probable membrane protein YLR241w - yeast (Saccharomyces cerevisiae) ; (U20865) Ylr241wp [Saccharomyces cerevisiae] mannitol-1-phosphate 5-dehydrogenase ; (U18943) mannitol-1-phosphate dehydrogenase [Bacillus stearothermophilus] (AE001015) acyl-CoA dehydrogenase (acd-9) [Archaeoglobus fulgidus] (U68040) polyketide synthase [Cochliobolus heterostrophus] N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa] (AL049500) T5C23.70 [Arabidopsis thaliana]
19294	ENU03088	ANI61C6709: 58-76 3506..2643	58-76	853-879	NAP		g2104455	456	98	8.00E-38	48	77	
19295	ENU03089	ANI61C9444: 22-49 1599..735	22-49	825-844	NAP		g1542843	397	162	4.00E-39	34	94	
19296	ENU03090	ANI61C2926: 67-86 4377..3210	67-86	867-890	NAP		g2645229	457	129	3.00E-43	37	58	
19297	ENU03091	ANI61C5745: 50-72 29..894	50-72	854-873	NAP		g1078626	1501	413	e-114	99	19	
19298	ENU03092	ANI61C9795: 24-55 3152..2286	24-55	829-848	NAP		g2388966	1410	294	4.00E-79	52	27	
19299	ENU03093	ANI61C3270: 22-43 1954..2821	22-43	828-847	NAP		g1363743	1110	168	6.00E-41	42	35	
19300	ENU03094	ANI61C7067: 55-74 928..61	55-74	861-880	NAP		g2494101	628	237	9.00E-62	41	74	
19301	ENU03095	ANI61C3705: 53-72 2000..1133	53-72	852-878	NAP		g2649289		103	2.00E-21			
19302	ENU03096	ANI61C1705: 27-52 3803..4670	27-52	825-852	NAP		g1546072	1002	112	4.00E-24	31	10	
19303	ENU03097	ANI61C322:1 26-45 1819..12688	26-45	834-853	NAP		g2507070	1257	299	2.00E-80	62	57	
19304	ENU03098	ANI61C1188: 24-48 9136..8271	24-48	832-852	NAP		g4539455	365	154	6.00E-37	40	69	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19305	ENU03099	ANI61C9049: 1749..879	22-52	827-850	NAP		g2500006	708	287	5.00E-77	52	99	formyl/tetrahydrofolate DEformylase (formyl-FH(4) hydrolase) ; formyl/tetrahydrofolate deformylase (EC 3.5.1.10) - Corynebacterium sp ; (U23955) 10-formyltetrahydrofolate hydrolase [Corynebacterium sp.] (AL023777) coenzyme a synthetase [Schizosaccharomyces pombe] (AL022197) putative protein [Arabidopsis thaliana] (AF034260) protein kinase NRC-2 [Neurospora crassa] "ribosomal protein L31.e.B, cytosolic - yeast (Saccharomyces cerevisiae) ; (U19729) Ylr406cp: member of L31E ribosomal protein family [Saccharomyces cerevisiae] " (AL022304) eukaryotic translation initiation factor 3 rna-binding subunit [Schizosaccharomyces pombe] vacuolar protein sorting-associated protein VPS16 ; vacuolar protein sorting-associated protein VPS16 - yeast (Saccharomyces cerevisiae) ; (U44030) Vsp16p: Vacuolar sorting protein [Saccharomyces cerevisiae] (AE000715) chorismate mutase/prephenate dehydratase [Aquifex aeolicus] hypothetical 36.4 KD protein in SMP1-MBA1 intergenic region ; probable membrane protein YBR183w - yeast (Saccharomyces cerevisiae) ; (Z36052) ORF YBR183w [Saccharomyces cerevisiae] ; (U02073) unknown [Saccharomyces cerevisiae] (AL022072) arginine n-methyltransferase [Schizosaccharomyces pombe] (AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa]
19306	ENU03100	ANI61C2649: 64-86	64-86	869-892	NAP		g3184098	307	142	4.00E-33	33	53	
19307	ENU03101	ANI61C1190: 25-44	25-44	825-853	NAP		g2980795	379	90	3.00E-40	45	97	
19308	ENU03102	ANI61C3127: 40-72	40-72	849-869	NAP		g2654106	1056	228	e-111	79	41	
19309	ENU03103	ANI61C1713: 31-49	31-49	840-860	NAP		g1084846	321	96	2.00E-19	68	40	
19310	ENU03104	ANI61C2402: 68-90	68-90	870-898	NAP		g3006180	545	121	8.00E-41	45	90	
19311	ENU03105	ANI61C5793: 33-57	33-57	843-863	NAP		g2507153	123	57	2.00E-10	24	33	
19312	ENU03106	ANI61C212:2 22-53	22-53	833-852	NAP		g2983461		139	2.00E-32			
19313	ENU03107	ANI61C1730: 39-59	39-59	851-870	NAP		g586314	199	47	3.00E-12	30	66	
19314	ENU03108	ANI61C8793: 24-51	24-51	836-855	NAP		g4008547	745	145	3.00E-47	42	55	
19315	ENU03109	ANI61C6738: 22-49	22-49	832-854	NAP		g2970667	293	101	6.00E-21	35	73	

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19316	ENU03110	ANI61C6877: 1..875	22-46	827-854	NAP		g3724291		64	8.00E-16			(AB011417) phosphate permease [Gibberella zeae]
19317	ENU03111	ANI61C9103: 23-46		836-855	NAP		g2951785	248	66	3.00E-11	41	95	(AB011822) clathrin light chain [Schizosaccharomyces pombe]
19318	ENU03112	ANI61C1065 24-46		837-856	NAP		g3881189	413	103	1.00E-21	52	98	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...
19319	ENU03113	ANI61C4534: 59-78		865-892	NAP		g4164400	574	93	2.00E-18	36	41	(AL035248) putative cell surface protein by similarity [Schizosaccharomyces pombe]
19320	ENU03114	ANI61C9963: 22-46		834-855	NAP		g585956	397	108	5.00E-28	34	95	"probable mitochondrial 40S ribosomal protein S9 precursor; ribosomal protein S9 precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z36015) ORF YBR146w [Saccharomyces cerevisiae] "
19321	ENU03115	ANI61C2000: 43-70		841-876	NAP		g585695		70	2.00E-11			pisatin demethylase (cytochrome P450 57A2) ; pisatin demethylase - fungus (Nectria haematococca) ; (X73145) pisatin demethylase [Nectria haematococca]

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19322	ENU03116	ANI50C5234_1:1735..859	28-50	843-862	NAP		g1170012		334	6.00E-91			UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase (GPT) (G1PT) (N-acetylglucosamine-1-phosphate transferase) (GLCNAC-1-P transferase); UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminophosphotransferase (EC 2.7.8.15) - fission yeast (Schizosaccharomyces pombe) ; (U09454) UDP-N-acetylglucosamine: dolichyl phosphate N-acetylglucosamine-1-phosphate transferase [Schizosaccharomyces pombe] ; (AL031349) N-acetylglucosamine-1-phosphate transferase [Schizosaccharomyces pombe]
19323	ENU03117	ANI61C9036: 22-50 1040..164	22-50	837-856	NAP		g2132491	210	78	2.00E-24	33	81	probable membrane protein YDR284c - yeast (Saccharomyces cerevisiae) ; (U51031) Ydr284cp [Saccharomyces cerevisiae]
19324	ENU03118	ANI61C1093 0:921..1797	22-51	835-856	NAP		g286165	498	217	6.00E-56	41	96	"(D14846) endo alpha-1,4 polygalactosaminidase precursor [Pseudomonas sp.]"
19325	ENU03119	ANI61C2150: 70-89 1557..1733	70-89	881-904	NAP		g1723784	264	75	7.00E-13	38	88	hypothetical 31.3 KD protein in TAF145-YOR1 intergenic region ; hypothetical protein YGR280c - yeast (Saccharomyces cerevisiae) ; (Z73065) ORF YGR280c [Saccharomyces cerevisiae]
19326	ENU03120	ANI61C8019: 66-85 1240..2119	66-85	874-903	NAP		g4154817	955	300	4.00E-87	61	86	(AE001466) putative [Helicobacter pylori J99]
19327	ENU03121	ANI61C5895: 23-46 3720..2841	23-46	841-860	NAP		g4490676	643	121	6.00E-63	68	98	(AL035655) ras-related protein [Schizosaccharomyces pombe]

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19328	ENU03122	ANI61C538:338..1218	45-65	864-883	NAP		g2132846	476	175	5.00E-43	32	55	probable membrane protein YOL119c - yeast [Saccharomyces cerevisiae]; (Z74861) ORF YOL119c [Saccharomyces cerevisiae]; (X95258) unknown protein [Saccharomyces cerevisiae]
19329	ENU03123	ANI61C10774:3056..3935	22-47	837-860	NAP		g482365	426	175	4.00E-43	51	97	protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) form II - bovine
19330	ENU03124	ANI61C8:2190..1309	56-78	876-895	NAP		g130858	650	201	2.00E-59			proteasome component C7-alpha (macropain subunit C7-alpha) (proteinase YSCE subunit 7) (multicatalytic endopeptidase complex C7) (component Y8) (SCL1 suppressor protein); multicatalytic endopeptidase complex (EC 3.4.99.46) chain YC7-alpha - yeast [Saccharomyces cerevisiae]; (M63641) proteasome Y8 [Saccharomyces cerevisiae]; (M55440) yeast proteasome subunit YC7-alpha [Saccharomyces cerevisiae]; (X56732) proteasome Y8 subunit [Saccharomyces cerevisiae]; (Z72533) ORF YGL011c [Saccharomyces cerevisiae]; (S58126) Unknown [Saccharomyces cerevisiae]; proteasome PRS2 [Saccharomyces cerevisiae]
19331	ENU03125	ANI61C10975:4012..3131	72-91	887-911	NAP		g1086919		84	1.00E-15			(U41279) similar to E. coli acyl-CoA thioesterase II (SP:P23911) [Caenorhabditis elegans]
19332	ENU03126	ANI61C8922:1914..2797	63-82	881-904	NAP		g2499790	1425	388	e-107	98	94	antigen 1 precursor (ASPND1); (Z50175) Aspergillus nidulans antigen 1 [Emmericella nidulans]
19333	ENU03127	ANI50C66411_1:889..6	40-59	862-881	NAP		g1526574		46	0.0002			(X98252) HA Vcr-1 protein [Chlorocebus aethiops]

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19334	ENU03128	ANI61C8587: 4021..3138	22-47	841-863	NAP		g731865	313	96	4.00E-19	26	50	hypothetical 59.6 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YIL121w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae]
19335	ENU03129	ANI61C905:2 334..3218	22-50	843-864	NAP		g4336889	961	189	2.00E-78	97	92	(AF107254) cyclophilin B; CYPB [Emicella nidulans]
19336	ENU03130	ANI61C6956: 112..996	53-76	865-895	NAP		g1710852	786	189	2.00E-55	93	94	GTP-binding protein SARA ; (Z67742) sarA [Aspergillus niger]
19337	ENU03131	ANI61C8618: 1156..2040	43-62	860-885	NAP		g4038630	523	122	1.00E-47	58	99	(AL032684) ER lumen protein retaining receptor protein [Schizosaccharomyces pombe]
19338	ENU03132	ANI61C1162: 1273..2157	71-90	882-913	NAP		g3702646	625	105	5.00E-25	34	47	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
19339	ENU03133	ANI61C9958: 948..63	47-66	871-890	NAP		g730502	721	277	1.00E-73			activator 1 41 KD subunit (replication factor C 41 KD subunit) ; replication factor C chain RFC2 - yeast (Saccharomyces cerevisiae) ; (D28499) Rfc2 protein [Saccharomyces cerevisiae] ; (U26028) Rfc2p [Saccharomyces cerevisiae]
19340	ENU03134	ANI61C7904: 526..1411	22-46	846-865	NAP		g585304	596	188	5.00E-47			[Saccharomyces cerevisiae] ; (Z49568) ORF YJR068w [Saccharomyces cerevisiae] ; (L47993) ORF YJR068w [Saccharomyces cerevisiae]
													[Saccharomyces cerevisiae] eukaryotic translation initiation factor 5 (EIF-5) ; translation initiation factor eIF-5 - yeast (Saccharomyces cerevisiae) ; (Z68111) Tif5p [Saccharomyces cerevisiae] ; (Z71255) Tif5p [Saccharomyces cerevisiae] ; (Z73616) eukaryotic translation initiation factor 5 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19341	ENU03135	ANI61C873:2 274..1388	26-45	843-870	NAP		g1350594	699	136	5.00E-70	79	95	RHO1 protein ; Rho1 protein - fission yeast (Schizosaccharomyces pombe) ; hypothetical protein SPAC1F7.04 - fission yeast (Schizosaccharomyces pombe) ; (D38180) Rho1 [Schizosaccharomyces pombe] ; [Schizosaccharomyces pombe] ; (Z67998) unknown [Schizosaccharomyces pombe] (U19882) FlibD [Emmericella nidulans] ; Myb-like DNA-binding protein [Emmericella nidulans] (AL034583) putative exonuclease [Schizosaccharomyces pombe] "putative D-3-phosphoglycerate dehydrogenase YIL074W (PGDH) ; hypothetical protein YIL074c - yeast (Saccharomyces cerevisiae) ; (Z37997) orf, len: 469, CAl: 0.23, similar to SERA_ECOLI P08328 D-3-phosphoglycerate dehydrogenase [Saccharomyces cerevisiae] "
19342	ENU03136	ANI61C9705: 45-64 4099..3213	45-64	870-889	NAP		g642577	1691	592	e-169	99	94	
19343	ENU03137	ANI61C4397: 50-71 29..917	50-71	876-895	NAP		g4056553	514	145	3.00E-34	42	43	
19344	ENU03138	ANI61C7016: 38-61 1144..2032	38-61	858-884	NAP		g731830	1371	277	1.00E-81	66	51	
19345	ENU03139	ANI61C7328: 43-63 1520..2409	43-63	870-889	NAP		g1665777	884	166	1.00E-48	44	41	
19346	ENU03140	ANI61C8058: 72-91 439..1327	72-91	888-918	NAP		g461925	408	188	4.00E-47	38	95	haloacetate dehalogenase H-1 ; haloacetate dehalogenase (EC 3.8.1.3) H-1 - Moraxella sp. plasmid pUOI ; (D90422) haloacetate dehalogenase H-1 [Moraxella sp.]
19347	ENU03141	ANI61C8183: 25-50 2180..3069	25-50	853-872	NAP		g132626	877	182	2.00E-70			ribonucleoside-Diphosphate reductase M2 chain (ribonucleotide reductase) ; ribonucleoside-diphosphate reductase (EC 1.17.4.1) chain M2 - mouse ; Protein R2 Of Ribonucleotide Reductase From Mouse ; (X15666) M2 ribonucleotide reductase [Mus musculus] ; (M14223) ribonucleotide reductase subunit M2 [Mus musculus]

Seq num	Seq id	Config Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19348	ENU03142	ANI61C6083: 63-83 1014..124	892-911	NAP			g131771	473	179	4.00E-45	36	53	"probable metabolite transport protein GTI1; probable membrane protein YCR098c - yeast (Saccharomyces cerevisiae); (X59720) YCR098c, len:518 [Saccharomyces cerevisiae]" putative transporter C11D3.18C; (Z68166) unknown [Schizosaccharomyces pombe] (AF039534) salicylate hydroxylase [Pseudomonas stutzeri] probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2); (U34740) putative p450 monooxygenase [Emmericella nidulans] TRNA-splicing endonuclease subunit SEN2 (TRNA-intron endonuclease); tRNA-splicing endonuclease beta chain - yeast (Saccharomyces cerevisiae); (M32336) tRNA splicing endonuclease beta-subunit [Saccharomyces cerevisiae]; (U53876) Sen2p: tRNA-splicing endonuclease beta-subunit [Saccharomyces cerevisiae]; (Z73277) ORF YLR105c [Saccharomyces cerevisiae] (Y16834) hexose transporter [Candida albicans] "(AL031228) dJ1033B10.9 (Short-chain alcohol dehydrogenase family member (HKE6, RING2)) [Homo sapiens]" (L07734) DNA polymerase delta [Schizosaccharomyces pombe] (AL021839) topoisomerase ii associated protein [Schizosaccharomyces pombe] (U78319) chitinase [Entamoeba histolytica]
19349	ENU03143	ANI61C6144: 43-70 24..915	870-892	NAP			g1351714		134	8.00E-31			
19350	ENU03144	ANI61C7133: 35-54 2531..3422	865-884	NAP			g4104775	177	95	6.00E-19	28	70	
19351	ENU03145	ANI61C5627: 53-80 952..61	882-902	NAP			g2493389	313	48	5.00E-13	30	45	
19352	ENU03146	ANI61C1479: 53-75 1081..189	879-903	NAP			g134427	269	87	1.00E-16			
19353	ENU03147	ANI61C7638: 64-84 647..1540	886-915	NAP			g3336839	365	108	8.00E-23	28	44	
19354	ENU03148	ANI61C5168: 26-45 2742..1848	857-878	NAP			g3820984	239	103	2.00E-21	36	91	
19355	ENU03149	ANI61C7755: 63-87 123..1018	895-916	NAP			g173384	1021	185	3.00E-94	66	25	
19356	ENU03150	ANI61C363:3 32-51 154..4049	864-885	NAP			g2894266	759	159	4.00E-41	35	35	
19357	ENU03151	ANI61C9942: 50-70 55..950	880-903	NAP			g1685362	459	179	3.00E-44	32	57	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19358	ENU03152	ANI61C7955: 57-76 1312..415		893-912	NAP		g544276	1444	291	e-110	76	70	glutathione-dependent FORMaldehyde dehydrogenase (FDH) (FALDH) ; FDH1 protein - yeast (Candida maltosa) ; (M58332) encoding formaldehyde resistance [Candida maltosa]
19359	ENU03153	ANI61C9825: 64-83 2422..1525		900-919	NAP		g3023753	328	138	7.00E-32	35	94	potential formate transporter ; (U52681) FdhC [Methanobacterium thermoformicum]
19360	ENU03154	ANI61C1073 43-62 3:22..919		879-898	NAP		g416643	770	153	1.00E-70	63	69	"aristolochene synthase (sesquiterpene cyclase) (AS) ; sesquiterpene cyclase, aristolochene synthase, AS - Penicillium roqueforti ; (L05193) aristolochene synthase [Penicillium roqueforti]"
19361	ENU03155	ANI61C5905: 61-85 3448..2551		890-916	NAP		g1730741	392	60	0.000000	25	47	hypothetical 65.3 KD protein in SUN4-MASS intergenic region ; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae) ; (U12141) membrane protein [Saccharomyces cerevisiae] ; (Z71341) ORF YNL065w [Saccharomyces cerevisiae]
19362	ENU03156	ANI61C1640: 49-68 2736..1839		883-904	NAP		g2583218	594	212	2.00E-54	51	21	(AF029913) beta glucosidase homolog [Cochliobolus heterostrophus]
19363	ENU03157	ANI61C7916: 72-93 4277..3378		910-929	NAP		g2132851	225	91	9.00E-18	29	55	probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae]
19364	ENU03158	ANI61C9393: 22-45 1639..2539		861-880	NAP		g1706221	106	55	0.000000	25	66	cytochrome B5 ; cytochrome b5 - yeast (Saccharomyces cerevisiae) ; (Z69382) Cytochrome B5 [Saccharomyces cerevisiae] ; (Z71387) ORF YNL111c [Saccharomyces cerevisiae]
19365	ENU03159	ANI61C6658: 22-50 1..901		847-880	NAP		g2257554	806	210	3.00E-81	57	34	[Saccharomyces cerevisiae] (AB004538) probable membrane protein YOL130w [Schizosaccharomyces pombe] ; (AL021766) hypothetical protein [Schizosaccharomyces pombe]

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19366	ENU03160	ANI61C7097: 69-88 1027..126	69-88	909-928	NAP		g1363775	295	136	2.00E-31	40	90	hypothetical protein YDR041w - yeast (Saccharomyces cerevisiae) ; (Z54075) unknown [Saccharomyces cerevisiae] (AL023554) 40s ribosomal protein s3. [Schizosaccharomyces pombe]
19367	ENU03161	ANI61C5156: 53-72 49..951	53-72	894-913	NAP		g3133108	648	182	4.00E-45	64	93	"(D89254) similar to Saccharomyces cerevisiae dihydroxy-acid dehydratase precursor, SWISS-PROT Accession Number P39522 [Schizosaccharomyces pombe]"
19369	ENU03163	ANI61C7052: 47-68 3943..3037	47-68	888-911	NAP		g4587302	1541	226	2.00E-73	54	35	[Schizosaccharomyces pombe] quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans]
19370	ENU03164	ANI61C1092 46-69 5:1380..474	46-69	876-911	NAP		g131768	178	62	3.00E-14	28	33	[Emericella nidulans] quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans]
19371	ENU03165	ANI61C2278: 22-43 1961..2868	22-43	868-887	NAP		g2257524	396	161	5.00E-39	40	95	(AB004537) hypothetical 47.4KD protein in SHPI-SEC17 intergenic region [Schizosaccharomyces pombe]
19372	ENU03166	ANI61C9199: 43-62 1466..557	43-62	882-909	NAP		g730753	863	235	7.00E-83			chromosome segregation protein SMC2 (DA-BOX protein SMC2) ; chromosome segregation protein SMC2 - yeast (Saccharomyces cerevisiae) ; (U05820) Smc2p [Saccharomyces cerevisiae] ; (D50617) chromosome segregation protein SMC2p [Saccharomyces cerevisiae] ; (D44602) DA-box protein Smc2p [Saccharomyces cerevisiae]
19373	ENU03167	ANI61C1000 22-45 4:4856..5763	22-45	865-888	NAP		g2388953	350	113	3.00E-37	42	96	[Saccharomyces cerevisiae] (Z98979) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19374	ENU03168	ANI61C6610: 24-59 1659..1842		869-890	NAP		g464862	503	498	e-140			26S protease regulatory subunit 7 homolog (CIM5 protein) (TAT-binding homolog 3); tat-binding protein homolog YTA3 - yeast (Saccharomyces cerevisiae); (X73571)
19375	ENU03169	ANI61C9449: 53-72 5985..5075		901-920	NAP		g3859663		70	5.00E-16			26S proteasome subunit Rpt1 [Saccharomyces cerevisiae]; (Z22817)
19376	ENU03170	ANI61C1038 2:3308..2399		866-889	NAP		g1708240	1190	379	e-104			putative ATPase [Saccharomyces cerevisiae]; (Z28145) ORF YKL145w [Saccharomyces cerevisiae]; 26S protease [Saccharomyces cerevisiae] (AL033502) uroporphyrinogen-III synthase [Candida albicans] hydroxymethylglutaryl-CoA synthase (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase); hydroxymethylglutaryl-CoA synthase - fission yeast (Schizosaccharomyces pombe); (U32187) 3-hydroxy-3-methylglutaryl coenzyme A synthase [Schizosaccharomyces pombe]; (Z98530) itr1; myo-inositol transporter [Schizosaccharomyces pombe]
19377	ENU03171	ANI61C7185: 36-56 648..1558		884-904	NAP		g117803	635	169	2.00E-41	38	47	cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR); L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala); (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] (AL031525) mitochondrial carrier protein [Schizosaccharomyces pombe]
19378	ENU03172	ANI61C7334: 22-49 1694..784		871-890	NAP		g3560163	925	201	8.00E-96	67	89	hypothetical 81.2 KD protein in MES1-FOL2 intergenic region; probable membrane protein YGR266w - yeast (Saccharomyces cerevisiae); (Z73051) ORF YGR266w [Saccharomyces cerevisiae]; (Y07893) ORF YGR266w [Saccharomyces cerevisiae]
19379	ENU03173	ANI61C5271: 22-56 67..978		872-891	NAP		g1723773	128	59	0.000000	23	28	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19380	ENU03174	ANI61C4304: 25-44 1882..971	25-44	875-894	NAP		g3169083	282	116	2.00E-25	34	79	(AL023705) hypothetical protein [Schizosaccharomyces pombe]
19381	ENU03175	ANI61C8225: 22-52 2145..3062	22-52	874-893	NAP		g4587575	220	77	1.00E-20	28	96	"(AC006550) Belongs to PF01121 Uncharacterized protein family UPF0038 containing ATP/GTP binding domain. ESTs gb AA585719, gb AA728503 and gb T22272 come from this gene. [Arabidopsis thaliana]" MAL3 protein ; (Z68198) putative chromosome segregation protein [Schizosaccharomyces pombe] ; (Y09518) MAL3 protein [Schizosaccharomyces pombe]
19382	ENU03176	ANI61C1734: 22-50 3869..2956	22-50	864-893	NAP		g1351729	388	87	1.00E-17	43	73	[Aquifex aeolicus] (X91837) G1315 [Saccharomyces cerevisiae] hypothetical oxidoreductase in MRPL44-MTF1 intergenic region ; hypothetical protein YMR226c - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae] cytochrome P450 51 (CYPL1) (P450-L1A1) (sterol 14-alpha demethylase) (eburicol 14-alpha-demethylase) (P450-14DM) ; lanosterol 14alpha-demethylase (EC 1.14.14.-) cytochrome P450 51 - Penicillium italicum ; (Z49750) cytochrome P-450 [Penicillium italicum]
19383	ENU03177	ANI61C1699: 24-55 950..35	24-55	878-897	NAP		g2983324	578	201	4.00E-51	43	89	Phosphatidylinositol-Specific Phospholipase C In Complex With Myo-Inositol ; Phosphatidylinositol-Specific Phospholipase C ; Phosphatidylinositol-Specific Phospholipase C In Complex With Glucosamine-(Alpha-1-6)-Myo-Inositol
19384	ENU03178	ANI61C379:6 23-42 647..5731	23-42	878-897	NAP		g1177632	187	91	9.00E-18	32	79	
19385	ENU03179	ANI61C499:5 40-59 008..5925	40-59	894-914	NAP		g2492763	572	112	1.00E-44	54	94	
19386	ENU03180	ANI61C9494: 59-78 1079..872	59-78	915-934	NAP		g2493386	1608	337	7.00E-92	58	57	
19387	ENU03181	ANI61C8220: 44-64 1681..764	44-64	898-919	NAP		g1633139	95	82	6.00E-15	29	91	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19388	ENU03182	ANI61C674:9 41..24	31-54	887-906	NAP		g1723510	446	108	2.00E-43	37	76	hypothetical 42.4 KD protein C1F12.05 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe] (AL031787) putative heavy metal transport protein
19389	ENU03183	ANI61C776:1 67-86 087..169	67-86	911-943	NAP		g3687489	432	69	4.00E-30	49	93	[Schizosaccharomyces pombe] (AL031787) putative heavy metal transport protein
19390	ENU03184	ANI61C3974: 42-62 3230..4149	42-62	892-919	NAP		g730655	923	280	8.00E-89	76	97	[Schizosaccharomyces pombe] "40S ribosomal protein RP10 ; ribosomal protein S0.e.B, cytosolic - yeast (Candida albicans) ; (X82017) ribosomal protein 10 [Candida albicans] "
19391	ENU03185	ANI61C8192: 34-53 13..118	34-53	893-912	NAP		g2842689	733	258	4.00E-68	53	59	hypothetical 50.4 KD protein C1F8.04C in chromosome I ; (Z81312) unknown [Schizosaccharomyces pombe]
19392	ENU03186	ANI61C3842: 38-57 1023..102	38-57	890-917	NAP		g3850125	399	161	5.00E-39	32	60	(AL033391) hypothetical membrane protein [Candida albicans]
19393	ENU03187	ANI61C2363: 48-67 1796..2717	48-67	900-927	NAP		g3242655	2990	316	1.00E-85	58	35	(AB015511) Avicelase III [Aspergillus aculeatus]
19394	ENU03188	ANI61C1084: 68-87 2338..1417	68-87	923-947	NAP		g4539262	321	73	5.00E-22	38	92	(AL049495) conserved phosducin-like hypothetical protein
19395	ENU03189	ANI61C6527: 62-81 457..1379	62-81	923-942	NAP		g2465150	419	86	4.00E-38	61	88	[Schizosaccharomyces pombe] (Z99753) rho protein
19396	ENU03190	ANI61C1037 9:857..1747	22-51	883-905	NAP		g2494084	335	134	9.00E-31	37	87	[Schizosaccharomyces pombe] glycerate dehydrogenase (NADH-dependent hydroxypyruvate reductase) (HPR) (GDH) (hydroxypyruvate dehydrogenase) (glyoxylate reductase) (HPR-A)
19397	ENU03191	ANI61C1103 2:3458..2532	24-47	883-908	NAP		g731385	329	73	2.00E-12	39	79	hypothetical 33.7 KD protein in ISC10 3'region ; hypothetical protein YER185w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer185wp [Saccharomyces cerevisiae]
19398	ENU03192	ANI61C9880: 60-80 5455..6381	60-80	920-944	NAP		g3116131	60	48	0.00007	27	32	(AL023288) hypothetical protein [Schizosaccharomyces pombe]

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19399	ENU03193	ANI61C1141 1:1275..348	65-84	929-949	NAP		g515503	634	192	7.00E-50	43	55	(U12013) 4-coumarate-CoA ligase enzyme [Pinus taeda] ; (U39404) 4-coumarate:CoA ligase [Pinus taeda] ; (U39405) 4-coumarate:CoA ligase [Pinus taeda]
19400	ENU03194	ANI61C6468: 48-67 620..1547	48-67	914-933	NAP		g2258125	892	171	6.00E-42	47	46	(Z83828) AmMst-1 [Amanita muscaria]
19401	ENU03195	ANI61C7752: 33-52 979..50	33-52	902-920	NAP		g4049518	592	210	1.00E-62	48	76	(AL031852) conserved hypothetical protein [Schizosaccharomyces pombe]
19402	ENU03196	ANI61C9305: 61-80 40..969	61-80	928-948	NAP		g2132923	747	287	7.00E-77	45	84	probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae) ; (Z75147) ORF YOR240w [Saccharomyces cerevisiae]
19403	ENU03197	ANI61C4048: 41-63 1855..2784	41-63	909-928	NAP		g2414604	1119	146	4.00E-46	43	49	(Z99295) dihydroxyacetone kinase [Schizosaccharomyces pombe] ; (AB010078) dihydroxyacetone kinase isoenzyme I [Schizosaccharomyces pombe]
19404	ENU03198	ANI61C460:1 23-53 255..324	23-53	893-912	NAP		g1709062	747	221	2.00E-84	55	71	galactosyltransferase MNN10 (BUD emergence delay protein 1) ; BED1 protein - yeast (Saccharomyces cerevisiae) ; (Z49701) unknown [Saccharomyces cerevisiae] ; (L42540) Mnn10p [Saccharomyces cerevisiae]
19405	ENU03199	ANI61C1122 25-44 5:2657..1725	25-44	895-914	NAP		g3293547	249	85	1.00E-18	30	95	(AF072709) putative oxidoreductase [Streptomyces lividans]
19406	ENU03200	ANI61C620:8 29-50 8..1022	29-50	894-921	NAP		g1709997	214	61	2.00E-17	40	18	DNA repair protein RAD18 ; (X80929) rad18 [Schizosaccharomyces pombe] ; (AL033406) dna repair protein rad18 [Schizosaccharomyces pombe]
19407	ENU03201	ANI61C1094: 39-58 1494..2429	39-58	913-932	NAP		g2494090		90	3.00E-17			hypothetical 33.3 KD protein in PERR-ARGF intergenic region ; (AE000134) putative lyase/synthase [Escherichia coli]
19408	ENU03202	ANI61C2632: 27-46 1105..2041	27-46	900-921	NAP		g2792328	370	152	3.00E-36	35	96	(AF040570) esterase [Amycolatopsis mediterranei]
19409	ENU03203	ANI61C8017: 36-55 4869..5806	36-55	911-930	NAP		g3378273	613	113	5.00E-50	43	79	(AF079317) benzyl alcohol dehydrogenase [Sphingomonas aromaticivorans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19410	ENU03204	ANI61S911:1 32..10	38-67	914-933	NAP		g1363737		129	2.00E-29	27	18	probable membrane protein YLR247c - yeast (Saccharomyces cerevisiae) ; (U20865) Ylr247cp [Saccharomyces cerevisiae]
19411	ENU03205	ANI61C3367: 46-65 455..1387	46-65	922-941	NAP		g4512354	216	98	1.00E-19	29	91	(AB011836) alkyl hydroperoxide reductase large subunit [Bacillus halodurans]
19412	ENU03206	ANI61C8472: 27-49 1870..933	27-49	901-922	NAP		g2133310	551	139	8.00E-59	46	93	hypothetical 32.0k protein - Neurospora crassa ; (L40806) open reading frame [Neurospora crassa] ; ORF [Neurospora crassa]
19413	ENU03207	ANI50346_1: 49-68 1529..590	49-68	927-946	NAP		g2492767		58	4.00E-23	35	98	putative short-chain type dehydrogenase/reductase Y4MP ; (AE000085) Y4mP [Rhizobium sp. NGR234]
19414	ENU03208	ANI61C6286: 59-79 187..705	59-79	934-957	NAP		g728797	797	405	e-133	80	77	actin-like protein (centractin) ; actin-related protein ro-4 - Neurospora crassa ; (L31505) centractin [Neurospora crassa]
19415	ENU03209	ANI61C1109 57-76 9:12037..1109	57-76	937-956	NAP		g3914053	1151	438	e-122	72	33	DNA mismatch repair protein MSH2 ; (AF030634) DNA mismatch repair protein [Neurospora crassa]
19416	ENU03210	ANI61C8920: 65-84 2082..1141	65-84	939-964	NAP		g2408039	785	196	2.00E-80	56	42	(Z99163) putative beta-glucan synthesis-associated protein [Schizosaccharomyces pombe]
19417	ENU03211	ANI61C1682: 56-76 1834..890	56-76	921-956	NAP		g131768	232	74	2.00E-12	25	54	quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans]
19418	ENU03212	ANI61C5444: 32-51 1810..867	32-51	914-933	NAP		g4008461		108	6.00E-23			(AL034489) predicted using Genefinder; cDNA EST yk367h5.3 comes from this gene; cDNA EST yk367h5.5 comes from this gene; cDNA EST EMBL:Z14572 comes from this gene [Caenorhabditis elegans]
19419	ENU03213	ANI61C4081: 30-49 1164..221	30-49	909-931	NAP		g2980819	226	96	4.00E-19	43	57	(AJ224865) IgE-binding protein [Aspergillus fumigatus]
19420	ENU03214	ANI61C5488: 61-81 269..1212	61-81	943-962	NAP		g3647337	268	100	2.00E-20	35	73	(AL031644) putative trna-splicing endonuclease subunit [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19421	ENU03215	ANI61C7354: 59-78 1885..939	63-82	947-966	NAP		g2769696	318	143	2.00E-33	33	80	(AC003982) unknown function; 60% similar to Z50177 (PID:g927403) (PID:g927402) [Homo sapiens]
19422	ENU03216	ANI61C1019 8:2387..1443	63-82	947-966	NAP		g2501598	411	120	2.00E-26	40	89	hypothetical 28.3 KD protein in PPR1-SNF7 intergenic region; hypothetical protein YLR022c - yeast (Saccharomyces cerevisiae); (Z73194) ORF YLR022c [Saccharomyces cerevisiae]
19423	ENU03217	ANI61C5194: 37-56 1513..567	37-56	922-941	NAP		g133961	801	128	2.00E-56	74	90	40S ribosomal protein S4 (omnipotent suppressor protein SUP44) (RP12) (S2E); ribosomal protein S2.e - yeast (Saccharomyces cerevisiae); (M59375) ribosomal protein S4 [Saccharomyces cerevisiae]; (Z72645) ORF YGL123w [Saccharomyces cerevisiae]; (X94106) SUP44 [Saccharomyces cerevisiae]
19424	ENU03218	ANI61C152:1 159..212	26-47	912-931	NAP		g3859681	446	198	7.00E-50	34	94	(AL033503) transcription regulatory protein [Candida albicans]
19425	ENU03219	ANI61C8982: 22-46 3165..2217	22-46	898-928	NAP		g755011	263	134	1.00E-30	34	81	(L39639) kievitone hydratase [Fusarium solani]
19426	ENU03220	ANI61C7190: 49-67 5784..6733	49-67	937-956	NAP		g544254	688	212	3.00E-68	55	95	esterase D; (AF112219) esterase D [Homo sapiens]
19427	ENU03221	ANI61C8388: 22-43 3577..2628	22-43	908-929	NAP		g2226414	258	74	9.00E-16	43	99	(Z97204) hypothetical protein [Schizosaccharomyces pombe]
19428	ENU03222	ANI61C4017: 30-49 1451..1846	30-49	918-938	NAP		g548584	793	228	4.00E-59			serine/threonine protein phosphatase ppe1 (phosphatase ESP1); cell shape control protein phosphatase ppe1 - fission yeast (Schizosaccharomyces pombe); (Z18925) type2A-like protein phosphatase [Schizosaccharomyces pombe]; (D13712) protein phosphatase [Schizosaccharomyces pombe]; (AL031540) serine-threonine protein phosphatase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19429	ENU03223	ANI61C7183: 1667..2617	25-56	912-933	NAP		g2498438	58	48	0.00007	18	48	transcriptional coactivator HFI1/ADA1 ; HFI1 protein - yeast (Saccharomyces cerevisiae) ; (Z67751) putative protein [Saccharomyces cerevisiae] ; (Z73610) ORF YPL254w [Saccharomyces cerevisiae] ; (U76735) putative transcriptional coactivator [Saccharomyces cerevisiae] (AF063095) SELIL [Mus musculus]
19430	ENU03224	ANI61C6626: 5169..6121	72-92	963-982	NAP		g4159995	577	130	2.00E-29	36	29	hypothetical 57.6 KD protein C30D10.15 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]
19431	ENU03225	ANI61C1070 6:6101..5146	22-50	916-935	NAP		g3219924	276	52	0.000005	29	34	hypothetical 44.9 KD protein in URA10-NRC1 intergenic region ; probable membrane protein YMR272c - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae]
19432	ENU03226	ANI61C6762: 994..1950	70-91	956-984	NAP		g2493967	854	151	2.00E-75	53	72	(U85909) hydroxylase [Aureobasidium pullulans]
19433	ENU03227	ANI61C8592: 19..976	40-59	934-954	NAP		g4099311	604	165	5.00E-40	44	62	(U68040) polyketide synthase [Cochliobolus heterostrophus]
19434	ENU03228	ANI61C2749: 1407..449	24-46	921-940	NAP		g1546072	373	173	2.00E-42	35	12	(U09358) Rca1p [Saccharomyces cerevisiae]
19435	ENU03229	ANI61C4206: 76..1034	50-70	944-966	NAP		g508233	1246	191	e-106	67	35	"(S83228) beta-isopropylmalate dehydrogenase [Aspergillus niger, strain A733, Peptide, 363 aa]
19436	ENU03230	ANI61C4920: 1744..784	51-77	949-969	NAP		g1911741	1223	326	e-121	82	82	[Aspergillus niger] ; isopropylmalate dehydrogenase [Aspergillus niger]"
19437	ENU03231	ANI61C9581: 3857..4819	24-46	925-944	NAP		g2492754	354	111	4.00E-33	38	87	sorbitol utilization protein SOU1 ; (AF002134) Sou1p [Candida albicans]
19438	ENU03232	ANI61C4572: 3699..2735	59-78	961-980	NAP		g3850070	1235	434	e-121	63	46	(AL033385) transketolase [Schizosaccharomyces pombe]
19439	ENU03233	ANI61C1071 8:1060..96	29-48	916-951	NAP		g3763927	329	99	2.00E-41	39	58	(AC004450) putative carboxyphosphoenolpyruvate mutase [Arabidopsis thaliana]

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19440	ENU03234	ANI61C8700: 32-49 17..982		927-955	NAP		g1703215	399	175	6.00E-43	31	51	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
19441	ENU03235	ANI61C8700: 32-49 17..982		927-955	NAP		g1703215	399	175	6.00E-43	31	51	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c [Saccharomyces cerevisiae]
19442	ENU03236	ANI61C8861: 50-69 169..1139		959-978	NAP		g2131729	702	189	7.00E-66	50	36	hypothetical protein YLL029w - yeast (Saccharomyces cerevisiae) ; (Z73134) ORF YLL029w [Saccharomyces cerevisiae]
19443	ENU03237	ANI61C4087: 40-59 2719..1749		949-968	NAP		g464435	1346	507	e-143	69	77	acid phosphatase precursor ; acid phosphatase (EC 3.1.3.2) - Aspergillus ficuum ; (L20566) acid phosphatase [Aspergillus niger]
19444	ENU03238	ANI61C9249: 22-52 7183..8155		932-952	NAP		g1781226	345	138	8.00E-32	34	92	(Z83867) fadB4 [Mycobacterium tuberculosis]
19445	ENU03239	ANI61C1997: 23-44 1399..426		933-954	NAP		g3183237	1374	244	8.00E-64	45	34	hypothetical 103.4 KD TRP-ASP repeats containing protein C3D6.12 in chromosome II ; (Z95620) trp asp repeat protein [Schizosaccharomyces pombe]
19446	ENU03240	ANI61C1025 25-46 5:1065..92		921-956	NAP		g1351660	526	222	4.00E-57	45	78	endonuclease III homolog (DNA- (apurinic or apyrimidinic site) lyase) ; endonuclease III (EC 3.1.-.-) - fission yeast (Schizosaccharomyces pombe) ; yeast (Schizosaccharomyces pombe) ; hypothetical protein SPAC30D11.07 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) endonuclease III homolog [Schizosaccharomyces pombe]
19447	ENU03241	ANI61C6477: 41-60 7088..6115		951-972	NAP		g3169050	118	68	8.00E-11	32	64	(AL023702) hypothetical protein SC1C3.24 [Streptomyces coelicolor]

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19448	ENU03242	ANI61C9181: 51-70 9526..8552		961-983	NAP		g2497056	183	52	6.00E-12			putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae] hypothetical protein C17H9.20 in chromosome I ; (Z98597) hypothetical protein [Schizosaccharomyces pombe] (D87681) acetyltransferase [Aspergillus awamori]
19449	ENU03243	ANI61C8589: 24-44 1475..501		926-956	NAP		g3183360	411	155	4.00E-37	27	57	
19450	ENU03244	ANI61C8537: 22-51 11961..10987		934-954	NAP		g1542843	1046	206	e-105	66	94	"DNA polymerase beta ; Dna Polymerase Beta (Beta Polymerase) (E.C.2.7.7.7) (Apo, Full Protein) ; Rattus norvegicus ; Rattus norvegicus ; Rattus norvegicus "
19451	ENU03245	ANI61C266:1 41-60 531..556		955-974	NAP		g585064	296	146	2.00E-34	28	95	(U59376) N-carbamoyl-D-amino acid amidohydrolase [Agrobacterium radiobacter] "hypothetical 29.7 KD protein in HRPA-ALDA intergenic region ; (D90780) ORF_ID:o270#1; similar to [SwissProt Accession Number P34209] [Escherichia coli] ; (D90781) ORF_ID:o270#1; similar to [SwissProt Accession Number P34209] [Escherichia coli] ; (AE000239) orf, hypothetical protein [Escherichia coli] "
19452	ENU03246	ANI61C9849: 47-67 2401..1424		950-982	NAP		g1401216	471	145	6.00E-34	41	95	(AB017112) mCAC [Mus musculus]
19453	ENU03247	ANI61C4859: 22-46 849..1829		931-960	NAP		g2506663	339	162	3.00E-39	38	99	hypothetical GTP-binding protein in POP2-HOL1 intergenic region ; hypothetical protein YNR053c - yeast (Saccharomyces cerevisiae) ; (Z71668) ORF YNR053c [Saccharomyces cerevisiae]
19454	ENU03248	ANI61C1038 32-58 3:2442..3423		942-971	NAP		g4239974		68	1.00E-10			
19455	ENU03249	ANI61C7390: 22-39 2129..2247		942-961	NAP		g1730685	1466	270	8.00E-72	67	44	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nobi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19456	ENU03250	ANI61C7332: 29-48 576..1557		933-968	NAP		g3122261	843	164	2.00E-84	74	99	eukaryotic translation initiation factor 6 (EIF-6) ; hypothetical protein YPR016c (Z49919) unknown [Saccharomyces cerevisiae] ; (U31900) Lpz15p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] (AL033391) hypothetical membrane protein [Candida albicans] (Z98944) hypothetical protein [Schizosaccharomyces pombe] (AB010465) lactonohydrolase [Fusarium oxysporum] "hypothetical 67.7 KD protein C23C11.03 in chromosome I ; (Z98559) SPAC23C11.03; len:598aa, similar eg. to YJR002W, YIX2_ yeast, p47083, hypothetical 67.0 kd protein, (593aa), fasta scores, opt:855, E(0:0, (33.0% identity in 610 aa overlap) [Schizosaccharomyces pombe] " tubulin alpha-2 chain ; tubulin alpha-2 chain - Emericella nidulans (AL035570) putative nitrilase homolog [Schizosaccharomyces pombe] (AF002660) aflatoxin [Aspergillus parasiticus] probable membrane protein YOR262w - yeast (Saccharomyces cerevisiae) ; (Z75170) ORF YOR262w [Saccharomyces cerevisiae] "2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase - Escherichia coli ; (Z47799) 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [Escherichia coli] ; (Z37980) hypothetical 2,4-dihydroxy-hepta-2-ene-1,7-dioate aldolase [Escherichia coli] " (AJ223327) rAsp f 9 [Aspergillus fumigatus]
19457	ENU03251	ANI61C8252: 58-77 3087..2106		977-997	NAP		g3850125	624	199	3.00E-50	35	63	
19458	ENU03252	ANI61C1118 31-53 5:2618..1636		946-971	NAP		g2370496	354	173	1.00E-42	33	35	
19459	ENU03253	ANI61C9343: 60-79 1910..2893		973-1001	NAP		g3810873	478	150	1.00E-35	41	76	
19460	ENU03254	ANI61C9255: 48-78 1781..798		969-989	NAP		g3183346	559	215	5.00E-55	38	53	
19461	ENU03255	ANI61C3731: 32-51 101..1084		954-973	NAP		g135407	1617	590	e-168	97	67	
19462	ENU03256	ANI61C1106 31-50 6:5032..6020		942-977	NAP		g4467274	575	206	2.00E-52	48	97	
19463	ENU03257	ANI61C6325: 45-65 1181..2169		970-991	NAP		g2738309	408	73	1.00E-27	31	70	
19464	ENU03258	ANI61C4666: 51-73 1164..175		980-998	NAP		g2132930	814	222	3.00E-57	47	83	
19465	ENU03259	ANI61C4278: 42-61 600..1590		955-990	NAP		g1073302	269	126	3.00E-28	30	100	
19466	ENU03260	ANI61C1072 29-50 3:1241..2230		955-977	NAP		g2879890	503	220	1.00E-56	37	99	

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19467	ENU03261	ANI61C9659: 1464..473	72-98	1002-1021	NAP		g1723239	784	314	6.00E-85	55	93	hypothetical 35.7 KD protein C26A3.11 in chromosome I; (Z69240) putative amidohydrolase [Schizosaccharomyces pombe]
19468	ENU03262	ANI61C7455: 65-84 6773..7764	65-84	995-1014	NAP		g417090	878	138	2.00E-84			GTP-binding nuclear protein GSP1/CNR1 ; GTP-binding protein GSP1 - yeast (Saccharomyces cerevisiae) ; (L08690) GTP-binding protein [Saccharomyces cerevisiae] ; (X71945) CNR2 [Saccharomyces cerevisiae] ; (U17243) GTP-binding nuclear protein. Highly similar to GSP2_yeast. Belongs to the Ran family of Ras proteins [Saccharomyces cerevisiae] (AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
19469	ENU03263	ANI61C5172: 33-52 3310..2318	33-52	964-983	NAP		g3702646	298	78	3.00E-26	31	54	[Schizosaccharomyces pombe] (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]
19470	ENU03264	ANI61C7232: 22-52 5559..4567	22-52	949-972	NAP		g3647335	145	67	2.00E-10	25	74	hypothetical 33.5 KD protein C1D4.02C in chromosome I; (Z69239) unknown [Schizosaccharomyces pombe]
19471	ENU03265	ANI61C3420: 22-46 1758..2750	22-46	940-972	NAP		g1723224	302	96	5.00E-19	32	99	cytochrome C PEROxidase precursor (CCP) ; cytochrome-c peroxidase (EC 1.11.1.5) precursor - yeast (Saccharomyces cerevisiae) ; (X62422) Cytochrome c peroxidase [Saccharomyces cerevisiae] ; (Z28291) ORF YKR066c [Saccharomyces cerevisiae]
19472	ENU03266	ANI61C9030: 66-85 2449..3441	66-85	997-1016	NAP		g543969	478	217	7.00E-56	44	74	hypothetical 32.6 KD protein in DAL5-THI11 intergenic region ; aryl-alcohol dehydrogenase homolog YJR155w - yeast (Saccharomyces cerevisiae) ; (Z49655) ORF YJR155w [Saccharomyces cerevisiae]
19473	ENU03267	ANI61C2045: 58-78 3325..2331	58-78	989-1008	NAP		g1352946	411	73	2.00E-21	42	94	

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19474	ENU03268	ANI61C1109 0:630..1622	22-57	953-973	NAP		g1293655	783	249	3.00E-65	44	49	(U51327) versicolorin B synthase [Aspergillus parasiticus]; (U51328) versicolorin B synthase [Aspergillus parasiticus]
19475	ENU03269	ANI61C9633: 3640..3430	38-57	970-989	NAP		g3668160	203	59	0.000000	23	47	(AL031764) hexose transporter. [Schizosaccharomyces pombe]; (AF098076) ght6p [Schizosaccharomyces pombe]
19476	ENU03270	ANI61C7613: 205..1199	22-45	950-974	NAP		g1353673	151	62	2.00E-17	30	75	(U42349) 39 kDa encoded by N33 [Homo sapiens]
19477	ENU03271	ANI61C1373: 141..1136	24-43	949-977	NAP		g3122964	432	129	3.00E-50	41	94	putative thiosulfate sulfurtransferase; hypothetical protein YOR251c - yeast (Saccharomyces cerevisiae); (Z75159) ORF YOR251c [Saccharomyces cerevisiae]
19478	ENU03272	ANI61C7897: 22..1017	43-62	976-996	NAP		g2131132	1110	444	e-124	66	22	UDPGlucose--glycoprotein glucosyltransferase (EC 2.7.8.19) - fission yeast (Schizosaccharomyces pombe); (U38417) UDP-Glc:Glycoprotein Glucosyltransferase [Schizosaccharomyces pombe]
19479	ENU03273	ANI61C1083 7:1059..63	22-46	957-976	NAP		g1708467	333	148	4.00E-35	35	82	branched-chain amino acid aminotransferase (transaminase B) (BCAT); branched-chain-amino-acid transaminase homolog - Haemophilus influenzae (strain Rd KW20); (U32798) branched-chain-amino-acid transaminase (ilvE) [Haemophilus influenzae Rd]
19480	ENU03274	ANI61C5227: 997..1	46-65	973-1000	NAP		g125935	578	76	2.00E-35	36	46	lactose permease; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (AL023780) DNA binding protein [Schizosaccharomyces pombe]
19481	ENU03275	ANI61C9068: 9..1006	26-48	951-981	NAP		g3184115	377	166	3.00E-40	30	63	(AB010442) PMR1 [Penicillium digitatum]
19482	ENU03276	ANI61C4858: 43..1040	54-74	981-1009	NAP		g3288709	1234	458	e-128	68	22	(AF010494) sorbitol dehydrogenase [Callitrix sp.]
19483	ENU03277	ANI61C1942: 3132..2133	45-65	975-1001	NAP		g2352843	715	104	5.00E-36	42	80	

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19484	ENU03278	ANI61C9666: 4320..3321	33-53	965-990	NAP		g2132925	517	263	2.00E-69	41	77	probable membrane protein YOR245c - yeast (Saccharomyces cerevisiae); (Z75153) ORF YOR245c [Saccharomyces cerevisiae]
19485	ENU03279	ANI61C4960: 53-72 3192..2193	53-72	988-1010	NAP		g729534	739	146	1.00E-75	51	58	UTR1 protein (unknown transcript 1 protein); UTR1 protein - yeast (Saccharomyces cerevisiae); (L26347) orf gtE530 [Saccharomyces cerevisiae]; (Z49549) ORF YJR049c [Saccharomyces cerevisiae]; (L36344) ORF; putative [Saccharomyces cerevisiae]
19486	ENU03280	ANI61C6471: 42-61 11749..10749	42-61	973-1000	NAP		g547648	949	280	2.00E-92			histidinol-phosphate aminotransferase (imidazole acetol-phosphate transaminase); his 3 protein - fission yeast (Schizosaccharomyces pombe); (L19523) imidazoleglycerol-phosphate dehydratase [Schizosaccharomyces pombe]; (L19524) imidazoleglycerol-phosphate dehydratase [Schizosaccharomyces pombe]; [Schizosaccharomyces pombe]; (AB004534) histidinol-phosphate aminotransferase [Schizosaccharomyces pombe] (Z99107) similar to hypothetical proteins [Bacillus subtilis] phosphate-repressible phosphate permease; phosphate-repressible phosphate permease - Neurospora crassa; (M31364) phosphate permease [Neurospora crassa] (AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe]; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe] (AL023706) apoptosis specific protein homologue [Schizosaccharomyces pombe]
19487	ENU03281	ANI61C7553: 40-59 299..1299	40-59	979-998	NAP		g2633013	351	145	1.00E-38	30	93	
19488	ENU03282	ANI61C1037 49-72 3:5272..6273	49-72	989-1008	NAP		g130117	869	214	7.00E-55	35	56	
19489	ENU03283	ANI61C1131: 34-53 1000..250	34-53	964-994	NAP		g2981103		107	2.00E-22	39	21	
19490	ENU03284	ANI61C7525: 23-47 7424..8426	23-47	964-983	NAP		g3169097	190	74	1.00E-12	28	85	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19491	ENU03285	ANI50C202_3:1765..2767	23-42	950-983	NAP		g2239196		257	6.00E-68	45	98	(Z97209) hypothetical protein [Schizosaccharomyces pombe]
19492	ENU03286	ANI61C8836:38-60	38-60	966-999	NAP		g135407	823	341	5.00E-93	60	62	tubulin alpha-2 chain; tubulin alpha-2 chain - Emericella nidulans
19493	ENU03287	ANI50C721_3785..4788	25-50	967-986	NAP		g116929		272	3.00E-75	49	63	hexaprenyl pyrophosphate synthetase precursor (HPS); trans-pentaprenyltransferase (EC 2.5.1.33) precursor - yeast (Saccharomyces cerevisiae); (J05547) hexaprenyl pyrophosphate synthetase (COQ1) [Saccharomyces cerevisiae]; (Z35872) ORF YBR003w [Saccharomyces cerevisiae]
19494	ENU03288	ANI61C1055 7:3124..4127	34-53	976-995	NAP		g549725	332	126	8.00E-31			"NADH-cytochrome B5 reductase precursor (P34/P32); cytochrome-b5 reductase (EC 1.6.2.2), mitochondrial outer membrane form - yeast (Saccharomyces cerevisiae); (Z26877) unknown [Saccharomyces cerevisiae]; (Z28150) ORF YKL150w [Saccharomyces cerevisiae]; (X81474) NADH-cytochrome b5 reductase [Saccharomyces cerevisiae]; ORF [Saccharomyces cerevisiae]"
19495	ENU03289	ANI61C562:1 854..850	22-48	964-984	NAP		g1346485	889	182	3.00E-54	41	53	malate oxidoreductase (malic enzyme) (ME) (NADP-dependent malic enzyme) (NADP-ME); (X56233) malic enzyme [Populus balsamifera subsp. trichocarpa]
19496	ENU03290	ANI61C30:36 23..2618	23-52	967-986	NAP		g172260	721	111	6.00E-38	67	52	(M96667) proteosome-related protein [Saccharomyces cerevisiae]
19497	ENU03291	ANI61C8552:8701..9708	72-94	1018-1037	NAP		g1176002	452	164	7.00E-40	32	60	hypothetical 55.1 KD protein in FAB1-PES4 intergenic region; probable membrane protein YFR021w - yeast (Saccharomyces cerevisiae); (D50617) YFR021W [Saccharomyces cerevisiae]
19498	ENU03292	ANI61C1658:3373..2365	22-44	968-988	NAP		g2398818	192	61	1.00E-23	36	73	(Z99126) hypothetical oxidoreductase [Schizosaccharomyces pombe]
19499	ENU03293	ANI61C1649:2056..1048	36-55	976-1002	NAP		g3183055	461	216	2.00E-55	41	47	probable serine/threonine-protein kinase C29A4.16; (Z97210) protein kinase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19500	ENU03294	ANI61C1183: 5335..4326	28-47	976-995	NAP		g418391	589	236	1.00E-61	39	88	"ZRT1 protein ; zinc transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (X67787) ORF1 [Saccharomyces cerevisiae] ; (X94357) ORF NRC376; EMBL:SCFZF1;X67787; PIR:DEBY4;S07614 [Saccharomyces cerevisiae] ; (Z72777) ORF YGL255w [Saccharomyces cerevisiae] " (Z98597) hypothetical nadh-cytochrome reductase [Schizosaccharomyces pombe] ubiquitin--protein ligase RSP5 ; hypothetical protein YER125w - yeast (Saccharomyces cerevisiae) ; (U18916) Rsp5p [Saccharomyces cerevisiae] (AB016895) Pop3 [Schizosaccharomyces pombe] glycerol-3-phosphate dehydrogenase (NAD+) 1 ; glycerol-3-phosphate dehydrogenase (NAD+) (EC 1.1.1.8) precursor - yeast (Saccharomyces cerevisiae) ; (Z24454) glycerol 3-phosphate dehydrogenase [Saccharomyces cerevisiae] ; (U04621) dihydroxyacetone phosphate reductase [Saccharomyces cerevisiae] ; (X76859) glycerol-3-phosphate dehydrogenase (NAD+) [Saccharomyces cerevisiae] ; (Z48432) glycerol-3-phosphate dehydrogenase (NAD+) (X76859) [Saccharomyces cerevisiae] ; (Z74071) ORF YDL022w [Saccharomyces cerevisiae] (AF092576) translation initiation factor eIF3 p40 subunit; eIF3p40 [Homo sapiens] (AB000703) phosphomannomutase [Schizosaccharomyces pombe] (AL023533) hypothetical protein [Schizosaccharomyces pombe]
19501	ENU03295	ANI61C6843: 46-65 2564..3573	46-65	994-1013	NAP		g2330719	105	73	2.00E-12	32	93	
19502	ENU03296	ANI61C9202: 22-48 2072..3082	22-48	968-990	NAP		g730684	2522	226	e-113	73	35	
19503	ENU03297	ANI61C6531: 22-55 1109..99	22-55	971-990	NAP		g3434986	778	255	1.00E-85	62	81	
19504	ENU03298	ANI61C1100 25-45 9:844..1854	25-45	973-993	NAP		g462197	726	223	6.00E-59			
19505	ENU03299	ANI61C4362: 31-51 872..1883	31-51	980-1000	NAP		g3986482	414	99	2.00E-40	37	80	
19506	ENU03300	ANI61C7112: 31-51 992..2003	31-51	967-1000	NAP		g1813335	721	176	2.00E-75	63	99	
19507	ENU03301	ANI61C1095: 34-55 3284..4296	34-55	985-1004	NAP		g3130060	914	115	5.00E-25	32	37	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19508	ENU03302	ANI50C66_1: 22-51 1364..2377	22-51	966-993	NAP		g2879890	245	245	e-101	70	91	(AJ223327) rAsp f 9 [Aspergillus fumigatus]
19509	ENU03303	ANI61C9775: 33-61 7754..8767	33-61	985-1004	NAP		g3873958	194	103	2.00E-21	26	95	(Z81458) similar to transposable element [Caenorhabditis elegans]
19510	ENU03304	ANI61C8634: 22-51 7809..6794	22-51	971-994	NAP		g538066	181	62	0.000000	25	96	(M77661) putative gag protein [Magnaporthe grisea]
19511	ENU03305	ANI61C8943: 55-80 1264..250	55-80	997-1027	NAP		g3426039	273	127	9.00E-29	49	25	(AC005168) unknown protein [Arabidopsis thaliana]
19512	ENU03306	ANI61C1622: 29-48 1355..341	29-48	974-1001	NAP		g549739	163	101	9.00E-21	34	37	hypothetical 55.4 KD protein in STE3-GIN10 intergenic region ; hypothetical protein YKL175w - yeast (Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28175) ORF YKL175w [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
19513	ENU03307	ANI61C9973: 38-57 1393..379	38-57	992-1011	NAP		g2318125	316	82	4.00E-18	38	75	[Saccharomyces cerevisiae] (AF014404) HIV-Nef associated acyl CoA thioesterase [Homo sapiens] ; (AL008726) dJ337O18.3.1 (Thioesterase II) (isoform 1) [Homo sapiens]
19514	ENU03308	ANI61C1292: 59-78 1044..26	59-78	1014-1034	NAP		g2271503	64	64	7.00E-17			(AF009672) unknown [Acinetobacter sp. ADP1]
19515	ENU03309	ANI61C1011 22-56 0:7268..6251	22-56	978-997	NAP		g2924499	331	124	8.00E-28	35	91	(AL022019) putative 3 beta-hydroxysteroid dehydrogenase/delta 5->4-isomerase(3beta-hsd) [Schizosaccharomyces pombe]
19516	ENU03310	ANI61C1143 68-91 4:1206..190	68-91	1022-1044	NAP		g3687478	1534	414	e-115	60	61	(AL031786) putative delta-1-pyrroline-5-carboxylate dehydrogenase [Schizosaccharomyces pombe]
19517	ENU03311	ANI61C541:2 23-49 380..1362	23-49	971-999	NAP		g2267603	246	121	9.00E-27	35	54	(AF009418) trichothecene biosynthesis transcription factor [Myrothecium roridum]
19518	ENU03312	ANI61C7921: 24-58 4205..3186	24-58	970-1001	NAP		g2879861	148	84	1.00E-17	25	97	(AL021815) hypothetical protein [Schizosaccharomyces pombe] ; (AL035675) adducin N terminal domain protein [Schizosaccharomyces pombe]
19519	ENU03313	ANI61C8093: 33-52 1073..52	33-52	992-1011	NAP		g3282211	1131	211	e-117	70	69	(U68714) isocitrate lyase 1 [Botryotinia fuckeliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19520	ENU003314	ANI61C1147 4:3071..2048	36-55	1000-1017	NAP		g3318897	337	161	8.00E-39	30	48	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum "
19521	ENU003315	ANI61C1118: 58-78 5506..6530	58-78	1020-1040	NAP		g3150262	713	178	4.00E-44	42	85	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
19522	ENU003316	ANI61C7162: 24-44 1316..291	24-44	984-1006	NAP		g2492816		74	3.00E-24			uracil permease ; (X98696) uracil permease [Schizosaccharomyces pombe]
19523	ENU003317	ANI61C4572: 38-71 1170..2195	38-71	1002-1021	NAP		g1174417	970	129	5.00E-42	71	65	spermidine synthase (putrescine aminopropyltransferase) (SPDSY) ; (Z54140) putrescine aminopropyltransferase
19524	ENU003318	ANI61C6048: 49-71 28..1055	49-71	1013-1034	NAP		g1723920	355	134	1.00E-31	40	77	[Schizosaccharomyces pombe] hypothetical 37.4 KD protein in SEC27-SSM1B intergenic region ; hypothetical protein YGL136c - yeast (Saccharomyces cerevisiae) ; (X92670) G2830 [Saccharomyces cerevisiae] ; (Z72658) ORF YGL136c
19525	ENU003319	ANI61C1082 6:2111..1083	27-46	993-1012	NAP		g1351122	1143	324	e-122	74	98	[Saccharomyces cerevisiae] thiazole biosynthetic enzyme (stress-inducible protein STI35) ; stress-inducible protein sti35 - fungus (Fusarium oxysporum) ; (M33643) STI35 protein [Fusarium oxysporum]
19526	ENU003320	ANI61C1026 5:1499..471	55-79	1012-1041	NAP		g3183345	259	127	1.00E-28	36	61	hypothetical 33.9 KD protein C14C4.12C in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe]
19527	ENU003321	ANI61C7819: 25-44 5645..4616	25-44	993-1012	NAP		g1083757	781	156	4.00E-55	44	25	plasma membrane Ca2+-ATPase isoform 4 - rat ; (U15408) plasma membrane Ca2+-ATPase isoform 4 [Rattus norvegicus]
19528	ENU003322	ANI61C1019 3:1386..356	22-47	991-1010	NAP		g2624697	1322	155	e-101	73	75	Pectin Lyase A

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19529	ENU03323	ANI61C7349: 62-80 274..1306		1032-1052	NAP		g1657510	628	175	8.00E-62	39	70	(U73857) betaine-aldehyde dehydrogenase [Escherichia coli]
19530	ENU03324	ANI61C1834: 54-73 4387..3355		1024-1044	NAP		g2500755	486	173	2.00E-47	57	31	response regulator MCS4 (mitotic catastrophe suppressor 4); (Y11927) Mcs4 protein [Schizosaccharomyces pombe]; (AF004694) Mcs4 [Schizosaccharomyces pombe]; [Schizosaccharomyces pombe]; (AL033388) response regulator mcs4 [Schizosaccharomyces pombe]; [Schizosaccharomyces pombe] (AL021837) hypothetical protein [Schizosaccharomyces pombe] (D90916) hypothetical protein [Synectocystis sp.] (AL031854) hypothetical zinc-finger protein [Schizosaccharomyces pombe] C-8 sterol isomerase (delta-8--delta-7 sterol isomerase); C-8 sterol isomerase - rice blast fungus; C-8 sterol isomerase - rice blast fungus; isomerase - rice blast fungus; (Z22775) C-8 sterol isomerase [Magnaporthe grisea] gluconolactonase precursor (D-glucono-delta-lactone lactonohydrolase); gluconolactonase (EC 3.1.1.17) precursor - Zymomonas mobilis; (X67189) gluconolactonase [Zymomonas mobilis] (X95074) Translin [Gallus gallus]
19531	ENU03325	ANI61C9207: 53-75 94..1126		1021-1043	NAP		g2894293	822	284	9.00E-76	43	65	
19532	ENU03326	ANI61C3172: 38-58 3489..2456		1004-1029	NAP		g1653791	159	104	1.00E-23	32	97	
19533	ENU03327	ANI61C1086 70-93 5:3495..2461		1033-1061	NAP		g3738189	314	131	6.00E-30	27	69	
19534	ENU03328	ANI61C8189: 71-101 1153..117		1043-1062	NAP		g462023	715	129	4.00E-29	65	62	
19535	ENU03329	ANI61C9130: 51-71 1173..139		1022-1043	NAP		g399766	100	78	7.00E-14	29	59	
19536	ENU03330	ANI61C9354: 24-49 1135..101		987-1016	NAP		g1770301	196	71	7.00E-14	36	94	
19537	ENU03331	ANI61C139:1 40-62 282..248		1011-1032	NAP		g731893	1070	128	9.00E-56	47	54	putative transporter YIL166C; probable membrane protein YIL166c - yeast (Saccharomyces cerevisiae); (Z46921) unknown [Saccharomyces cerevisiae]
19538	ENU03332	ANI61C1034 72-91 0:1354..319		1030-1065	NAP		g2370487	1901	444	e-124	65	48	(Z98849) glutamyl-tRNA synthetase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19539	ENU03333	ANI61C4602: 902..1937	49-75	1023-1042	NAP		g1723769	269	55	3.00E-11			putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
19540	ENU03334	ANI61C7359: 28-47 1489..454	28-47	1002-1021	NAP		g3925755	533	246	2.00E-64	39	65	(AL034352) putative phosphodiesterase-nucleotide pyrophosphatase precursor [Schizosaccharomyces pombe]
19541	ENU03335	ANI61C1897: 24-51 2896..1859	24-51	999-1018	NAP		g3434937	503	158	5.00E-38	61	94	(AB000281) krev-1 [Neurospora crassa]
19542	ENU03336	ANI61C8156: 69-89 2505..3542	69-89	1043-1064	NAP		g3551511	910	320	9.00E-87	47	83	(AB016807) flavohemoglobin [Fusarium oxysporum]
19543	ENU03337	ANI61C6276: 31-56 133..1170	31-56	1007-1026	NAP		g129781	355	175	4.00E-43	32	87	Pepsinogen II-2/3 precursor (pepsinogen A) ; (M59235) pepsinogen [Oryctolagus cuniculus]
19544	ENU03338	ANI61C7530: 22-48 4427..3389	22-48	993-1018	NAP		g4008577	348	111	8.00E-24	32	98	(AL034491) conserved hypothetical protein [Schizosaccharomyces pombe]
19545	ENU03339	ANI61C5932: 59-78 6356..5318	59-78	1033-1055	NAP		g4512354	224	83	5.00E-20			(AB011836) alkyl hydroperoxide reductase large subunit [Bacillus halodurans]
19546	ENU03340	ANI61C8268: 32-67 4374..5413	32-67	1010-1029	NAP		g2879890	782	185	4.00E-77	52	98	(AJ223327) rAsp f 9 [Aspergillus fumigatus]
19547	ENU03341	ANI61C1048 5:5667..6705	27-47	1005-1024	NAP		g3915140	678	89	2.00E-46	36	63	Isotrichodermin C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides]
19548	ENU03342	ANI61C8858: 22-41 1041..1	22-41	996-1020	NAP		g2293194	303	152	3.00E-36	28	89	(AF008220) yteR [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19549	ENU03343	ANI61C2233: 24-46 3..1043		1003-1022	NAP		g585542	541	223	1.00E-57			putative NADH-cytochrome B5 reductase (P35) ; cytochrome-b5 reductase (EC 1.6.2.2) - yeast (Saccharomyces cerevisiae) ; (Z28365) cytochrome b5 reductase [Saccharomyces cerevisiae] ; (Z46861) cytochrome b5 reductase [Saccharomyces cerevisiae] ; cytochrome b reductase [Saccharomyces cerevisiae] hypothetical protein YDR489w - yeast (Saccharomyces cerevisiae) ; (U33050) Ydr489wp; CAI: 0.16 [Saccharomyces cerevisiae]
19550	ENU03344	ANI61C3401: 22-52 493..1534		998-1021	NAP		g2131525	108	39	0.01	25	94	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe] (AL022071) hypothetical protein [Schizosaccharomyces pombe] Heat shock protein HSP1 (65 KD IGE-binding protein) ; (U92465) heat shock protein [Aspergillus fumigatus] glucosamine-6-phosphate isomerase (glucosamine-6-phosphate deaminase) ; glucosamine-6-phosphate deaminase protein (nagB) homolog - Haemophilus influenzae (strain Rd KW20) ; (U32700) glucosamine-6-phosphate isomerase (nagB) [Haemophilus influenzae Rd] protein transport protein SEC13 ; SEC13 protein - yeast (Saccharomyces cerevisiae) ; (L05929) Sec13p [Saccharomyces cerevisiae] ; (U14913) Sec13p [Saccharomyces cerevisiae] (AL034583) related to yeast zds family proteins [Schizosaccharomyces pombe] (L39639) kievitone hydratase [Fusarium solani]
19551	ENU03345	ANI61C9825: 47-66 5460..4418		1028-1047	NAP		g3850084	230	63	5.00E-17	29	90	
19552	ENU03346	ANI61C1042 51-77 7:30..1072		1032-1051	NAP		g2950464	1087	312	e-102	67	58	
19553	ENU03347	ANI61C5619: 65-84 2226..1184		1046-1065	NAP		g2851483	1706	493	e-138	93	78	
19554	ENU03348	ANI61C41:20 44-64 88..1046		1025-1044	NAP		g1171641	795	316	1.00E-85	59	96	
19555	ENU03349	ANI61C7807: 64-84 1969..3013		1044-1065	NAP		g417748	807	150	4.00E-77	62	90	
19556	ENU03350	ANI61C4411: 37-56 1439..396		1014-1038	NAP		g4056558	130	74	2.00E-12	35	18	
19557	ENU03351	ANI61C3627: 53-73 6985..5942		1032-1054	NAP		g755011	496	217	1.00E-55	36	92	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19558	ENU03352	ANI61C5159: 2737..1690	22-47	1008-1027	NAP		g1171024	542	169	9.00E-49	46	87	"mitochondrial RNA splicing protein MRS3 ; splicing protein MRS3, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X56445) MRS3 protein [Saccharomyces cerevisiae] ; (X87371) mitochondrial splicing unit [Saccharomyces cerevisiae] ; (Z49408) ORF YJL133w [Saccharomyces cerevisiae]"
19559	ENU03353	ANI61C1040 9:3163..2116	23-45	1009-1028	NAP		g3024013	949	203	6.00E-57	66	94	eukaryotic translation initiation factor 2 alpha subunit (EIF-2-alpha) ; (AL021046) translational initiation factor 2 alpha [Schizosaccharomyces pombe]
19560	ENU03354	ANI61C2163: 53-72 580..1631	53-72	1027-1060	NAP		g1523784	140	83	1.00E-25	32	38	(Z79750) acid phosphatase [Emmericella nidulans]
19561	ENU03355	ANI61C766:1 22-49 329..279	22-49	1008-1030	NAP		g2414631	65	61	0.000000	28	48	(Z99260) hypothetical protein [Schizosaccharomyces pombe]
19562	ENU03356	ANI61C8382: 64-83 3380..2329	64-83	1052-1072	NAP		g3135990	765	167	2.00E-50	41	64	(AL023589) membrane transporter [Schizosaccharomyces pombe]
19563	ENU03357	ANI61C9268: 22-55 688..1739	22-55	1011-1031	NAP		g1351310	1415	514	e-145	83	96	Thioredoxin reductase ; 72k broad-range disulfide reductase (NADPH) (EC 1.-.-) - Penicillium chrysogenum ; (X76119) thioredoxin reductase [Penicillium chrysogenum]
19564	ENU03358	ANI61C6529: 22-47 5556..6607	22-47	1012-1031	NAP		g127112	758	204	6.00E-57	56	97	MAK16 protein ; MAK16 protein - yeast (Saccharomyces cerevisiae) ; (J03852) MAK16 protein [Saccharomyces cerevisiae] ; (U12980) Mak16p: putative nuclear protein [Saccharomyces cerevisiae]
19565	ENU03359	ANI61C3092: 23-42 1866..2919	23-42	1014-1034	NAP		g125271	1258	389	e-107	72	94	"Casein kinase II, alpha chain (CK II) (CK2-alpha) ; casein kinase II (EC 2.7.1.-) alpha chain - maize ; Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays ; (X61387) casein kinase II alpha subunit [Zea mays]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
19566	ENU03360	ANI61C8693: 59-91 76..1129		1048-1070	NAP		g1170603	1038	375	e-103	53	32	probable serine/threonine-protein C2F7.03C; hypothetical protein SPAC2F7.03c - fission yeast (Schizosaccharomyces pombe); (Z50142) protein kinase [Schizosaccharomyces pombe] (L35487) mannanase [Aspergillus aculeatus] (AF054824) delta 5 microsomal desaturase [Mortierella alpina] GCY protein; GCY1 protein - yeast (Saccharomyces cerevisiae); (X13228) GCY protein (AA 1-312) [Saccharomyces cerevisiae]; (X90518) ORF O31567 [Saccharomyces cerevisiae]; (X94335) YOR3269w [Saccharomyces cerevisiae]; (X96740) GCY protein [Saccharomyces cerevisiae]; (Z75028) ORF YOR120w [Saccharomyces cerevisiae] NADPH dehydrogenase 1 (old yellow enzyme 1); NADPH dehydrogenase (EC 1.6.99.1) chain OYE1 - yeast (Saccharomyces cerevisiae); Old Yellow Enzyme (Oxidized) (Oye) (E.C.1.6.99.1) Complexed With P-Hydroxybenzaldehyde; Old Yellow Enzyme (Reduced) (Oye) (E.C.1.6.99.1); Old Yellow Enzyme (Oxidized) (Oye) (E.C.1.6.99.1); (X53597) NADPH dehydrogenase [Saccharomyces pastorianus] (Z11701) putative protein kinase [Saccharomyces cerevisiae] (Y14766) alk8 [Candida albicans]
19567	ENU03361	ANI61C51:26 47-68 ..1080		1040-1059	NAP		g558311	1144	254	e-118	65	82	
19568	ENU03362	ANI61C980:5 22-57 747..4693		1001-1034	NAP		g3342268	95	57	0.000000 2	38	14	
19569	ENU03363	ANI61C5185: 22-47 1040..2099		1020-1039	NAP		g121087	556	217	5.00E-57			
19570	ENU03364	ANI61C1024 65-84 9:1587..527		1052-1083	NAP		g417431	604	254	1.00E-66			
19571	ENU03365	ANI61C8885: 32-51 3652..2592		1024-1050	NAP		g3836	697	186	2.00E-76	47	29	
19572	ENU03366	ANI61C8063: 22-50 1..1062		1013-1041	NAP		g3395458	212	56	1.00E-22	39	35	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19573	ENU03367	ANI61C5331: 1285..223	36-56	1027-1056	NAP		g117178	2183	640	0	85	68	Benzoate 4-monoxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) ; benzoate 4-monoxygenase (EC 1.14.13.12) cytochrome P450 53 - Aspergillus niger ; (X52521) benzoate 4-monoxygenase [Aspergillus niger] hypothetical 48.7 KD protein C6G10.03C in chromosome I ; (Z98603) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein (MEL3-10 3' region) - yeast (Saccharomyces cerevisiae) ; (Z37509) ORF near MEL [Saccharomyces cerevisiae] (Z97992) zootin like protein [Schizosaccharomyces pombe] Salicylate hydroxylase (salicylate 1-monoxygenase) ; salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida (strain PpG7) ; (M60055) salicylate hydroxylase [Pseudomonas putida] (AL023534) putative methionine aminopeptidase 1 [Schizosaccharomyces pombe] Salicylate hydroxylase (salicylate 1-monoxygenase) ; salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida (strain PpG7) ; (M60055) salicylate hydroxylase [Pseudomonas putida]
19574	ENU03368	ANI61C9104: 1830..2897	49-68	1049-1070	NAP		g3183387	608	109	3.00E-37	40	71	
19575	ENU03369	ANI61C2888: 4069..5135	24-42	1029-1048	NAP		g1077195	884	136	3.00E-31	34	56	
19576	ENU03370	ANI61C2922: 22-53	22-53	1020-1047	NAP		g2276350	899	290	1.00E-77	56	99	
19577	ENU03371	ANI61C6515: 38-57	38-57	1032-1064	NAP		g1346660		77	4.00E-22			
19578	ENU03372	ANI61C9024: 29-61	29-61	1034-1055	NAP		g3130036	1225	299	e-115	61	87	
19579	ENU03373	ANI61C6515: 274..1342	44-63	1038-1070	NAP		g1346660		77	4.00E-22			
19580	ENU03374	ANI61C860:2 594..1524	27-46	1036-1055	NAP		g1078613	1726	301	e-171	88	74	stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces capsulata ; (X85963) delta-9 fatty acid desaturase [Ajellomyces capsulatus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19581	ENU03375	ANI61C6203: 25-45 3521..2451		1031-1053	NAP		g4503653	590	211	8.00E-54	40	52	"fatty-acid-Coenzyme A ligase, very long-chain 1 ; very-long-chain acyl-CoA synthetase (very-long-chain-fatty-acid-CoA ligase) ; (D88308) very-long-chain acyl-CoA synthetase [Homo sapiens] ; (AF096290) very long-chain acyl-CoA synthetase [Homo sapiens]"
19582	ENU03376	ANI61C5100: 70-90 1151..81		1077-1098	NAP		g3859693		75	7.00E-13			(AL033497) transport protein [Candida albicans]
19583	ENU03377	ANI61C3804: 50-69 3421..4492		1052-1079	NAP		g731684	590	192	2.00E-52	42	98	hypothetical 35.1 KD protein in NAM8-GAR1 intergenic region ; hypothetical protein YHR088w - yeast (Saccharomyces cerevisiae) ; (U00060) Yhr088wp [Saccharomyces cerevisiae] (U62917) glucose transporter TGT2 [Taenia solium]
19584	ENU03378	ANI61C9031: 63-82 342..579		1072-1093	NAP		g1480799		37	0.000000			(AB011211) pectin methyltransferase [Aspergillus oryzae]
19585	ENU03379	ANI61C3234: 52-71 725..1797		1063-1082	NAP		g4514622	469	107	4.00E-44	41	89	hypothetical 37.0 KD protein in SPOIIR-GLYC intergenic region ; SUA5 homolog ipc-29d - Bacillus subtilis ; (Z38002) Similar to Saccharomyces cerevisiae SUA5 protein [Bacillus subtilis] ; (Z99122) alternate gene name: ipc-29d; similar to hypothetical proteins [Bacillus subtilis] ; ipc-29d gene [Bacillus subtilis]
19586	ENU03380	ANI61C8984: 59-81 3629..2556		1054-1089	NAP		g732384	519	107	8.00E-41			"proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 ; (AB009398) 26S proteasome subunit p40.5 [Homo sapiens]"
19587	ENU03381	ANI61C1139 65-84 7:730..1805		1079-1098	NAP		g4506223	545	205	5.00E-52	36	84	(AJ001732) rAsp f 4 [Aspergillus fumigatus]
19588	ENU03382	ANI61C7637: 50-72 1107..2184		1060-1084	NAP		g3005839	410	110	1.00E-23	45	31	probable calcium-transporting ATPase 9 ; probable membrane protein
19589	ENU03383	ANI61C7016: 63-83 6581..5505		1068-1097	NAP		g2493012	538	99	5.00E-34	41	17	YOR291w - yeast (Saccharomyces cerevisiae) ; (Z75199) ORF YOR291w [Saccharomyces cerevisiae]
19590	ENU03384	ANI61C567:3 26-48 434..4511		1029-1061	NAP		g1870209		46	0.0004			(AC000133) ORF [Emeritella nidulans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19591	ENU03385	ANI61C8963: 1834..2913	26-45	1044-1063	NAP		g2132210	665	268	4.00E-71	41	98	hypothetical protein YPL152w - yeast (Saccharomyces cerevisiae); (Z73508) ORF YPL152w [Saccharomyces cerevisiae]; (X96770) P2591 protein [Saccharomyces cerevisiae] "(S83194) Ca2+/calmodulin-dependent protein kinase IV kinase isoform, CaM-kinase kinase alpha [rats, brain, Peptide, 505 aa] [Rattus sp.]; (AB023658) Ca/calmodulin-dependent protein kinase alpha, CaM-kinase kinase alpha [Rattus norvegicus]
19592	ENU03386	ANI61C4714: 40-61 2661..3740	40-61	1053-1077	NAP		g1836161	530	212	1.00E-56	38	64	(L48074) secreted dipeptidyl peptidase [Aspergillus fumigatus] (AE001098) conserved hypothetical protein [Archaeoglobus fulgidus] hypothetical protein YDR214w - yeast (Saccharomyces cerevisiae); (Z68195) unknown [Saccharomyces cerevisiae]; (Z68194) unknown [Saccharomyces cerevisiae] hypothetical 27.0 KD protein C12B10.13 in chromosome I; (Z70721) conserved hypothetical protein. [Schizosaccharomyces pombe] (AL049522) putative dolichol kinase [Schizosaccharomyces pombe] 2-nitropropane dioxygenase precursor (nitroalkane oxidase) (2-NPD); (U22530) 2-nitropropane dioxygenase precursor [Neurospora crassa] hypothetical 48.0 KD protein C4G8.06C in chromosome I; hypothetical protein SPAC4G8.06c - fisston yeast (Schizosaccharomyces pombe); (Z56276) hypothetical protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (AL023589) membrane transporter [Schizosaccharomyces pombe]
19593	ENU03387	ANI61C129:3 29-48 071..4150	29-48	1036-1066	NAP		g2340046	2589	326	e-105	79	42	
19594	ENU03388	ANI61C5996: 22-42 6212..7291	22-42	1031-1059	NAP		g2650534	128	74	2.00E-12	29	54	
19595	ENU03389	ANI61C7595: 23-51 1374..295	23-51	1039-1060	NAP		g2131398	463	120	2.00E-45	37	92	
19596	ENU03390	ANI61C1118 47-66 7:2732..3811	47-66	1063-1084	NAP		g1723555		83	2.00E-15			
19597	ENU03391	ANI61C8085: 52-71 3337..2254	52-71	1074-1093	NAP		g4539603	263	91	1.00E-17	36	37	
19598	ENU03392	ANI61C1118: 22-53 10357..9272	22-53	1043-1065	NAP		g2498094	348	162	4.00E-39	34	93	
19599	ENU03393	ANI61C4327: 27-47 1150..2235	27-47	1047-1071	NAP		g1351597	376	203	2.00E-51	40	72	
19600	ENU03394	ANI61C238:1 22-49 0..1096	22-49	1047-1066	NAP		g3135988	201	89	1.00E-19	35	36	

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19601	ENU03395	ANI61C7744: 7338..6252	33-54	1058-1077	NAP		g130684	910	314	7.00E-85	66	93	Outer mitochondrial membrane protein porin ; porin - Neurospora crassa ; (X05824) major protein (AA 1-283) [Neurospora crassa]
19602	ENU03396	ANI61C3311: 24-55	24-55	1050-1069	NAP		g4581517		83	3.00E-33			(AL049559) putative d-amino acid oxidase [Schizosaccharomyces pombe]
19603	ENU03397	ANI61C2398: 58-77	58-77	1084-1104	NAP		g113712	600	147	6.00E-40	35	61	Amidase ; amidase (EC 3.5.1.4) - Brevibacterium sp. (strain R312) ; amidase - Rhodococcus sp. (strain N-774) ; (X54074) amidase [Rhodococcus sp.] ; (M60264) enantiomer-selective amidase [Brevibacterium sp.] ; (AB016078) amidase [Rhodococcus sp. N-771]
19604	ENU03398	ANI61C7272: 24-43	24-43	1046-1071	NAP		g3183379	405	144	9.00E-34	36	83	"putative 38.2 KD phosphatase 2C in chromosome 1 ; (Z98762) SPAC4A8.03c, putative protein phosphatase, len:339aa, similar eg. to P2C1_SCHPO, P40371, protein phosphatase 2c homolog 1, (347aa), fasta scores, opt:276, E(0):3.2e-11, (29.4% identity in 282 aa overlap), also simi..."
19605	ENU03399	ANI61C1068 50-70	50-70	1079-1098	NAP		g4507713	505	203	4.00E-51	36	69	tetratricopeptide repeat domain 2 ; (U46571) tetratricopeptide repeat protein [Homo sapiens]
19606	ENU03400	ANI61C6636: 23-42	23-42	1051-1071	NAP		g2213547	476	183	1.00E-48	52	59	(Z97052) putative ubiquinone biosynthesis methyltransferase [Schizosaccharomyces pombe]
19607	ENU03401	ANI61C8531: 38-58	38-58	1068-1090	NAP		g2879890	627	264	7.00E-70	46	89	(AJ223327) rAsp f 9 [Aspergillus fumigatus]
19608	ENU03402	ANI61C6472: 69-88	69-88	1090-1122	NAP		g3914593	236	132	4.00E-30	39	91	putative ribokinase ; (AL023554) ribokinase [Schizosaccharomyces pombe]
19609	ENU03403	ANI61C2203: 48-67	48-67	1083-1102	NAP		g1352904	296	69	1.00E-24	34	84	hypothetical 37.5 KD protein in YUH1-URA8 intergenic region ; hypothetical protein YJR100c - yeast (Saccharomyces cerevisiae) ; (Z49600) ORF YJR100c [Saccharomyces cerevisiae]

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19610	ENU03404	ANI61C9708: 3952..5050	58-77	1095-1114	NAP		g1168269	1196	222	e-118	72	95	"Arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A); (L23430) endo-1,5-alpha-L-arabinase [Aspergillus niger]; endo-1,5-alpha-L-arabinase [Aspergillus niger]"
19611	ENU03405	ANI61C9805: 42-61 1380..282	42-61	1079-1098	NAP		g4512702	567	70	3.00E-11	35	24	(AC006569) hypothetical protein [Arabidopsis thaliana]
19612	ENU03406	ANI61C1031 63-82 6:2340..3438	63-82	1096-1119	NAP		g731746	302	130	2.00E-29	36	80	hypothetical 42.4 KD protein in ENO2-STB5 intergenic region; hypothetical protein YHR176w - yeast (Saccharomyces cerevisiae); (U00027)
19613	ENU03407	ANI61C1067: 69-88 1112..2210	69-88	1104-1125	NAP		g3024986	129	59	1.00E-10			Yhr176vp [Saccharomyces cerevisiae] hypothetical zinc-type alcohol dehydrogenase-like protein in AHFP-RNK intergenic region; (U82598) FadH homolog [Escherichia coli]; (AE000166) putative oxidoreductase [Escherichia coli]; (D90701) Glutathione-dependent formaldehyde dehydrogenase (EC 1.2.1.1) (FDH) (FALDH). [Escherichia coli]; (D90702) Glutathione-dependent formaldehyde dehydrogenase (EC 1.2.1.1) (FDH) (FALDH). [Escherichia coli]
19614	ENU03408	ANI50C1743 37-64 6_1:16..1114	37-64	1060-1093	NAP		g2132293		157	1.00E-37	32	90	hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae); (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325) [Saccharomyces cerevisiae]
19615	ENU03409	ANI61C7138: 45-65 1323..2422	45-65	1082-1102	NAP		g135142	1945	270	9.00E-72	44	36	"Leucyl-tRNA synthetase, mitochondrial precursor (leucine--tRNA ligase) (LEURS); leucine--tRNA ligase (EC 6.1.1.4) precursor, mitochondrial - Neurospora crassa; (M30472) leucyl-tRNA synthetase [Neurospora crassa]"

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19616	ENU03410	ANI61C7147: 56-83 7618..6518		1093-1114	NAP		g128847	1614	603	e-173	90	69	NADH-ubiquinone oxidoreductase 49 KD subunit precursor (complex I-49KD) (CI-49KD) ; NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 49K chain - Neurospora crassa ; (X54508) NADH dehydrogenase 49 kD subunit [Neurospora crassa] (X53840) mitochondrial ribosomal protein YmL20 [Saccharomyces cerevisiae]
19617	ENU03411	ANI61C9007: 22-51 2391..3492		1061-1080	NAP		g3976	198	71	1.00E-11	31	59	"putative dihydroxy-acid dehydratase precursor (DAD) (2,3-Dihydroxy acid hydrolyase) ; (Z69795) unknown [Schizosaccharomyces pombe] "
19618	ENU03412	ANI61C6616: 43-61 2489..1387		1081-1102	NAP		g1708464	1270	222	e-108	67	56	"ATP synthase alpha chain, mitochondrial precursor ; H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - Neurospora crassa ; (M84191) mitochondrial ATPase alpha-subunit [Neurospora crassa] "
19619	ENU03413	ANI61C953:2 55-74 815..1713		1093-1115	NAP		g584806	1920	661	0	88	66	(AJ001909) transcriptional activator [Aspergillus niger]
19620	ENU03414	ANI61C1699: 27-47 2563..1461		1065-1087	NAP		g2808634	3172	522	e-147	80	39	"Exopolysaccharuronase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) ; (X99795) exopolysaccharuronase [Aspergillus tubingensis] "
19621	ENU03415	ANI61C8652: 34-54 93..1201		1080-1099	NAP		g2499716	226	77	2.00E-13	29	67	"hypothetical 52.3 KD protein in FRE2 5'region ; hypothetical protein YKL221w - yeast (Saccharomyces cerevisiae) ; (X75950) ORF4, B473 [Saccharomyces cerevisiae] ; (Z28221) ORF YKL221w [Saccharomyces cerevisiae] ; ORF 4 [Saccharomyces cerevisiae] "
19622	ENU03416	ANI61C1106 33-52 6:144..1255		1082-1101	NAP		g549759	630	185	5.00E-58	31	78	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
19623	ENU03417	ANI61C5477: 22-48 81..1191		1068-1090	NAP		g1834342	750	190	3.00E-78	48	21	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19624	ENU03418	ANI61C7673: 64-89	64-89	1108-1133	NAP		g4495126	1033	269	3.00E-71	37	35	(AL035583) putative helicase [Schizosaccharomyces pombe]
19625	ENU03419	ANI61C8010: 22-51	22-51	1056-1091	NAP		g1173405	733	169	2.00E-71			"protein phosphatase PP1 regulatory subunit SDS22 ; protein suppressor sds22 - fission yeast (Schizosaccharomyces pombe) ; (Z98762) SPAC4A8.12c, sds22; protein phosphatases pp1 regulat ory subunit, len:332aa, identical to SD22_SCHPO, P22194, (3 32aa), similar eg. to yeast Q15435, SDS22 homolog, (360aa), fasta scores, opt:837, E0:0, (47.6% identi... (Z99531) ubiquitin system protein [Schizosaccharomyces pombe]
19626	ENU03420	ANI61C8479: 62-82	62-82	1111-1132	NAP		g2440180	1508	542	e-153	69	11	(D90917) hypothetical protein [Synecocystis sp.]
19627	ENU03421	ANI61C9176: 22-51	22-51	1072-1092	NAP		g1653915	415	203	2.00E-51	32	96	"uracil-DNA glycosylase precursor (UDG) ; uracil-DNA glycosylase (EC 3.2.2.-) - yeast (Saccharomyces cerevisiae) ; (J04470) uracil-DNA-glycosylase [Saccharomyces cerevisiae] ; (Z46659) UNG1 gene, len: 359, CAI: 0.12, uracil-DNA-glycosylase [Saccharomyces cerevisiae]"
19628	ENU03422	ANI61C1899: 47-66	47-66	1098-1117	NAP		g137043	489	149	4.00E-53	44	84	(AL033503) peptide transport protein [Candida albicans]
19629	ENU03423	ANI61C8616: 22-47	22-47	1066-1093	NAP		g3859684	404	140	1.00E-42	32	53	(AL023592) acetamidase [Schizosaccharomyces pombe]
19630	ENU03424	ANI61C4044: 23-42	23-42	1073-1095	NAP		g3136052	320	147	2.00E-36	33	61	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) ; (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
19631	ENU03425	ANI61C1103 68-88	68-88	1122-1140	NAP		g2132651	664	80	2.00E-33	30	61	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
19632	ENU03426	ANI61C6686: 34-56	34-56	1085-1106	NAP		g1351714	288	90	3.00E-17	25	68	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19633	ENU03427	ANI61C1032 0:1321..2437	22-50	1076-1096	NAP		g126918	310	92	9.00E-32	36	95	Mono- and diacylglycerol lipase precursor (MDGL) ; mono- and diacylglycerol lipase (EC 3.1.1.-) precursor - Penicillium camembertii ; (D90315) MDGL precursor [Penicillium camemberti]
19634	ENU03428	ANI61C2335: 57-75 3069..1952	57-75	1111-1132	NAP		g1346703	1482	468	e-142	78	96	Polygalacturonase precursor (pectinase) (PGL) ; polygalacturonase (EC 3.2.1.15) precursor - Aspergillus parasiticus ; (U17167) polygalacturonase precursor [Aspergillus parasiticus] ; (L23523) polygalacturonase [Aspergillus parasiticus]
19635	ENU03429	ANI61C6897: 66-97 2289..1172	66-97	1108-1141	NAP		g3646379	657	161	2.00E-59	41	60	(AJ001540) phenylacetyl-CoA ligase [Penicillium chrysogenum]
19636	ENU03430	ANI61C2091: 39-58 2554..1436	39-58	1087-1114	NAP		g4454019		62	2.00E-12			(AL035396) SRG1-like protein [Arabidopsis thaliana]
19637	ENU03431	ANI61C6093: 28-51 4053..2935	28-51	1077-1104	NAP		g4107289	467	192	2.00E-50	35	66	(AL035076) putative carboxylesterase-lipase family member [Schizosaccharomyces pombe]
19638	ENU03432	ANI61C9179: 35-54 2067..949	35-54	1091-1112	NAP		g1077295	175	102	4.00E-21	31	92	probable membrane protein YOL107w - yeast (Saccharomyces cerevisiae) ; (Z48149) similarity with P. tetraurelia cytochrome C oxidase [Saccharomyces cerevisiae] ; (Z74849) ORF YOL107w [Saccharomyces cerevisiae]
19639	ENU03433	ANI61C7538: 22-46 2343..1223	22-46	1081-1100	NAP		g730272	625	238	3.00E-77	43	92	Peroxisomal targeting signal 2 receptor (PTS2 receptor) (peroxisome import protein PAS7) (peroxin-7) ; PAS7 protein - yeast (Saccharomyces cerevisiae) ; (X81424) Pas7p [Saccharomyces cerevisiae] ; (X83704) Peb1 [Saccharomyces cerevisiae]
19640	ENU03434	ANI61C6107: 62-82 3168..4289	62-82	1122-1141	NAP		g2956780	608	108	1.00E-57	46	90	(AL022103) deoxycytidylate deaminase [Schizosaccharomyces pombe]
19641	ENU03435	ANI61C9017: 71-91 1203..81	71-91	1133-1151	NAP		g1754596	398	97	2.00E-19	31	54	(D45893) acr-2 [Neurospora crassa]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19642	ENU03436	ANI61C9774: 3928..5051	65-85	1127-1146	NAP		g549443	8521	690	0	99	18	Conidial green pigment synthase ; probable polyketide synthase - Emericella nidulans ; (X65866) putative polyketide or fatty acid synthase [Emericella nidulans] ; wA gene [Emericella nidulans] (AJ005253) ClpP protease [Mus musculus] ; (AJ012249) ClpP protease [Mus musculus] "NMT1 protein homolog ; nmt1 protein - Aspergillus parasiticus ; (U15196) the expression of this gene has been shown to be completely inhibited by thiamine as was observed for the Schizosaccharomyces pombe nmt1, Swiss-Prot Accession Number P36597 [Aspergillus parasiticus] ; nmt1 gene [Aspergillus parasiticus] " cytochrome C PERoxidase precursor (CCP) ; cytochrome-c peroxidase (EC 1.11.1.5) precursor - yeast (Saccharomyces cerevisiae) ; (X62422) Cytochrome c peroxidase [Saccharomyces cerevisiae] ; (Z28291) ORF YKR066c [Saccharomyces cerevisiae]
19643	ENU03437	ANI61C1695: 22-52 1352..1600	22-52	1069-1103	NAP		g3559935	425	141	5.00E-47	55	54	chromosome 22 open reading frame 1 ; (U84894) 239AB [Homo sapiens] (U59214) MAP protein kinase MPKA [Emericella nidulans] (U26463) NADPH-dependent aldehyde reductase [Sporidiobolus salmonicolor] (U41278) contains similarity to G beta repeats (PROSITE:PS00670) of the beta-transducin family [Caenorhabditis elegans]
19644	ENU03438	ANI61C6466: 22-57 615..1739	22-57	1085-1104	NAP		g1171741	1602	512	e-144	92	99	probable membrane protein YOR380w - yeast (Saccharomyces cerevisiae) ; (Z75288) ORF YOR380w [Saccharomyces cerevisiae]
19645	ENU03439	ANI61C1045 1:4390..3264	70-89	1124-1154	NAP		g543969	593	135	5.00E-61	42	95	
19646	ENU03440	ANI61C7019: 64-83 5621..4493	64-83	1128-1149	NAP		g4502497	280	71	1.00E-11	38	89	
19647	ENU03441	ANI61C3212: 38-58 2345..1218	38-58	1104-1123	NAP		g4580577	2092	412	0	97	81	
19648	ENU03442	ANI61C1118 46-65 2:2717..3848	46-65	1114-1135	NAP		g1142698	719	120	3.00E-50	57	94	
19649	ENU03443	ANI61C8239: 22-52 1151..20	22-52	1090-1111	NAP		g1086900	178	59	9.00E-12	31	39	
19650	ENU03444	ANI61C1097 60-79 9:7353..6221	60-79	1131-1150	NAP		g2132958	353	153	1.00E-36	30	65	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19651	ENU03445	ANI61C8387: 2051..918	72-92	1139-1163	NAP		g3560241	373	85	4.00E-21	40	26	(AL031532) putative amino acid permease [Schizosaccharomyces pombe]
19652	ENU03446	ANI61C5168: 4266..3132	25-52	1088-1116	NAP		g1171946	615	183	1.00E-71	41	93	NADPH dehydrogenase 3 (old yellow enzyme 3) ; NADPH dehydrogenase (EC 1.6.99.1) OYE3 - yeast (Saccharomyces cerevisiae) ; (L29279) NADPH dehydrogenase [Saccharomyces cerevisiae] ; (Z73527) ORF YPL171c [Saccharomyces cerevisiae]
19653	ENU03447	ANI61C1113 3:7531..6395	46-65	1110-1139	NAP		g1730251	724	192	4.00E-84	56	91	GTP cyclohydrolase II ; GTP-cyclohydrolase - Pichia guilliermondii ; GTP-cyclohydrolase - Pichia guilliermondii ; (Z49093) GTP-cyclohydrolase [Pichia guilliermondii] Triosephosphate isomerase (TIM) ; triose-phosphate isomerase (EC 5.3.1.1) - Emericella nidulans ; (D10019) triosephosphate isomerase [Emericella nidulans]
19654	ENU03448	ANI61C2332: 1195..2329	27-50	1094-1120	NAP		g136053	1099	187	e-111	98	99	hypothetical 30.0 KD protein C13F4.14 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (AL031322) conserved hypothetical protein [Schizosaccharomyces pombe]
19655	ENU03449	ANI61C6376: 58-77 592..1727	58-77	1131-1151	NAP		g1723274	275	96	4.00E-19	36	94	hypothetical 51.6 KD protein in SSB2-SPX18 intergenic region ; hypothetical protein YNL206c - yeast (Saccharomyces cerevisiae) ; (X78898) possibly expressed during the late G1 /S phase; homology with the SSRP proteins [Saccharomyces cerevisiae] ; (Z71482) ORF YNL206c [Saccharomyces cerevisiae]
19656	ENU03450	ANI61C2623: 2420..3555	71-89	1145-1164	NAP		g732190		81	6.00E-16			[AF031376] LIM-domain binding factor 2; LDB2 [Danio rerio] Hexokinase ; (L04480) hexokinase [Schistosoma mansoni]
19657	ENU03451	ANI61C9329: 1338..203	69-88	1142-1162	NAP		g3078001		36	0.66			
19658	ENU03452	ANI61C3576: 634..1771	55-75	1120-1150	NAP		g2833327		76	4.00E-13			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19659	ENU03453	ANI61C4140: 43-63 135..1273		1116-1139	NAP		g1705465	1079	414	e-119	58	88	Biotin synthase (biotin synthetase) ; biotin synthetase - yeast (Saccharomyces cerevisiae) ; (Z73071) ORF YGR286c [Saccharomyces cerevisiae]
19660	ENU03454	ANI61C9438: 31-50 91..1229		1100-1127	NAP		g3929362	362	174	9.00E-43	32	70	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVI]
19661	ENU03455	ANI61C6611: 30-57 1466..2605		1105-1127	NAP		g2492777	604	220	1.00E-56	47	88	hypothetical zinc-type alcohol dehydrogenase-like protein in PRE5-FET4 intergenic region ; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae) ; (Z54141) unknown [Saccharomyces cerevisiae]
19662	ENU03456	ANI61C7326: 23-45 515..1656		1093-1122	NAP		g585668	807	192	5.00E-48	49	90	Polygalacturonase precursor (PG) (pectinase) ; (L02239) endopolygalacturonase [Gibberella fujikuroi]
19663	ENU03457	ANI61C5335: 22-41 2897..4040		1103-1125	NAP		g2501210	1300	420	e-135	69	99	putative disulfide isomerase TIGA precursor ; (X98748) tigA [Aspergillus niger]
19664	ENU03458	ANI61C2777: 52-71 1206..2352		1137-1156	NAP		g1408294	565	220	1.00E-56	39	94	(U61983) benzyl alcohol dehydrogenase [Acinetobacter calcoaceticus]
19665	ENU03459	ANI61C4098: 72-91 690..1836		1154-1176	NAP		g1199853	292	140	2.00E-32	36	90	(X95720) O6357 [Saccharomyces cerevisiae]
19666	ENU03460	ANI61C3743: 67-86 4765..5912		1152-1171	NAP		g3914390	685	150	2.00E-35	45	91	Pectin lyase precursor ; (L22857) pectin lyase [Colletotrichum gloeosporioides]
19667	ENU03461	ANI61C1756: 50-79 3030..1882		1134-1156	NAP		g113792	1500	466	e-130	63	59	"glucoamylase precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosylhydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor -- Aspergillus sp ; (D10460) glucoamylase [Aspergillus shirousami]"
19668	ENU03462	ANI61C9390: 67-94 2443..1293		1149-1175	NAP		g3915606	251	86	1.00E-24	30	52	Amine oxidase [flavin-containing] (monoamine oxidase) (MAO)

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19669	ENU03463	ANI61C348:2 ..1154	23-58	1109-1133	NAP		g3493591	647	279	3.00E-74	44	56	(AF063231) cytoplasmic dynein intermediate chain 2 [Mus musculus]
19670	ENU03464	ANI61C323:2 848..1695	25-44	1118-1136	NAP		g140479	785	148	9.00E-35	36	37	"probable transporter FEN2 ; probable membrane protein YCR028c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR028c, len:512 [Saccharomyces cerevisiae] "
19671	ENU03465	ANI61C1037 2:81..1234	29-50	1121-1140	NAP		g66290	554	217	9.00E-56	34	59	laccase (EC 1.10.3.2) I - Emericella nidulans
19672	ENU03466	ANI61C843:3 768..2614	23-46	1111-1134	NAP		g3913072	143	86	5.00E-16	39	24	probable 2-dehydropanoate 2-reductase (ketopantoate reductase) (KPA reductase) ; (AE000986)
19673	ENU03467	ANI61C843:3 768..2614	41-64	1129-1152	NAP		g3913072	143	86	5.00E-16	39	24	thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus]
19674	ENU03468	ANI61C9542:45..1198	28-53	1120-1139	NAP		g3183308	392	143	2.00E-33	37	38	probable 2-dehydropanoate 2-reductase (ketopantoate reductase) (KPA reductase) ; (AE000986)
19675	ENU03469	ANI61C6702:1884..728	36-60	1129-1150	NAP		g2132851	146	53	9.00E-12	29	44	thiamine biosynthesis protein (apbA) [Archaeoglobus fulgidus]
19676	ENU03470	ANI61C9502:1289..133	55-74	1150-1169	NAP		g3323397	1563	518	e-163	83	92	hypothetical 49.6 KD protein C5D6.04 in chromosome I ; (Z98056) hypothetical protein [Schizosaccharomyces pombe]
19677	ENU03471	ANI61C546:14..1171	35-55	1129-1150	NAP		g2499517	578	181	3.00E-66	41	56	probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae] (U89991) mannose-1-phosphate guanylyltransferase [Hypocrea jecorina]
													hypothetical 71.1 KD protein in DSK2-CAT8 intergenic region ; hypothetical protein YMR278w - yeast (Saccharomyces cerevisiae) ; (Z49704) unknown [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19678	ENU03472	ANI61C11:71 3..1872	67-87	1163-1183	NAP		g1730840	935	190	1.00E-47	36	45	putative cysteinyl-TRNA synthetase C29E6.06C (cysteine--TRNA ligase) (CYRS) ; probable membrane protein YNL247w - yeast (Saccharomyces cerevisiae) ; (X96722) ORF N0885 [Saccharomyces cerevisiae] ; (Z71523) ORF YNL247w [Saccharomyces cerevisiae]
19679	ENU03473	ANI61C8853: 29-48 1981..821	29-48	1114-1147	NAP		g1730193	703	291	5.00E-78			UDP-glucose 4-epimerase (galactowaldenase) (UDP-Galactose 4-epimerase) ; (X99339) UDP-glucose 4-epimerase [Bacillus subtilis] ; (D83026) highly homologous to UDP-glucose 4-epimerases (SwissProt:GALE_HAEIN and GALE_ECOLI); hypothetical [Bacillus subtilis] ; (Z99123) UDP-glucose 4-epimerase [Bacillus subtilis] (M11621) putative [Saccharomyces cerevisiae]
19680	ENU03474	ANI61C676:4 44-65 319..3155	44-65	1145-1164	NAP		g806323	295	93	2.00E-27	39	58	"(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]"
19681	ENU03475	ANI61C9629: 22-43 4604..3440	22-43	1124-1143	NAP		g4006818	832	135	9.00E-80	55	96	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
19682	ENU03476	ANI61C1097 49-68 5:5843..4679	49-68	1152-1171	NAP		g2132942		112	4.00E-24			[AF007270] contains similarity to syntaxin [Arabidopsis thaliana] (AL033497) unknown hypothetical protein [Candida albicans]
19683	ENU03477	ANI50C1823 27-46 6:2180..3345	27-46	1128-1150	NAP		g2191179		72	6.00E-12	31	72	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19684	ENU03478	ANI61C5073: 39-58 1205..40	39-58	1143-1162	NAP		g3859696	361	123	4.00E-38	34	78	
19685	ENU03479	ANI61C4357: 53-73 1174..6	53-73	1159-1179	NAP		g2507070	383	105	4.00E-38	36	65	

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19686	ENU03480	ANI61C11:71 3..1882	67-87	1173- 1193	NAP		g1730840	935	196	2.00E-49	36	45	putative cysteinyl-TRNA synthetase C29E6.06C (cysteine--TRNA ligase) (CYSRS); probable membrane protein YNL247w - yeast (Saccharomyces cerevisiae); (X96722) ORF N0885 [Saccharomyces cerevisiae]; (Z71523) ORF YNL247w [Saccharomyces cerevisiae]
19687	ENU03481	ANI61C7427: 32-54 2413..1245		1139- 1158	NAP		g4038613	681	184	8.00E-46	50	91	(Z98602) conserved uncharacterized protein domain-containing protein [Schizosaccharomyces pombe]
19688	ENU03482	ANI61C4324: 71-94 1338..168		1180- 1199	NAP		g3821271	1076	351	4.00E-96	64	66	(AJ009956) alpha-galactosidase 1 [Penicillium simplicissimum]
19689	ENU03483	ANI61C9384: 37-63 2716..1542		1148- 1169	NAP		g2981103	375	140	1.00E-32	33	64	(AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe]; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe]
19690	ENU03484	ANI61C1005 59-78 2..1724..2899		1173- 1192	NAP		g131768	568	159	4.00E-38	32	69	quininate permease (quininate transporter); quininate transport protein - Emericella nidulans; (X13525) quininate permease [Emericella nidulans]
19691	ENU03485	ANI61C1024: 26-45 1957..3134		1143- 1161	NAP		g2388912	499	80	1.00E-36	49	99	(Z98974) putative small nuclear ribonucleoprotein [Schizosaccharomyces pombe]
19692	ENU03486	ANI61C6064: 52-71 1924..747		1159- 1187	NAP		g3581921	198	53	0.000004	45	58	(AL031546) ubiquinol-cytochrome c reductase complex subunit [Schizosaccharomyces pombe]
19693	ENU03487	ANI61C7603: 67-87 1265..88		1173- 1202	NAP		g3859693		68	1.00E-10			(AL033497) transport protein [Candida albicans]
19694	ENU03488	ANI61C7603: 67-87 1265..88		1173- 1202	NAP		g3859693		68	1.00E-10			(AL033497) transport protein [Candida albicans]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19695	ENU03489	ANI61C7187: 65-84 7398..6219	1167-1201		NAP		g112940	532	134	1.00E-40			Acyl-coenzyme A:6-aminopenicillanic-acid-acyltransferase precursor (isopenicillin N acyltransferase) ; acyltransferase AAT - Emericella nidulans ; isopenicillin N acyltransferase (EC 2.3.1.-) - Emericella nidulans ; (X53310) Acyl-CoA [Emericella nidulans] ; (M58293) acyl-coenzyme A:Isopenicillin N acyltransferase [Emericella nidulans] (AL031603) putative glycosyl transferase [Schizosaccharomyces pombe]
19696	ENU03490	ANI61C9634: 52-71 5874..7054	1165-1189		NAP		g3646449	753	206	3.00E-62	48	69	hypothetical 61.8 KD protein C12B10.03 in chromosome I ; (Z70721) WD repeat protein [Schizosaccharomyces pombe]
19697	ENU03491	ANI61C352:5 22-48 571..6752	1142-1161		NAP		g1723547	701	170	8.00E-80	46	59	membrane protein YDR331w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr331wp [Saccharomyces cerevisiae] (Z80108) lipI [Mycobacterium tuberculosis]
19698	ENU03492	ANI61C8306: 60-79 1238..2422	1180-1202		NAP		g1351809	956	397	e-109	53	94	hypothetical 61.8 KD protein C12B10.03 in chromosome I ; (Z70721) WD repeat protein [Schizosaccharomyces pombe]
19699	ENU03493	ANI61C1105 37-56 9:1448..263	1161-1180		NAP		g1542908		96	6.00E-19			GPI-anchor transamidase ; probable membrane protein YDR331w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr331wp [Saccharomyces cerevisiae] (Z80108) lipI [Mycobacterium tuberculosis]
19700	ENU03494	ANI61C1056 59-89 6:2316..1131	1180-1202		NAP		g3560245	168	79	5.00E-14	26	51	hypothetical 61.8 KD protein C12B10.03 in chromosome I ; (Z70721) WD repeat protein [Schizosaccharomyces pombe]
19701	ENU03495	ANI61C2603: 22-48 2277..1092	1138-1165		NAP		g4490992	188	76	3.00E-13	30	79	hydroxylase [Streptomyces coelicolor] (Z99116) yqkA [Bacillus subtilis] (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis]
19702	ENU03496	ANI61C6589: 55-74 1064..777	1174-1199		NAP		g731468	299	114	1.00E-24	38	56	hypothetical 47.0 KD protein in PET117-CEM1 intergenic region ; hypothetical protein YER059w - yeast (Saccharomyces cerevisiae) ; (U18813) Yer059wp [Saccharomyces cerevisiae]
19703	ENU03497	ANI61C9095: 22-50 1401..215	1147-1166		NAP		g1731087	67	56	0.000000	21	59	hypothetical 39.0 KD protein in GLNQ-ANSR intergenic region ; (D84432) YqkA [Bacillus subtilis] ; (Z99116) yqkA [Bacillus subtilis] (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis]
19704	ENU03498	ANI61C1082: 63-82 204..1391	1181-1208		NAP		g1929089	393	133	3.00E-30	30	65	hypothetical 39.0 KD protein in GLNQ-ANSR intergenic region ; (D84432) YqkA [Bacillus subtilis] ; (Z99116) yqkA [Bacillus subtilis] (Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis]
19705	ENU03499	ANI61C4013: 34-55 519..1708	1161-1181		NAP		g2804298	792	241	6.00E-63	36	70	[AB010439] steroid monooxygenase [Rhodococcus rhodochrous]

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19706	ENU03500	ANI61C410:1 386..195	55-74	1179-1204	NAP		g2131476	626	210	7.00E-69	44	89	hypothetical protein YDR415c - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr415cp; CAI: 0.14 [Saccharomyces cerevisiae]
19707	ENU03501	ANI61C8114: 64-83 330..1523	64-83	1181-1215	NAP		g1706694	609	178	1.00E-46	35	49	"Lanosterol synthase (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene--lanosterol cyclase) (OSC) ; lanosterol synthase (EC 5.4.99.7) - fission yeast (Schizosaccharomyces pombe) ; (U41368) lanosterol synthase [Schizosaccharomyces pombe] "
19708	ENU03502	ANI61C9917: 22-41 2839..1646	22-41	1153-1173	NAP		g3581896	443	138	8.00E-32	24	70	(AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
19709	ENU03503	ANI61C6104: 28-47 2458..1265	28-47	1158-1179	NAP		g4106687	432	86	6.00E-20	34	97	(AL035065) putative nadh-dependent flavin oxidoreductase [Schizosaccharomyces pombe]
19710	ENU03504	ANI61C6105: 57-75 599..1793	57-75	1190-1209	NAP		g3560215	956	252	2.00E-80	49	81	"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe] "
19711	ENU03505	ANI61C650:3 22-49 29..1525	22-49	1155-1176	NAP		g1711370	326	107	5.00E-34	32	96	nuclear pore protein SEH1 ; SEC13 protein homolog YGL100w - yeast (Saccharomyces cerevisiae) ; (X90994) Sec13p-like protein [Saccharomyces cerevisiae] ; (Z72622) ORF YGL100w [Saccharomyces cerevisiae]
19712	ENU03506	ANI61C1054 24-43 0:6432..6182	24-43	1148-1179	NAP		g2648302	290	108	1.00E-32	42	97	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus] "
19713	ENU03507	ANI61C8859: 22-41 1375..177	22-41	1153-1178	NAP		g4587097	104	65	0.000000	32	67	(AB019045) OMPdecarboxylase [Rhizomucor pusillus]
19714	ENU03508	ANI61C9217: 22-41 1731..2931	22-41	1150-1180	NAP		g1169696		36	0.7			Flagellin 1 ; flagellin fliC-1 - Proteus mirabilis ; (L07270) flagellin [Proteus mirabilis]
19715	ENU03509	ANI61C6534: 23-47 1344..1248	23-47	1166-1183	NAP		g549699	427	41	0.021	27	89	hypothetical 50.5 KD protein in MDH1-VMA5 intergenic region ; hypothetical protein YKL082c - yeast (Saccharomyces cerevisiae) ; (Z28082) ORF YKL082c [Saccharomyces cerevisiae]

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19716	ENU03510	ANI61C6741: 614..1817	48-67	1186-1209	NAP		g1174552	564	99	1.00E-54	43	95	tryptophan YL-TRNA synthetase (tryptophan--TRNA ligase) (TRPRS) ; tryptophan--tRNA ligase (EC 6.1.1.2) - Haemophilus influenzae (strain Rd KW20) ; (U32746) tryptophanyl-tRNA synthetase (trpS) [Haemophilus influenzae Rd] (AJ005824) Ufd1 protein [Schizosaccharomyces pombe] ; (AJ005825) Ufd1 protein [Schizosaccharomyces pombe] type II proteinS geranylgeranyltransferase beta subunit (type II protein geranyl-geranyltransferase beta subunit) (GGTASE-II-beta) (PGGT) (YPT1/SEC4 proteins geranylgeranyltransferase beta subunit) ; probable protein prenyltransferase (EC 2.5.1.-) BET2 - yeast (Saccharomyces cerevisiae) ; (U25842) Protein Geranyl-geranyltransferase beta subunit (Swiss Prot. accession number P20133; P32433) [Saccharomyces cerevisiae] (D43950) KIAA0098 is a human counterpart of mouse chaperonin containing TCP-1 gene. [Homo sapiens] hypothetical 49.3 KD protein C30D11.06C in chromosome I ; hypothetical protein SPAC30D11.06c - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein YLR114c - yeast (Saccharomyces cerevisiae) ; (U53878) Ylr114cp [Saccharomyces cerevisiae] ; (X89514) putative orf [Saccharomyces cerevisiae] ; (Z73286) ORF YLR114c [Saccharomyces cerevisiae]
19717	ENU03511	ANI61C1046 0:2203..999	22-49	1152-1184	NAP		g3123677	610	254	1.00E-66	46	99	
19718	ENU03512	ANI61C8443: 24-55 4113..2909	24-55	1154-1186	NAP		g1352074	792	282	3.00E-77			
19719	ENU03513	ANI61C3364: 56-76 94..1299	56-76	1185-1219	NAP		g603955	1280	349	e-122	71	64	
19720	ENU03514	ANI61C5704: 24-50 3..1208	24-50	1159-1187	NAP		g1351659	766	311	5.00E-84	46	88	
19721	ENU03515	ANI61C7052: 67-87 180..1388	67-87	1213-1233	NAP		g2131781	369	102	8.00E-44	35	42	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19722	ENU03516	ANI61C9393: 62-81	2303..3511	1208-1228	NAP		g3261633	452	200	2.00E-50	35	95	(Z79700) fadE13 [Mycobacterium tuberculosis]
19723	ENU03517	ANI61C8651: 23-44	2941..1731	1172-1191	NAP		g2499591	1035	296	2.00E-79	69	68	mitogen-activated protein kinase HOG1 (MAP kinase HOG1) ; (X90586) unnamed protein product [Candida albicans]
19724	ENU03518	ANI61C9381: 45-67	579..1789	1194-1213	NAP		g135025	905	297	7.00E-84	69	83	"succinyl-CoA ligase (GDP-FORMING), alpha-chain precursor (succinyl-CoA synthetase, alpha chain) (SCS-alpha) ; succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) alpha chain precursor - rat ; (J03621) succinyl-CoA synthetase alpha subunit (EC 6.2.1.4) [Rattus norvegicus]" (AF054512) endoglucanase V [Aspergillus aculeatus]
19725	ENU03519	ANI61C6226: 44-63	14274..13064	1193-1212	NAP		g2997731	992	229	3.00E-59	64	92	putative DNA repair protein C12B10.12C ; (Z70721) putative dna repair protein [Schizosaccharomyces pombe]
19726	ENU03520	ANI61C1227: 69-95	4360..3149	1216-1238	NAP		g1723554	619	237	1.00E-61	39	60	protein [Schizosaccharomyces pombe]
19727	ENU03521	ANI50C7567 22-54	2_1:1300..88	1172-1192	NAP		g3560212		68	5.00E-25	29	20	(AL031536) hypothetical zinc finger protein [Schizosaccharomyces pombe]
19728	ENU03522	ANI61C263:1 22-40	418..2631	1159-1193	NAP		g3875242	181	66	3.00E-22	30	90	(Z75532) similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene [Caenorhabditis elegans]
19729	ENU03523	ANI61C1056 71-90	8:3268..2054	1223-1243	NAP		g747710	231	117	1.00E-25	30	20	(X16609) alt. ankyrin (variant 2.2) [Homo sapiens]
19730	ENU03524	ANI61C1086: 41-60	3065..4279	1194-1213	NAP		g1175958	571	233	1.00E-60	36	55	hypothetical 70.5 KD protein in AGP3-DAK3 intergenic region ; probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae) ; (D50617) YFL054C [Saccharomyces cerevisiae] ; (D44603) unknown [Saccharomyces cerevisiae]
19731	ENU03525	ANI61C5132: 22-51	376..1591	1170-1195	NAP		g2160161		43	0.003			(AC000132) F21M12.7 gene product [Arabidopsis thaliana]
19732	ENU03526	ANI61C1064 63-88	4:6301..5085	1209-1237	NAP		g4049527	391	71	1.00E-30	45	97	(AL034565) putative transcription initiation factor tfiif small subunit [Schizosaccharomyces pombe]

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19733	ENU03527	ANI61C6659: 1179..2398	61-80	1213-1238	NAP		g2633018	395	205	7.00E-52	32	63	(Z99107) similar to hypothetical proteins from <i>B. subtilis</i> [<i>Bacillus subtilis</i>]
19734	ENU03528	ANI61C9013: 22-41		1180-1199	NAP		g465483	869	261	7.00E-69	48	61	protein kinase WIS1 ; protein kinase wis1 (EC 2.7.1.-) - fission yeast (<i>Schizosaccharomyces pombe</i>) ; (X62631) protein kinase [Schizosaccharomyces pombe]
19735	ENU03529	ANI61C6231: 23-46		1182-1201	NAP		g3810833	405	132	6.00E-30	33	36	(AL032684) putative pre-tRNA nuclear export receptor [Schizosaccharomyces pombe]
19736	ENU03530	ANI61C7020: 65-84		1226-1245	NAP		g2498763	496	142	5.00E-46	41	89	peroxisomal membrane protein PEX13 (peroxin-13) ; (U70067) integral peroxisomal membrane protein PpPex13p [<i>Pichia pastoris</i>]
19737	ENU03531	ANI61C1021 45-64		1201-1225	NAP		g1351714	223	73	2.00E-16	35	59	putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
19738	ENU03532	ANI61C1046 22-52		1177-1202	NAP		g586479	934	294	e-105			phosphatidate cytidyltransferase (CDP-diglyceride synthetase) (CDP-diglyceride pyrophosphorylase) (CDP-diacylglycerol synthase) (CDS) (CTP-phosphatidate cytidyltransferase) (CDP-DAG synthase) ; probable membrane protein YBR029c - yeast (<i>Saccharomyces cerevisiae</i>) ; (X76078) YBR0313 [Saccharomyces cerevisiae] ; (Z35898) ORF YBR029c [Saccharomyces cerevisiae] ; ORF YBR0313 [Saccharomyces cerevisiae]
19739	ENU03533	ANI61C9016: 27-49		1189-1208	NAP		g3150248	797	304	3.00E-91	53	65	(AL023634) GTPase activating protein [Schizosaccharomyces pombe]
19740	ENU03534	ANI61C6369: 63-82		1226-1245	NAP		g2649648	601	208	3.00E-62	37	95	(AE001038) acyl-CoA dehydrogenase (acd-6) [<i>Archaeoglobus fulgidus</i>]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19741	ENU03535	ANI61C2490: 35-54 67..1292		1199-1218	NAP		g2507436	922	333	1.00E-90	49	46	glutamyl ¹ -TRNA synthetase (glutamine--TRNA ligase) (GLNRS) ; glutamine--TRNA ligase (EC 6.1.1.18) - yeast (Saccharomyces cerevisiae) ; (U55021) Gln4p [Saccharomyces cerevisiae] ; (Z75076) ORF YOR168w [Saccharomyces cerevisiae]
19742	ENU03536	ANI61C5804: 22-47 1290..65		1183-1205	NAP		g125886	618	169	2.00E-53	41	86	lactate 2-monooxygenase (lactate oxidase) ; lactate 2-monooxygenase (EC 1.13.12.4) - Mycobacterium smegmatis ; (J05402) L-lactate 2-monooxygenase [Mycobacterium smegmatis]
19743	ENU03537	ANI61C1809: 22-47 1295..2523		1174-1207	NAP		g2498337	722	242	2.00E-64	42	78	squalene monooxygenase (squalene epoxidase) (SE) ; (D88252) squalene epoxidase [Candida albicans] ; (U69674) squalene epoxidase [Candida albicans]
19744	ENU03538	ANI61C7512: 64-84 1907..678		1228-1251	NAP		g2408022	357	125	8.00E-28	47	35	(Z99162) ER protein-translocation complex subunit [Schizosaccharomyces pombe]
19745	ENU03539	ANI61C7486: 57-75 4470..3238		1225-1246	NAP		g117803	1224	452	e-126	62	67	cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase) (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala]
19746	ENU03540	ANI61C676:1 32-51 800..3031		1203-1221	NAP		g544261		46	0.0006			RNA-binding protein EWS ; RNA-binding protein EWS - human ; (X66899) RNA binding protein [Homo sapiens] ; (X72990) EWS [Homo sapiens] ; (Y07848) RNA binding protein [Homo sapiens] ; EWS gene [Homo sapiens]
19747	ENU03541	ANI61C5627: 55-74 5260..4027		1227-1246	NAP		g3914984	208	113	3.00E-24	25	10	ferrichrome siderophore peptide synthetase ; (U62738) ferrichrome siderophore peptide synthetase [Ustilago maydis]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19748	ENU03542	ANI61C164;1 024..2255	36-55	1195-1227	NAP		g1750122	1071	163	3.00E-64	42	75	"(U66480) xylan beta-1,4-xylosidase [Bacillus subtilis]; (Z99113) xylan beta-1,4-xylosidase [Bacillus subtilis]"
19749	ENU03543	ANI61C9610; 72-96 1578..347	72-96	1244-1264	NAP		g118298	463	200	2.00E-50			S-adenosylmethionine decarboxylase PROenzyme (ADOMETDC); adenosylmethionine decarboxylase (EC 4.1.1.50) precursor - yeast (Saccharomyces cerevisiae); (M38434) S-adenosylmethionine decarboxylase [Saccharomyces cerevisiae]; (X91067) adenosylmethionine decarboxylase [Saccharomyces cerevisiae]; (Z74794) ORF YOL052c [Saccharomyces cerevisiae]
19750	ENU03544	ANI61C5499; 57-77 269..1504	57-77	1215-1250	NAP		g2132395	346	150	3.00E-48	36	71	polyadenylated RNA-binding protein PUB1 - yeast (Saccharomyces cerevisiae); (Z71292) ORF YNL016w [Saccharomyces cerevisiae]
19751	ENU03545	ANI61C3215; 72-91 1248..12	72-91	1247-1266	NAP		g730251	626	208	5.00E-64	49	89	protein phosphatase 2C homolog 1 (PP2C-1); phosphoprotein phosphatase (EC 3.1.3.16) 2C - fission yeast (Schizosaccharomyces pombe); (L26970) protein phosphatase 2C [Schizosaccharomyces pombe]
19752	ENU03546	ANI61C9596; 22-56 2267..3504	22-56	1196-1216	NAP		g1078613	1662	534	e-151	69	80	stearoyl-CoA desaturase (EC 1.14.99.5) - Ajellomyces capsulata; (X85963) delta-9 fatty acid desaturase [Ajellomyces capsulatus]
19753	ENU03547	ANI61C6355; 38-57 17..1253	38-57	1207-1232	NAP		g730615	978	393	e-108	47	28	DNA-directed RNA polymerase mitochondrial precursor; (L25087) mitochondrial RNA polymerase [Neurospora crassa]; cyt-5 gene [Neurospora crassa]
19754	ENU03548	ANI61C1028 33-55 1:47..1284	33-55	1207-1228	NAP		g1723906	542	206	3.00E-52	39	48	hypothetical 80.0 KD protein in SNF4-TAF60 intergenic region; probable membrane protein YGL114w - yeast (Saccharomyces cerevisiae); (Z72636) ORF YGL114w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19755	ENU03549	ANI61C1118: 4267..3029	69-88	1246-1264	NAP		g2132958	354	110	2.00E-23	26	73	probable membrane protein YOR380w - yeast (Saccharomyces cerevisiae) ; (Z75288) ORF YOR380w [Saccharomyces cerevisiae] (AF009672) unknown [Acinetobacter sp. ADP1]
19756	ENU03550	ANI61C5525: 26-45	26-45	1201-1221	NAP		g2271503	247	83	1.00E-20	30	91	ATP10 protein ; (J05463) ATP10 protein [Saccharomyces cerevisiae] (U78597) kinesin light chain [Plectonema boryanum]
19757	ENU03551	ANI61C8624: 47-68	47-68	1223-1242	NAP		g114699	158	85	9.00E-16	29	67	hypothetical 102.3 KD protein in DAL82-RFA2 intergenic region ; hypothetical protein YNL313c - yeast (Saccharomyces cerevisiae) ; (Z46259) NO364 [Saccharomyces cerevisiae] ; (Z71589) ORF YNL313c [Saccharomyces cerevisiae]
19758	ENU03552	ANI61C1080 72-92	72-92	1242-1269	NAP		g2645229	358	95	1.00E-18	34	29	probable ATP-dependent RNA helicase DBP8 ; helicase homolog - yeast (Saccharomyces cerevisiae) ; (U00027) Yhr169wp [Saccharomyces cerevisiae]
19759	ENU03553	ANI61C431:3 22-44	22-44	1200-1220	NAP		g1176586	579	157	1.00E-37	36	36	(AL023780) DNA binding protein [Schizosaccharomyces pombe]
19760	ENU03554	ANI61C1007 44-63	44-63	1223-1242	NAP		g731740	990	363	1.00E-99	50	91	alcohol dehydrogenase II ; alcohol dehydrogenase (EC 1.1.1.1) II - Emericella nidulans ; (Z48000) alcohol dehydrogenase II [Emericella nidulans] ; alcohol dehydrogenase II [Emericella nidulans]
19761	ENU03555	ANI61C1111: 66-88	66-88	1232-1265	NAP		g3184115	634	250	1.00E-65	35	80	(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]
19762	ENU03556	ANI61C3965: 66-86	66-86	1242-1265	NAP		g1703172	1802	433	e-163	98	93	zinc finger protein 207 ; (AF046001) zinc finger transcription factor [Homo sapiens]
19763	ENU03557	ANI61C290:9 26-47	26-47	1207-1226	NAP		g3646450	1005	148	9.00E-35	41	53	
19764	ENU03558	ANI61C7312: 66-85	66-85	1250-1269	NAP		g4508017	242	58	4.00E-18	27	76	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19765	ENU03559	ANI61C1036 6:1735..490	25-55	1209-1228	NAP		g549077	974	375	e-103	51	98	"3-ketoacyl-CoA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase) ; acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica) ; (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica] " (Z79750) acid phosphatase [Emericella nidulans]
19766	ENU03560	ANI61C170:3 233..1986	55-74	1232-1260	NAP		g1523784	2260	840	0	97	67	Uroporphyrinogen decarboxylase (UPD) ; uroporphyrinogen decarboxylase (EC 4.1.1.37) - yeast (Saccharomyces cerevisiae) ; (X63721) uroporphyrinogen decarboxylase [Saccharomyces cerevisiae] ; (Z19089) uroporphyrinogen decarboxylase [Saccharomyces cerevisiae] ; (Z49209) Hem12p [Saccharomyces cerevisiae] (AL035076) putative glutamate-1-semialdehyde aminotransferase [Schizosaccharomyces pombe] (Y16748) malate dehydrogenase [Pirromyces sp. E2] (AL034393) predicted using Genefinder; cDNA EST yk343c12.5 comes from this gene; cDNA EST yk402e12.5 comes from this gene; cDNA EST yk457e8.5 comes from this gene; cDNA EST yk470f2.5 comes from this gene; cDNA EST yk281e3.5 comes...
19768	ENU03562	ANI61C8571:1770..523	71-94	1257-1276	NAP		g4107288	922	216	5.00E-84	52	88	
19769	ENU03563	ANI61C3737:2726..3975	51-70	1236-1257	NAP		g4029338	627	112	5.00E-41	49	95	
19770	ENU03564	ANI61C8574:85..1333	24-48	1204-1230	NAP		g3979938	105	36	0.73	34	31	
19771	ENU03565	ANI61C1023 5:1602..354	33-56	1220-1239	NAP		g3367626	867	163	7.00E-87	59	94	(AJ007712) replication factor C subunit [Arxula adenivorans] (AL031788) uv excision repair protein rad23 homolog [Schizosaccharomyces pombe]
19772	ENU03566	ANI61C6252:5320..4069	31-52	1219-1239	NAP		g3687502	605	65	3.00E-20	48	90	probable serine/threonine-protein kinase C1D4.11C ; (Z69239) unknown [Schizosaccharomyces pombe]
19773	ENU03567	ANI61C1155:4035..2784	22-48	1211-1231	NAP		g1708616	896	175	3.00E-82	57	48	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19774	ENU03568	ANI61C4414: 2075..3328	22-40	1207-1233	NAP		g1077358	523	196	6.00E-55	37	66	probable membrane protein YLR361c - yeast (Saccharomyces cerevisiae) ; (U19103) Ylr361cp [Saccharomyces cerevisiae]
19775	ENU03569	ANI61C7023: 59-78	59-78	1254-1273	NAP		g1351643	674	161	2.00E-70	41	93	hypothetical 43.0 KD protein C8A4.09C in chromosome I ; hypothetical protein SPAC8A4.09c - fission yeast (Schizosaccharomyces pombe) ; (Z66569) unknown [Schizosaccharomyces pombe] ; [Schizosaccharomyces pombe] ; (AL032824) hypothetical protein [Schizosaccharomyces pombe] (AL033385) conserved hypothetical protein [Schizosaccharomyces pombe] (X58121) SMP3 protein [Saccharomyces cerevisiae] (AL031743) putative protein transport protein [Schizosaccharomyces pombe] "(AL033388) hypothetical integral membrane protein, putative involvement in lipid metabolism [Schizosaccharomyces pombe] "
19776	ENU03570	ANI61C8693: 37-56	37-56	1232-1252	NAP		g3850069	254	85	1.00E-15	32	95	hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN49 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Yal060wp [Saccharomyces cerevisiae]
19777	ENU03571	2175..3432	60-83	1257-1276	NAP		g4498	445	163	3.00E-45	35	69	(AF104312) glycolate oxidase; short-chain alpha-hydroxy acid oxidase [Mus musculus]
19778	ENU03572	ANI61C3740: 55-75	55-75	1242-1272	NAP		g3650391	831	201	1.00E-50	50	78	(AE001684) Oxononanoate Synthase [Chlamydia pneumoniae]
19779	ENU03573	88..1346	36-59	1235-1254	NAP		g3850111	561	94	2.00E-45	41	98	probable serine/threonine-protein kinase C24B11.11C ; hypothetical protein SPAC24B11.11c - fission yeast (Schizosaccharomyces pombe) ; (Z67757) unknown [Schizosaccharomyces pombe]
19780	ENU03574	ANI61C2194: 46-65	46-65	1246-1266	NAP		g731293	286	138	1.00E-31	33	90	[Schizosaccharomyces pombe]
19781	ENU03575	ANI61C5263: 32-51	32-51	1231-1252	NAP		g4585221	330	101	3.00E-24	39	88	hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region ; FUN49 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Yal060wp [Saccharomyces cerevisiae]
19782	ENU03576	ANI61C1054	42-61	1243-1262	NAP		g4377376	462	165	1.00E-52	39	94	(AF104312) glycolate oxidase; short-chain alpha-hydroxy acid oxidase [Mus musculus]
19783	ENU03577	6:3353..2091	59-78	1256-1280	NAP		g1346360	542	231	6.00E-60	47	31	(AE001684) Oxononanoate Synthase [Chlamydia pneumoniae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19784	ENU03578	ANI61C4008: 1935..3199	58-77	1259-1280	NAP		g2276351	329	93	4.00E-18	55	42	putative transcriptional regulator [Schizosaccharomyces pombe]
19785	ENU03579	ANI61C1160: 6131..7397	32-51	1225-1255	NAP		g585007	63	57	0.000000	2		cell division protein kinase 2 homolog CRK1 ; protein kinase (EC 2.7.1.37) cdc2-related CRK1 - Leishmania mexicana ; (X60385) cdc2-like protein [Leishmania mexicana]
19786	ENU03580	ANI61C4268: 227..1494	22-42	1228-1247	NAP		g400766	447	201	1.00E-50	36	62	phenol 2-monoxygenase (phenol hydroxylase) ; phenol 2-monoxygenase (EC 1.14.13.7) - Pseudomonas sp. plasmid EST1412 (AL031534) protein kinase kin1 [Schizosaccharomyces pombe]
19787	ENU03581	ANI61C8771: 3..1223	22-48	1213-1247	NAP		g3560139	157	50	0.00003	27	39	maackiain detoxification protein 1 - fungus (Nectria haematococca) ; (U35892) predicted flavin-containing mono-oxygenase [Nectria haematococca]
19788	ENU03582	ANI61C4868: 634..1905	71-90	1279-1299	NAP		g2133295	1263	182	4.00E-96	54	77	Meiotic recombination protein DLH1 (DMC1 homolog) ; DMC1/LIM15 homolog 1 - yeast (Candida albicans) ; (U39808) Dlh1p [Candida albicans]
19789	ENU03583	ANI61C1074: 2..366..1636	22-46	1230-1250	NAP		g1706446	876	208	5.00E-90	63	99	hypothetical 40.0 KD protein C4G8.14C in chromosome I ; hypothetical protein SPAC4G8.14c - fission yeast (Schizosaccharomyces pombe)
19790	ENU03584	ANI61C1113: 1..2093..824	22-46	1225-1250	NAP		g1351604	337	123	2.00E-35	35	96	(U52963) mitogen-activated protein kinase [Nectria haematococca var. brevicornis]
19791	ENU03585	ANI61C9449: 3534..4806	29-48	1235-1259	NAP		g1279911	1596	555	e-167	91	99	hypothetical protein YPR023c - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
19792	ENU03586	ANI61C6804: 7842..6567	50-77	1262-1281	NAP		g1084946	276	96	4.00E-25	29	83	(D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]
19793	ENU03587	ANI61C1101: 1341..68	26-51	1235-1257	NAP		g434759	1403	232	e-147	64	41	(AL023777) hypothetical protein [Schizosaccharomyces pombe]
19794	ENU03588	ANI61C1171: 4..1281	25-52	1240-1259	NAP		g3184099	637	193	5.00E-51	36	69	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19795	ENU03589	ANI61C7713: 6808..5530	22-43	1234-1258	NAP		g3183342	519	135	5.00E-31	38	96	hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe] (U58946) transposase [Aspergillus awamori] (Z98979) hypothetical protein [Schizosaccharomyces pombe] (AF032386) aldose-1-epimerase-like protein [Nicotiana tabacum] (AJ001330) orfT [Lactobacillus sakei] (AJ001330) precursor - alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkoae) NADH-ubiquinone oxidoreductase 51 KD subunit precursor (complex I-51KD) (Cl-51KD) ; (X64402) NADH dehydrogenase [Aspergillus niger] (AL034353) probable metabolite transport protein [Schizosaccharomyces pombe] (AL021428) hypothetical protein Rv0068 [Mycobacterium tuberculosis] (Y14749) MDM10 [Podospira anserina] (AF016448) Similar to glycolate oxidase; coded for by C. elegans cDNA yk151h10.5; coded for by C. elegans cDNA yk151h10.3 [Caenorhabditis elegans] "3-ketoacyl-CoA thiolase peroxisomal A precursor (beta-ketothiolase A) (acetyl-CoA acyltransferase A) (peroxisomal 3-oxoacyl-CoA thiolase A) ; acetyl-CoA C-acyltransferase (EC 2.3.1.16) A precursor, peroxisomal - rat ; (D90058) 3-ketoacyl-CoA thiolase A [Rattus norvegicus] " (AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]
19796	ENU03590	ANI61C8371: 22-46		1235-1259	NAP		g1805251	366	166	4.00E-40	29	74	
19797	ENU03591	1861..3140	25-47	1241-1262	NAP		g2388971	1133	260	e-119	57	99	
19798	ENU03592	ANI61C1137 7:5545..4266	22-45	1228-1260	NAP		g2739168	229	148	7.00E-35	31	98	
19799	ENU03593	ANI61C822:1 658..2938		1241-1261	NAP		g2764614	510	128	7.00E-58	40	98	
19800	ENU03594	ANI61C1918: 22-55		1242-1262	NAP		g2144467	1212	135	2.00E-84	59	52	
19801	ENU03595	ANI61C9032: 22-41 4163..2881	70-89	1292-1311	NAP		g2499312	2312	591	e-168	92	77	
19802	ENU03596	ANI61C5905: 70-89 524..1807		1272-1304	NAP		g3925778	835	78	1.00E-17	44	26	
19803	ENU03597	ANI61C6334: 63-83 1851..3134		1246-1276	NAP		g2808725	159	78	1.00E-13	34	53	
19804	ENU03598	ANI61C3320: 35-55 1285..2	64-87	1283-1307	NAP		g2407968	415	164	9.00E-40	35	87	
19805	ENU03599	ANI61C2332: 3982..2697	23-42	1237-1266	NAP		g2315453	463	123	5.00E-43	40	98	
19806	ENU03600	ANI61C5370: 23-42 1552..266		1247-1266	NAP		g135746	730	182	2.00E-83	46	93	
19807	ENU03601	ANI61C6496: 22-56 4395..5681		1296-1315	NAP		g2625138	2012	190	5.00E-94	48	23	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19808	ENU03602	ANI61C9767: 3929..2643	23-56	1248-1267	NAP		g1723533	220	109	4.00E-23	38	39	hypothetical 33.6 KD protein C25G10.01 in chromosome I ; (Z70691) mna binding protein [Schizosaccharomyces pombe] (Z75532) similar to mitochondrial carrier protein; cDNA EST yk264h5.5 comes from this gene [Caenorhabditis elegans]
19809	ENU03603	ANI61C263:1 22-41 584..2871	22-41	1242-1267	NAP		g3875242	181	66	3.00E-22	30	96	
19810	ENU03604	ANI61C526:3 72-93 333..2046	72-93	1290-1317	NAP		g125935	165	65	0.000000	26	64	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] "(D83732) endo-1,4-beta-glucanase [Aspergillus oryzae]"
19811	ENU03605	ANI61C1086 24-56 7:367..1654	24-56	1243-1269	NAP		g2467375	1275	527	e-149	63	98	probable membrane protein YOR161c - yeast (Saccharomyces cerevisiae) ; (U55021) O3568p [Saccharomyces cerevisiae] ; (Z75069) ORF YOR161c [Saccharomyces cerevisiae]
19812	ENU03606	ANI61C3295: 31-52 10..1297	31-52	1255-1277	NAP		g2132901	833	178	4.00E-75	40	78	hypothetical 56.4 KD protein in RPL32-CWH41 intergenic region precursor ; probable membrane protein YGL028c - yeast (Saccharomyces cerevisiae) ; (Z72550) ORF YGL028c [Saccharomyces cerevisiae]
19813	ENU03607	ANI61C435:4 49-68 685..3397	49-68	1269-1295	NAP		g1723809	380	152	7.00E-36	27	78	[Saccharomyces cerevisiae] (AL033391) hypothetical membrane protein [Candida albicans] Arginine metabolism regulation protein III ; regulatory protein ARGRIII - yeast (Saccharomyces cerevisiae) ; (X05328) ARGRIII protein (AA 1-355) [Saccharomyces cerevisiae] ; (Z46727) Arg3p [Saccharomyces cerevisiae] (AE001015) acyl-CoA dehydrogenase (acd-9) [Archaeoglobus fulgidus] hypothetical 34.2 KD protein in CUS1-RPL18A1 intergenic region ; hypothetical protein YMR241w - yeast (Saccharomyces cerevisiae) ; (Z48756) unknown [Saccharomyces cerevisiae]
19814	ENU03608	ANI61C2205: 64-84 2001..712	64-84	1290-1310	NAP		g3850125	458	131	9.00E-31	33	76	
19815	ENU03609	ANI61C80:12 55-74 97..8	55-74	1283-1302	NAP		g114134	236	93	4.00E-18	33	86	
19816	ENU03610	ANI61C9725: 53-72 1421..131	53-72	1282-1301	NAP		g2649289	300	118	8.00E-26	33	88	
19817	ENU03611	ANI61C6152: 45-64 1746..3037	45-64	1273-1293	NAP		g2497200	1006	332	1.00E-92	70	97	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19818	ENU03612	ANI61C1077	67-86	1295-1316	NAP		g1363051	468	113	2.00E-24	28	76	P58 protein - bovine : (U04631) PKR inhibitor P58 [Bos taurus]
19819	ENU03613	ANI61C8876: 43-63		1271-1295	NAP		g1170767	1490	383	e-154	77	96	26S protease regulatory subunit 8 homolog (LET1 protein) ; transcription factor SUG1 homolog - fission yeast (Schizosaccharomyces pombe) ; (U02280) Let1 [Schizosaccharomyces pombe] ; (AL035065) 26s protease regulatory subunit 8 homolog [Schizosaccharomyces pombe]
19820	ENU03614	ANI61C59:19 26-45		1259-1278	NAP		g2492825	374	141	5.00E-41	32	96	"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus]"
19821	ENU03615	ANI61C59:19 26-45		1259-1278	NAP		g2492825	374	141	5.00E-41	32	96	"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus]"
19822	ENU03616	ANI61C1100 29-49		1256-1283	NAP		g1854443	474	180	2.00E-44	39	92	(D83970) CPRD8 protein [Vigna unguiculata]
19823	ENU03617	ANI61C9270: 26-51		1249-1280	NAP		g2500938	115	71	2.00E-11	32	42	Myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
19824	ENU03618	ANI61C9270: 26-51		1249-1280	NAP		g2500938	115	71	2.00E-11	32	42	Myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
19825	ENU03619	ANI61C3627: 22-42		1257-1277	NAP		g4240421		99	1.00E-22			(AF080235) reductase homolog [Streptomyces cyanogenus]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19826	ENU03620	ANI61C9039: 3292..4589	28-51	1264-1283	NAP		g2330781	972	328	e-103	51	84	"(Z98559) SPAC23C11.17; len:485aa, similar eg. to YPR125W, Q06493, chromosome xvi orf, (454aa), fasta scores, opt:1063, E(0:0, (43.5% identity in 418 aa overlap)
19827	ENU03621	ANI61C3441: 72-93 705..2002	72-93	1292-1327	NAP		g731716	646	270	4.00E-73	42	88	[Schizosaccharomyces pombe] "hypothetical 49.8 KD protein in ACT3-YCK1 intergenic region precursor ; hypothetical protein YHR132c - yeast (Saccharomyces cerevisiae) ; (U10398) Ecm14p [Saccharomyces cerevisiae] "hypothetical 39.4 KD protein in SGA1-KTR7 intergenic region ; hypothetical protein YIL096c - yeast (Saccharomyces cerevisiae) ; (Z38125) orf, len: 336, CAI: 0.14
19828	ENU03622	ANI61C1057 23-42 2:2746..1446	23-42	1262-1281	NAP		g731846	159	53	0.000003	27	70	[Saccharomyces cerevisiae] "ATPase C subunit) ; H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar - bovine ; (J05681) H+ - ATPase C subunit [Bos taurus] "probable ATP-dependent RNA helicase PRH1 ; PRH1 protein - fission yeast (Schizosaccharomyces pombe) ; (Z54354) probable atp-dependent rna helicase prh1 [Schizosaccharomyces pombe]
19829	ENU03623	ANI50C1282 50-69 7_1:1701..400	50-69	1277-1309	NAP		g137471		134	1.00E-30	38	94	(Y16748) malate dehydrogenase [Piromyces sp. E2]
19830	ENU03624	ANI61C5190: 68-90 2421..1118	68-90	1310-1329	NAP		g1172616	1087	326	2.00E-88	49	54	(AB016720) carboxylesterase precursor [Aphis gossypii] putative polyketide biosynthesis protein PKSJ ; (U11039) unknown [Bacillus subtilis] ; (Z99112) pksJ [Bacillus subtilis] ; (Z99113) pksJ [Bacillus subtilis]
19831	ENU03625	ANI61C8056: 65-84 641..1944	65-84	1306-1326	NAP		g4029338	632	145	6.00E-65	57	96	(AB011157) KIAA0585 protein [Homo sapiens]
19832	ENU03626	ANI61C6841: 22-42 5143..3838	22-42	1267-1285	NAP		g3426006	302	140	2.00E-32	39	32	(Y14749) MDM10 [Podospira anserina]
19833	ENU03627	ANI61C5500: 50-71 2517..1207	50-71	1299-1318	NAP		g730334	379	173	2.00E-42	28	76	
19834	ENU03628	ANI61C1029 22-42 4:4056..2745	22-42	1271-1290	NAP		g3043694	243	137	2.00E-31	29	64	
19835	ENU03629	ANI61C2332: 64-87 3982..2670	64-87	1315-1334	NAP		g2407968	415	164	9.00E-40	34	88	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19836	ENU03630	ANI61C8090: 1445..129	22-41	1277-1296	NAP		g2984184	398	157	2.00E-37	29	82	(AE000763) N-methylhydantoinase B [Aquifex aeolicus]
19837	ENU03631	ANI61C4285: 46-68		1302-1321	NAP		g2664292	1594	447	e-171	81	95	(Y15744) cellular aspartic protease [Aspergillus fumigatus] ; (AJ132504) aspartic protease [Aspergillus fumigatus]
19838	ENU03632	ANI61C7950: 57-77		1304-1333	NAP		g2493391		96	4.00E-19			probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emericella nidulans]
19839	ENU03633	ANI61C4230: 47-75		1289-1323	NAP		g1351673	367	113	6.00E-32	38	96	hypothetical 37.7 KD protein C1F7.12 in chromosome I ; hypothetical protein SPAC1F7.12 - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown
19840	ENU03634	ANI61C3599: 29-52		1288-1307	NAP		g522302	4000	589	e-167	63	36	[Schizosaccharomyces pombe] (L35053) endonuclease [Magnaporthe grisea]
19841	ENU03635	ANI61C4299: 57-80		1316-1335	NAP		g1351606	196	67	3.00E-10	29	25	hypothetical 54.3 KD protein C23D3.03C in chromosome I ; hypothetical protein SPAC23D3.03c - fission yeast (Schizosaccharomyces pombe) ; (Z64354) unknown
19842	ENU03636	ANI61C406:2	30-57	1290-1310	NAP		g135184	2357	266	e-118	54	38	[Schizosaccharomyces pombe] "Valyl-TRNA synthetase, mitochondrial precursor (valine--TRNA ligase) (VALRS) ; valine--tRNA ligase (EC 6.1.1.9) - Neurospora crassa "
19843	ENU03637	ANI61C4412: 45-65		1307-1326	NAP		g1469396	692	226	8.00E-75	43	94	(U43775) secreted aspartic proteinase precursor [Glomerella cingulata]
19844	ENU03638	ANI61C1527: 25-56		1290-1309	NAP		g730338	1840	565	e-160	58	72	Lysophospholipase precursor (phospholipase B) ; lysophospholipase (EC 3.1.1.5) - Penicillium notatum (fragment) ; (X60348)
19845	ENU03639	ANI61C188:1	56-77	1321-1340	NAP		g1346290	802	166	2.00E-81	45	69	lysophospholipase [Penicillium chrysogenum] high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]

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19846	ENU03640	ANI61C1118 0:5077..3751	71-94	1334-1355	NAP		g2621739	762	227	2.00E-87	51	68	(AE000845) long-chain-fatty-acid-CoA ligase [Methanobacterium thermoautotrophicum]
19847	ENU03641	ANI61C3898: 65-90 1348..20	65-90	1331-1351	NAP		g2498971	627	130	3.00E-29	34	75	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emericella nidulans] (AL031856) putative golgi uridine diphosphate-N-acetylglucosamine transporter [Schizosaccharomyces pombe]
19848	ENU03642	ANI61C1085 22-51 7:1133..2463	22-51	1282-1310	NAP		g3738167	452	173	2.00E-42	41	100	probable histone DEacetylase HOS2 ; probable transcription regulator YGL194c - yeast (Saccharomyces cerevisiae) ; (Z72716) ORF YGL194c [Saccharomyces cerevisiae]
19849	ENU03643	ANI61C1018 44-63 7:4272..2941	44-63	1314-1333	NAP		g1723948	1150	469	e-131	55	95	probable histone DEacetylase HOS2 ; probable transcription regulator YGL194c - yeast (Saccharomyces cerevisiae) ; (Z72716) ORF YGL194c [Saccharomyces cerevisiae]
19850	ENU03644	ANI61C8914: 51-70 1895..3227	51-70	1315-1341	NAP		g2826168	62	7.00E-13				(AB010714) salicylate hydroxylase [Pseudomonas putida]
19851	ENU03645	ANI61C1926: 22-42 59..1393	22-42	1295-1314	NAP		g2131429	236	119	4.00E-26	25	96	hypothetical protein YDR322w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr322wp [Saccharomyces cerevisiae]
19852	ENU03646	ANI61C8043: 65-84 2221..884	65-84	1340-1360	NAP		g3150104	251	129	4.00E-29	36	33	(AL023596) hypothetical protein MLCB2407.16c [Mycobacterium leprae]
19853	ENU03647	ANI61C7152: 40-61 4223..2886	40-61	1314-1335	NAP		g2132817	222	75	2.00E-21	33	41	probable membrane protein YOL003c - yeast (Saccharomyces cerevisiae) ; (U43491) hypothetical protein UNE378 [Saccharomyces cerevisiae] ; (Z74745) ORF YOL003c [Saccharomyces cerevisiae]
19854	ENU03648	ANI61C3804: 22-41 2043..705	22-41	1299-1318	NAP		g1711632	2083	396	e-149	62	65	putative glycyl-TRNA synthetase (glycine--TRNA ligase) (GLYRS) ; (Z69369) glycyl tRNA synthetase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19855	ENU03649	ANI61C4864: 57-76 635..1973		1333-1353	NAP		g1176339	517	136	4.00E-57	36	87	"hypothetical 50.8 KD protein in MIR1-STE18 intergenic region ; indoleamine-pyrrrole 2,3-dioxygenase homolog YJR078w - yeast (Saccharomyces cerevisiae) ; (Z49578) ORF YJR078w [Saccharomyces cerevisiae] ; (L47993) ORF YJR078w [Saccharomyces cerevisiae] " [AL033534] carbamoyl-phosphate synthase [Schizosaccharomyces pombe] (Y13975) phospholipase C [Candida albicans] (U62917) glucose transporter TGTP2 [Taenia solium] hypotheatcal protein YDR322w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr322wp [Saccharomyces cerevisiae] " (U62928) multidrug resistance protein, ABC transporter protein [Aureobasidium pullulans] ; (U85909) multidrug resistance-like protein [Aureobasidium pullulans] " (U31348) G4p1 [Saccharomyces cerevisiae] (X81067) probable mitochondrial protein; nearly identical to YME1 [Saccharomyces cerevisiae] Galactose-1-phosphate uridylyltransferase ; UDPglucose--hexose-1-phosphate uridylyltransferase (EC 2.7.7.12) - yeast (Kluyveromyces marxianus var. lactis) ; (X07039) epimerase (GAL 7) (AA 1 - 370) [Kluyveromyces lactis] (AB025252) reverse transcriptase [Magnaporthe grisea]
19856	ENU03650	ANI61C7945: 72-91 1416..2755		1349-1369	NAP		g3873545	3360	293	e-150	66	36	
19857	ENU03651	ANI61C1092 47-66 8:3792..2452		1323-1345	NAP		g2462982	244	103	8.00E-35	34	23	
19858	ENU03652	ANI61C9031: 63-82 342..579		1335-1362	NAP		g1480799		37	0.000000			
19859	ENU03653	ANI61C1926: 22-42 59..1401		1302-1322	NAP		g2131429	236	119	4.00E-26	25	96	
19860	ENU03654	ANI61C6211: 49-71 1869..3212		1324-1350	NAP		g4097503	1671	313	2.00E-84	42	34	
19861	ENU03655	ANI61C3588: 64-84 2903..2660		1347-1366	NAP		g1002712	351	64	0.000000	54	12	
19862	ENU03656	ANI61C4066: 58-77 1651..306		1342-1361	NAP		g531752	1288	418	e-116	56	57	
19863	ENU03657	ANI61C7448: 22-48 1277..2623		1305-1325	NAP		g120909	856	314	2.00E-92	51	96	
19864	ENU03658	ANI61C5998: 50-69 5415..4069		1334-1354	NAP		g4586458	151	108	1.00E-22	32	62	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19865	ENU03659	ANI61C8751: 4049..5395	22-45	1307-1326	NAP		g2498440	926	297	4.00E-99	48	88	"Homogentisate 1,2-dioxygenase (homogentisicase) (homogentisate oxygenase) (homogentisic acid oxidase) ; 3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15) - Emericella nidulans ; (U30797) 2,5 dihydroxyphenylacetate oxidase [Emericella nidulans] ; (AJ001836) homogentisate dioxygenase [Emericella nidulans] "
19866	ENU03660	ANI61C2872: 28-50	28-50	1315-1334	NAP		g1717973	1184	499	e-140	61	56	"Glycogen (starch) synthase, isoform 2 ; UDPglucose--starch glucosyltransferase (EC 2.4.1.11) 2 - yeast (Saccharomyces cerevisiae) ; (U17244) Gsy2p: Glycogen Synthase (UDP-glucose--starch glucosyltransferase) [Saccharomyces cerevisiae] "
19867	ENU03661	ANI61C5204: 42-61	42-61	1325-1349	NAP		g4558826	2307	553	e-156	99	98	(AF076691) aureobasidin-resistance protein; AurA [Emericella nidulans]
19868	ENU03662	ANI61C4343: 39-69	39-69	1328-1347	NAP		g1176967	88	71	1.00E-11	28	32	hypothetical 37.6 KD protein in GNTR-HTPG intergenic region ; (AB005554) see SWISS_PROT ACC#: P42106 [Bacillus subtilis] ; (Z99124) yxaG [Bacillus subtilis]
19869	ENU03663	ANI61C236:1	45-65	1328-1353	NAP		g2266941	1681	559	e-168	87	93	(AF009036) NAD(+)-isocitrate dehydrogenase subunit I [Ajellomyces capsulatus]
19870	ENU03664	ANI61C4864: 635..1985	57-76	1333-1365	NAP		g1176339	517	136	4.00E-57	35	88	"hypothetical 50.8 KD protein in MIR1-STE18 intergenic region ; indoleamine-pyrrole 2,3-dioxygenase homolog YJR078w - yeast (Saccharomyces cerevisiae) ; (Z49578) ORF YJR078w [Saccharomyces cerevisiae] ; (L47993) ORF YJR078w [Saccharomyces cerevisiae] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19871	ENU03665	ANI61C8878: 23-42 2850..1496		1307-1335	NAP		g1351651	784	220	1.00E-56	45	99	hypothetical 43.7 KD protein C24B11.08C in chromosome I ; hypothetical protein SPAC24B11.08c - fission yeast (Schizosaccharomyces pombe) ; (Z67757) unknown [Schizosaccharomyces pombe] (AC000133) ORF [Emericella nidulans] (AL021748) major facilitator superfamily protein [Schizosaccharomyces pombe] DNA-3-methyladenine glycosidase (3-methyladenine DNA glycosylase) (3MEA DNA glycosylase) ; DNA-3-methyladenine glycosidase I (EC 3.2.2.20) - fission yeast (Schizosaccharomyces pombe) ; (U76637) 3-methyladenine DNA glycosylase [Schizosaccharomyces pombe]
19872	ENU03666	ANI61C3420: 37-56 1372..18		1326-1349	NAP		g1870209	419	158	7.00E-38	95	13	
19873	ENU03667	ANI61C6436: 57-76 2965..1611		1350-1369	NAP		g2842516	589	83	1.00E-34	30	66	
19874	ENU03668	ANI61C6064: 22-41 92..1449		1315-1337	NAP		g2494171		80	3.00E-14			
19875	ENU03669	ANI61C313:2 22-41 655..1296		1319-1338	NAP		g1711561		105	3.00E-27			Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae] (AL021710) hypothetical protein [Arabidopsis thaliana] cytochrome B2 precursor (L-lactate dehydrogenase (cytochrome)) (L-lactate ferricytochrome C oxidoreductase (L-LCR) ; L-lactate dehydrogenase (cytochrome) (EC 1.1.2.3) precursor - yeast (Pichia anomala) ; (X16051) L-lactate:cytochrome c oxidoreductase preprotein [Pichia anomala] protein kinase C-like ; protein kinase C homolog PKCA - Aspergillus niger ; (U10549) protein kinase C [Aspergillus niger]
19876	ENU03670	ANI61C8049: 69-90 2384..1025		1367-1386	NAP		g2832659	249	100	2.00E-20	27	71	
19877	ENU03671	ANI61C8377: 50-69 88..1447		1344-1367	NAP		g117803	591	262	3.00E-69	39	71	
19878	ENU03672	ANI61C722:3 42-61 078..1715		1342-1362	NAP		g2499576	2827	357	e-177	85	35	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19879	ENU03673	ANI61C9491: 1576..1664	27-46	1328-1347	NAP		g4154089	286	98	2.00E-32	35	100	(Z98981) putative pyridoxal kinase [Schizosaccharomyces pombe]
19880	ENU03674	ANI61C9160: 1151..1495	68-95	1370-1389	NAP		g4512109	470	176	2.00E-43	36	40	(AF125185) origin recognition complex subunit 4-related protein Orp4p [Schizosaccharomyces pombe]
19881	ENU03675	ANI61C2242: 56-75	56-75	1356-1377	NAP		g729014	1043	146	1.00E-95	46	74	Arginine permease; arginine transport protein - yeast (Saccharomyces cerevisiae); (M11724) amino acid permease [Saccharomyces cerevisiae]; (U18795) Can1p: arginine permease [Saccharomyces cerevisiae]
19882	ENU03676	ANI61C7470: 65-84	65-84	1366-1390	NAP		g3135990	1056	287	1.00E-76	42	78	(AL023589) membrane transporter [Schizosaccharomyces pombe]
19883	ENU03677	ANI61C1036 35-58	35-58	1343-1362	NAP		g2465156	701	255	5.00E-67	45	94	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
19884	ENU03678	ANI61C1018 22-50	22-50	1334-1353	NAP		g2058345	1215	168	e-110	70	96	(Y12693) oxysterol-binding protein [Neurospora crassa]
19885	ENU03679	ANI61C310:1 64-83	64-83	1380-1399	NAP		g3261633	321	83	5.00E-17	33	94	(Z79700) fadE13 [Mycobacterium tuberculosis]
19886	ENU03680	ANI61C1090 36-56	36-56	1352-1372	NAP		g3122213	667	236	3.00E-61	39	96	histidinol dehydrogenase (HDH); (AE000809) histidinol dehydrogenase [Methanobacterium thermoautotrophicum]
19887	ENU03681	ANI61C4094: 22-55	22-55	1339-1358	NAP		g1465805	274	87	7.00E-21	32	85	(U64852) coded for by C. elegans cDNA cm17d4; Similar to epoxide hydrolase. [Caenorhabditis elegans]
19888	ENU03682	ANI61C3456: 70-99	70-99	1388-1407	NAP		g2492816	582	156	5.00E-62	32	73	uracil permease; (X98696) uracil permease [Schizosaccharomyces pombe]
19889	ENU03683	ANI61C7433: 35-54	35-54	1354-1373	NAP		g121855	1110	182	7.00E-76			"Exoglucanase II precursor (exocellobiohydrolase II) (CBHII) (1,4-beta-cellobiohydrolase); cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei); cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus (Trichoderma viride); (M16190) cellobiohydrolase II [Trichoderma reesei]; cellobiohydrolase II [Trichoderma reesei]"

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19890	ENU03684	ANI61C1092 8:1312..2692	57-76	1376-1395	NAP		g461915	829	108	2.00E-43			Dipeptidyl aminopeptidase A (DPAP A) (YSCIV) ; dipeptidyl aminopeptidase (EC 3.4.14.-) - yeast (Saccharomyces cerevisiae) ; (L21944) dipeptidyl aminopeptidase [Saccharomyces cerevisiae] ; (U08230) dipeptidyl aminopeptidase A [Saccharomyces cerevisiae] ; (X92441) YOR50-9 [Saccharomyces cerevisiae] ; (Z75127) ORF YOR219c [Saccharomyces cerevisiae] (AF016452) Similar to aldehyde dehydrogenase; coded for by C. elegans cDNA yk144e3.3; coded for by C. elegans cDNA yk144e3.5 [Caenorhabditis elegans] hypothetical protein YOR197w - yeast (Saccharomyces cerevisiae) ; (Z75105) ORF YOR197w [Saccharomyces cerevisiae]
19891	ENU03685	ANI61C2498: 47-67 402..1785	47-67	1367-1388	NAP		g2315524	682	129	1.00E-67	37	81	
19892	ENU03686	ANI61C8615: 23-42 471..1854	23-42	1329-1364	NAP		g2132083	929	353	2.00E-96	49	95	
19893	ENU03687	ANI61C8941: 64-83 2802..1417	64-83	1388-1407	NAP		g4589366	542	226	3.00E-58	39	65	(AF140505) DEAD box RNA helicase [Candida albicans]
19894	ENU03688	ANI61C7867: 69-88 425..1811	69-88	1391-1413	NAP		g3123294	781	79	2.00E-70	61	97	"Endo-1,4-beta-xylanase (xylanase) (1,4-beta-D-xylan xylanohydrolase)"
19895	ENU03689	ANI61C1061 35-56 9:2216..830	35-56	1360-1380	NAP		g1703361	1592	467	e-169			"ARG-6 protein precursor (contains: N-acetyl-gamma-glutamyl-l-phosphate reductase (N-acetyl-glutamate smilaldehyde dehydrogenase) (NAGSA dehydrogenase), and acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-... ; acetylglutamate kinase (EC 2.7.2.8) / N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) precursor, mitochondrial - Neurospora crassa ; (L27746) arg-6 gene product [Neurospora crassa] "
19896	ENU03690	ANI61C7037: 22-56 2809..1421	22-56	1337-1368	NAP		g436466	162	68	1.00E-10	25	89	(Z29102) putative transposase [Drosophila hydei] ; transposase [Drosophila hydei]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19897	ENU03691	ANI61C3244: 152..1540	25-46	1344-1371	NAP		g1708319	820	349	4.00E-95	45	82	cell cycle protein kinase HSK1 ; protein kinase hsk1 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe) ; (D50493) hsk1+ protein kinase [Schizosaccharomyces pombe] ; (AL035263) cell cycle protein kinase hsk1 [Schizosaccharomyces pombe] (Z29102) putative transposase [Drosophila hydei] ; transposase [Drosophila hydei] NADPH dehydrogenase 2 (old yellow enzyme 2) ; NADPH dehydrogenase (EC 1.6.99.1) chain OYE2 - yeast (Saccharomyces cerevisiae) ; (L06124) NAD(P)H:oxidoreductase [Saccharomyces cerevisiae] ; (U00027) Oye2p: NAD(P)H oxidoreductase (Old Yellow Enzyme) [Saccharomyces cerevisiae]
19898	ENU03692	ANI61C9575: 22-56 4095..2707	22-56	1337-1368	NAP		g436466	143	64	0.000000 002	24	89	Conidium-specific protein ; SpoC1-C1D protein - Emericella nidulans ; (X54668) SpoC1-C1D product [Emericella nidulans]
19899	ENU03693	ANI61C9932: 32-59 1268..2657	32-59	1359-1379	NAP		g417432	613	280	1.00E-74	40	91	(AE000955) 2-nitropropane dioxygenase (ncd2) [Archaeoglobus fulgidus] Zn/Cd resistance gene [Saccharomyces cerevisiae] hypothetical protein YDR330w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr330wp [Saccharomyces cerevisiae] ATP-dependent bile acid permease ; probable membrane protein YLL048c - yeast (Saccharomyces cerevisiae) ; (Z73153) ORF YLL048c [Saccharomyces cerevisiae]
19900	ENU03694	ANI61C7763: 26-45 59..1451	26-45	1353-1376	NAP		g134270	146	54	0.000003	33	31	
19901	ENU03695	ANI61C1560: 44-64 3104..1711	44-64	1376-1395	NAP		g2648355	167	60	0.000000 03	38	96	
19902	ENU03696	ANI61C410:5 41-62 030..6425	41-62	1371-1394	NAP		g227157	333	107	2.00E-22	32	85	
19903	ENU03697	ANI61C1048 59-79 2:1595..200	59-79	1387-1412	NAP		g2131432	441	155	5.00E-37	32	83	
19904	ENU03698	ANI61C1128 67-87 3:1939..544	67-87	1401-1420	NAP		g3915963	742	159	3.00E-73	38	26	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19905	ENU03699	ANI61C2134: 4169..5564	26-45	1347-1379	NAP		g730893	283	54	7.00E-13			tryptophan permease (tryptophan amino acid transporter) ; tryptophan transport protein - yeast (Saccharomyces cerevisiae) ; (L33461)
													tryptophan permease [Saccharomyces cerevisiae] ; (X79150) tryptophan amino acid permease [Saccharomyces cerevisiae] ; (Z74762) ORF YOL020w [Saccharomyces cerevisiae] ; (U66834) suppressor of ABF1 [Saccharomyces cerevisiae]
19906	ENU03700	ANI61C2438: 160..1556	72-93	1407-1426	NAP		g731880	520	191	8.00E-48	27	64	"hypothetical 80.5 KD protein in SLN1-RAD25 intergenic region ; hypothetical protein YIL144w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 691, CAI: 0.15, possible coiled-coil [Saccharomyces cerevisiae] "
19907	ENU03701	ANI61C2438: 160..1556	72-93	1407-1426	NAP		g731880	520	191	8.00E-48	27	64	"hypothetical 80.5 KD protein in SLN1-RAD25 intergenic region ; hypothetical protein YIL144w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 691, CAI: 0.15, possible coiled-coil [Saccharomyces cerevisiae] "
19908	ENU03702	ANI61C1724: 30-51 2191..3589	30-51	1356-1386	NAP		g461508	925	393	e-108			"vacuolar aminopeptidase I precursor (polypeptidase) (leucine aminopeptidase IV) (LAPIV) (aminopeptidase III) (aminopeptidase YSC1) ; aminopeptidase ysc1 (EC 3.4.11.-) precursor, vacuolar - yeast (Saccharomyces cerevisiae) ; (M25548) aminopeptidase I [Saccharomyces cerevisiae] ; (X71133) vacuolar aminopeptidase YSC1 [Saccharomyces cerevisiae] ; (Z28103) ORF YKL103c [Saccharomyces cerevisiae] "
19909	ENU03703	ANI61C7948: 41-60 5069..4253	41-60	1375-1401	NAP		g3925779	71	47	0.0003	28	35	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19910	ENU03704	ANI61C3294: 2140..735	58-77	1401-1421	NAP		g3201958	368	159	4.00E-40	39	62	(AF068116) eIF4E-like protein 4E-LP [Mus musculus]
19911	ENU03705	ANI61C3573: 68-90		1398-1431	NAP		g1078218	961	195	3.00E-80	45	93	probable membrane protein YDR105c - yeast (Saccharomyces cerevisiae); (Z47746) unknown [Saccharomyces cerevisiae]; (Z48758) unknown [Saccharomyces cerevisiae]
19912	ENU03706	ANI61C7316: 30-57		1375-1394	NAP		g4388565	1265	424	e-125	52	91	[Saccharomyces cerevisiae] (Z35875) ORF YBR006w [Saccharomyces cerevisiae]
19913	ENU03707	ANI61C2435: 51-71		1386-1417	NAP		g1749554	618	213	7.00E-64	47	95	"(D89173) similar to Saccharomyces cerevisiae hypothetical 36.4KD protein in SOD1-CPA2 intergenic region, SWISS-PROT Accession Number P47143 [Schizosaccharomyces pombe]; (AL023781) adenosine kinase [Schizosaccharomyces pombe]"
19914	ENU03708	ANI61C9254: 23-52		1370-1389	NAP		g3738169	1087	314	7.00E-99	58	97	(AL031856) putative mitochondrial protein import protein - DNAJ protein [Schizosaccharomyces pombe]
19915	ENU03709	ANI61C1115 22-48		1370-1390	NAP		g3183342	353	130	2.00E-29	38	96	[Schizosaccharomyces pombe] hypothetical 44.5 KD protein C14C4.09 in chromosome I; (Z98596) hypothetical protein
19916	ENU03710	ANI61C3949: 66-85		1415-1434	NAP		g1345704	233	62	0.000000	27	33	[Schizosaccharomyces pombe] cell division control protein 15; cell division control protein cdc15 - fission yeast (Schizosaccharomyces pombe); (Z95334) Cdc15p [Schizosaccharomyces pombe]
19917	ENU03711	ANI61C9367: 22-42		1362-1391	NAP		g131828	998	282	5.00E-98	44	79	LOW-affinity glucose transporter; glucose transport protein RAG1 - yeast (Kluyveromyces marxianus var. lactis) (X53752) putative sugar transporter [Kluyveromyces lactis]
19918	ENU03712	ANI61C212:3 23-42		1367-1393	NAP		g2996008	1881	666	0	85	99	(AF053983) translation release factor subunit 1 [Podospora anserina]
19919	ENU03713	ANI61C7848: 37-55		1384-1408	NAP		g3023951	470	205	5.00E-52	30	43	Histone transcription regulator 1 homolog; (Z97204) putative hira protein; histone transcription regulator [Schizosaccharomyces pombe]
19920	ENU03714	ANI61C9794: 23-50		1367-1394	NAP		g2271477	1012	194	e-106	49	97	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19921	ENU03715	ANI61C7561: 258..87	45-64	1391-1421	NAP		g117619	135	50	0.00004	34	18	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603)
													choline transport protein [Saccharomyces cerevisiae] ; (Z72599)
													ORF YGL077c [Saccharomyces cerevisiae]
19922	ENU03716	ANI61C9917: 22-41	22-41	1380-1399	NAP		g3581896	443	138	9.00E-32	24	75	(AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
19923	ENU03717	ANI61C7944: 36-55	36-55	1392-1414	NAP		g1077336	466	127	2.00E-52	35	96	hypothetical protein YLR380w - yeast (Saccharomyces cerevisiae) ; (U19104)
		3165..4585											Ylr380wp [Saccharomyces cerevisiae]
19924	ENU03718	ANI61C2369: 22-44	22-44	1380-1402	NAP		g586465	233	88	2.00E-20	26	94	hypothetical 50.8 KD protein in COQ1-FLR1 intergenic region precursor ; probable membrane protein YBR004c - yeast (Saccharomyces cerevisiae) ; (Z35873) ORF YBR004c [Saccharomyces cerevisiae]
19925	ENU03719	ANI61C1133 22-44	22-44	1383-1403	NAP		g2746775	414	139	9.00E-37	36	82	(AF040640) similar to peptidase family C19 (ubiquitin carboxyl-terminal hydrolase) [Caenorhabditis elegans]
		0:963..2385											mevalonate kinase (MVK) ; mevalonate kinase (EC 2.7.1.36) - yeast (Saccharomyces cerevisiae) ; (X55875) mevalonate kinase [Saccharomyces cerevisiae] ; (X06114)
19926	ENU03720	ANI61C7948: 42-61	42-61	1391-1424	NAP		g125407	523	179	1.00E-47	36	95	ORF1 (put. RAR1 protein) (AA 1-443) [Saccharomyces cerevisiae] ; (Z49809)
		2803..4226											Rar1p [Saccharomyces cerevisiae]
19927	ENU03721	ANI61C316:3 58-84	58-84	1423-1442	NAP		g2492782	551	219	5.00E-56	38	97	alpha-galactosidase precursor (melibiase) (alpha-D-galactoside galactohydrolase) ; (L27992) alpha-galactosidase [Coffea arabica]
		290..1864											"DLTE protein ; hypothetical protein - Bacillus subtilis ; dltE product[putative cytosolic oxidoreductase [Bacillus subtilis, Peptide, 252 aa] ; (X73124)
19928	ENU03722	ANI61C1271: 22-44	22-44	1379-1408	NAP		g729344		45	0.000000			ipa-1r [Bacillus subtilis] ; (Z99123)
		2312..2792								01			alternate gene name: ipa-1r [Bacillus subtilis] "

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19929	ENU03723	ANI61C8203: 68-88	1429-1459	1429-1459	NAP		g4249560	1229	291	e-133	52	96	(AB003109) beta-glucosidase [Humicola grisea var. thermoides]
19930	ENU03724	ANI61C1036: 49-68	1421-1441	1421-1441	NAP		g1730771	1269	330	1.00E-89	41	43	hypothetical 110.9 KD protein in spC98-TOM70 intergenic region; probable membrane protein YNL123w - yeast (Saccharomyces cerevisiae); (Z69382) N1897 [Saccharomyces cerevisiae]; (Z71399) ORF YNL123w [Saccharomyces cerevisiae]
19931	ENU03725	ANI61C8805: 24-49	1396-1417	1396-1417	NAP		g4105567	184	105	9.00E-22	31	93	(AF047707) UDP-glucose:ceramide glycosyltransferase [Rattus norvegicus]
19932	ENU03726	ANI61C1038: 23-42	1397-1416	1397-1416	NAP		g2894272	351	141	1.00E-32	38	76	(AL021839) hypothetical protein [Schizosaccharomyces pombe]
19933	ENU03727	ANI61C9835: 51-69	1425-1445	1425-1445	NAP		g2132357	148	84	2.00E-15	40	35	NBP2 protein - yeast (Saccharomyces cerevisiae); (Z50046) Nbp2p [Saccharomyces cerevisiae]; (D43693) Nap1-binding protein [Saccharomyces cerevisiae]
19934	ENU03728	ANI61C8985: 57-75	1432-1451	1432-1451	NAP		g3915140	562	127	2.00E-54	34	94	isotrichodermin C-15 hydroxylase (cytochrome P450 65A1); (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides]
19935	ENU03729	ANI61C7943: 40-59	1419-1438	1419-1438	NAP		g632081		103	3.00E-21			hypothetical protein 4 - Xanthobacter sp.; (X79863) orf4 [Xanthobacter sp. Py2]
19936	ENU03730	ANI61C9526: 22-44	1401-1420	1401-1420	NAP		g2501674	185	61	2.00E-18	39	20	DRAP deaminase; RIB2 protein - yeast (Saccharomyces cerevisiae); (Z21618) DRAP deaminase [Saccharomyces cerevisiae]; (Z74808) ORF YOL066c [Saccharomyces cerevisiae]
19937	ENU03731	ANI61C8286: 55-74	1426-1453	1426-1453	NAP		g1172703	484	191	8.00E-48	44	32	"peptide transporter PTR2-A; (U01171) similar to S. cerevisiae PTR2 gene, GenBank Accession Number L11994 [Arabidopsis thaliana]" (X63029) Uhu [Drosophila heteroneura]
19938	ENU03732	ANI61C408:7	52-79	1425-1453	NAP		g7464		75	1.00E-12			(Z98529) putative RNA-binding protein [Schizosaccharomyces pombe]
19939	ENU03733	ANI61C9882: 22-49	1405-1424	1405-1424	NAP		g2462671	413	129	4.00E-29	33	97	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19940	ENU03734	ANI61C2898: 131..1579	72-91	1458-1477	NAP		g1709679	753	238	6.00E-85	40	59	probable mitochondrial intermediate peptidase precursor (MIP) ; (Z70690) unknown [Schizosaccharomyces pombe]
19941	ENU03735	ANI61C6436: 2965..1517	57-76	1436-1463	NAP		g2842516	589	92	3.00E-37	30	72	(AL021748) major facilitator superfamily protein [Schizosaccharomyces pombe]
19942	ENU03736	ANI61C8998: 2873..1424	39-58	1427-1446	NAP		g2398820	524	221	8.00E-57	34	43	(Z99126) hypothetical protein. [Schizosaccharomyces pombe]
19943	ENU03737	ANI61C8998: 2873..1424	39-58	1427-1446	NAP		g2398820	524	221	8.00E-57	34	43	(Z99126) hypothetical protein. [Schizosaccharomyces pombe]
19944	ENU03738	ANI61C7853: 3528..4978	22-48	1411-1430	NAP		g1345707	387	108	6.00E-42	38	73	CCC1 protein ; CCC1 protein - yeast (Saccharomyces cerevisiae) ; (U19027) CCC1p: putative transmembrane Ca2+ transporter [Saccharomyces cerevisiae] ; (L24112) Ccc1p [Saccharomyces cerevisiae]
19945	ENU03739	ANI61C5260: 588..2042	62-81	1441-1474	NAP		g1709784	955	347	8.00E-95			gamma-glutamyl phosphate reductase (GPR) (glutamate-5-semialdehyde dehydrogenase) (glutamyl-gamma-semialdehyde dehydrogenase) ; glutamate-5-semialdehyde dehydrogenase (EC 1.2.1.41) - yeast (Saccharomyces cerevisiae) ; (X90565) orf 06155 [Saccharomyces cerevisiae] ; (U43565) gamma-glutamyl phosphate reductase [Saccharomyces cerevisiae] ; (Z75231) ORF YOR323c [Saccharomyces cerevisiae] (AF127176) trichothecene 3-O-acetyltransferase [Fusarium sporotrichioides]
19946	ENU03740	ANI61C7017: 6649..8103	22-55	1409-1434	NAP		g4378882		150	3.00E-35			hypothetical 42.3 KD protein in YTA2-DIT1 intergenic region ; hypothetical protein YDR400w - yeast (Saccharomyces cerevisiae) ; (U32274) Ydr400wp; CAI: 0.14 [Saccharomyces cerevisiae]
19947	ENU03741	ANI61C6489: 8671..7216	24-50	1417-1437	NAP		g2497466	344	73	3.00E-34	35	98	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19948	ENU03742	ANI61C1056 5:1238..2697	22-41	1406-1439	NAP		g3881508	259	75	1.00E-12	33	91	(Z47357) cDNA EST EMBL:T00822 comes from this gene; cDNA EST EMBL:T00823 comes from this gene [Caenorhabditis elegans]
19949	ENU03743	ANI61C7184: 3218..4678	32-53	1428-1450	NAP		g1710597	292	121	2.00E-30	33	73	"mitochondrial 60S ribosomal protein L7 precursor (YML7) ; ribosomal protein Yml7, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49701) unknown [Saccharomyces cerevisiae] " (AF095898) siderophore biosynthesis repressor SREA [Emricella nidulans] "3-ketoacyl-CoA thiolase peroxisomal precursor (beta-ketothiolase) (acetyl-CoA acyltransferase) (peroxisomal 3-oxoacyl-CoA thiolase) ; acetyl-CoA C-acyltransferase (EC 2.3.1.16), peroxisomal - yeast (Yarrowia lipolytica) ; (X69988) acetyl-CoA acyltransferase [Yarrowia lipolytica] " choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
19950	ENU03744	ANI61C9446: 3377..4838	67-86	1452-1486	NAP		g4585213	2852	484	0	99	81	
19951	ENU03745	ANI61C6203: 5604..7069	68-87	1465-1491	NAP		g549077	840	275	1.00E-75	53	95	
19952	ENU03746	ANI61C3969: 238..1703	29-48	1420-1452	NAP		g117619	632	213	2.00E-54	33	82	
19953	ENU03747	ANI61C1041 7:2853..2916	69-90	1467-1493	NAP		g2507070	369	88	1.00E-18	35	61	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19954	ENU03748	ANI61C9290: 3960..2492	55-86	1460-1481	NAP		g1237183	434	146	2.00E-53	33	83	(D43773) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
19955	ENU03749	ANI61C6471: 6161..7630	24-50	1432-1451	NAP		g3947853	663	232	9.00E-65	53	73	(AL034381) transcriptional regulator [Schizosaccharomyces pombe]
19956	ENU03750	ANI61C222:1 257..1567	23-43	1430-1450	NAP		g403179	263	129	5.00E-29	37	25	(L24441) kinesin light chain [Loligo pealii]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19957	ENU03751	ANI61C7471: 6428..4957	65-84	1474-1494	NAP		g2507070	442	113	1.00E-50	35	83	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19958	ENU03752	ANI61C1144 35-64 6:2721..1249	35-64	1442-1465	NAP		g127024	1418	417	e-163	60	93	homoserine O-acetyltransferase (homoserine O-trans-acetylase) ; homoserine O-acetyltransferase (EC 2.3.1.31) - fungus (Ascobolus immersus) ; (M26662) met2 [Ascobolus immersus]
19959	ENU03753	ANI61C2369: 58-77 810..2283	58-77	1467-1489	NAP		g586465	233	88	2.00E-20	26	94	hypothetical 50.8 KD protein in COQ1-FLR1 intergenic region precursor ; probable membrane protein YBR004c - yeast (Saccharomyces cerevisiae) ; (Z35873) ORF YBR004c [Saccharomyces cerevisiae]
19960	ENU03754	ANI61C1056 62-81 5:1164..2638	62-81	1474-1494	NAP		g3881508	259	76	7.00E-13	32	96	(Z47357) cDNA EST EMBL:T00822 comes from this gene; cDNA EST EMBL:T00823 comes from this gene [Caenorhabditis elegans]
19961	ENU03755	ANI61C5215: 27-54 4956..3482	27-54	1440-1459	NAP		g1172824	337	57	0.000000	56	11	DNA repair and recombination protein RAD52 ; (X75086) K.lactis Rad52 [Kluyveromyces lactis]
19962	ENU03756	ANI61C9290: 55-86 3960..2484	55-86	1470-1489	NAP		g1237183	434	146	2.00E-53	33	84	(D43773) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]
19963	ENU03757	ANI61C1118 22-53 5:6237..4760	22-53	1438-1457	NAP		g3025028	482	217	2.00E-55	33	83	"hypothetical 47.3 KD protein in OMPX-MOEB intergenic region ; (AE000184) orf, hypothetical protein [Escherichia coli] ; (D90719) ORF_ID:o207#4 [Escherichia coli] ; (D90720) ORF_ID:o207#4 [Escherichia coli] "
19964	ENU03758	ANI61C9356: 23-42 1498..19	23-42	1440-1460	NAP		g3150152	1177	372	e-121	70	78	(AJ006219) clathrin-associated protein [Drosophila melanogaster]
19965	ENU03759	ANI61C3300: 22-41 478..1957	22-41	1440-1459	NAP		g2388977	152	56	0.000000	39	16	(Z98980) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19966	ENU03760	ANI61C7237: 3570..5051	42-63	1451-1481	NAP		g1708578	63	0.000000	006			myo-inositol transporter 1 ; myo-inositol transport protein ITR1 - yeast (Saccharomyces cerevisiae) ; (U33057)
													It1p: myo-inositol transporter; YDR497C; CAI: 0.19 [Saccharomyces cerevisiae]
19967	ENU03761	ANI61C8669: 2812..1331	46-68	1453-1485	NAP		g1176670	262	90	4.00E-17	33	96	hypothetical 37.7 KD protein C08B11.7 in chromosome II ; (Z46676) similar to thiolesterase; cDNA EST yk221d9.5 comes from this gene [Caenorhabditis elegans] (U59421) Band 17 [Gallus gallus]
19968	ENU03762	ANI61C9412: 33..1515	54-74	1471-1494	NAP		g2795769	36	0.0004				dicarboxylic amino acid permease ; dicarboxylic amino acid permease DIP5 - yeast (Saccharomyces cerevisiae) ; (X95802) dicarboxylic amino acids Dip5p permease [Saccharomyces cerevisiae] ; (Z73621)
19969	ENU03763	ANI61C3441: 4345..2860	37-59	1450-1480	NAP		g1706439	1343	469	e-131	56	77	ORF YPL265w [Saccharomyces cerevisiae]
19970	ENU03764	ANI61C5996: 2135..3623	30-55	1454-1475	NAP		g2507070	323	101	1.00E-35	28	93	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
19971	ENU03765	ANI61C3862: 3232..1743	68-95	1495-1515	NAP		g4204312	652	271	1.00E-71	38	42	(AC003027) lclprt seq No definition line found [Arabidopsis thaliana]
19972	ENU03766	ANI61C2424: 2002..510	72-96	1503-1522	NAP		g1723562	778	291	2.00E-81	46	30	probable eukaryotic initiation factor C17C9.03 ; (Z73099) probable initiation factor [Schizosaccharomyces pombe]
19973	ENU03767	ANI61C2430: 934..2426	39-58	1470-1489	NAP		g1399818	863	337	1.00E-96	45	98	(U59234) biotin carboxylase [Synecococcus PCC7942]
19974	ENU03768	ANI61C276:1 620..126	72-94	1505-1524	NAP		g4127990	375	142	5.00E-33	34	83	(AJ006487) propionyl-CoA carboxylase [Homo sapiens]
19975	ENU03769	ANI61C7856: 2906..1412	26-49	1449-1478	NAP		g3702646	458	81	5.00E-26			(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19976	ENU03770	ANI61C1113 3:1690..192	38-57	1476-1495	NAP		g416582	1318	276	e-127			actin-like protein ARP2 ; actin-like protein ACT2 - yeast (Saccharomyces cerevisiae) (strain X2180) ; (X61502)
													actin-like protein [Saccharomyces cerevisiae] ; (Z71781) actin-like protein ACT2 [Saccharomyces cerevisiae] ; (Z74077) ORF YDL029w [Saccharomyces cerevisiae] ; actin-like protein ACT2 [Saccharomyces cerevisiae]
19977	ENU03771	ANI61C1093 5:1563..64	53-79	1480-1510	NAP		g3006137	942	324	9.00E-88	44	53	(AL022299) Cu ⁺⁺ -transporting ATPase [Schizosaccharomyces pombe]
19978	ENU03772	ANI61C3308: 2458..957	58-77	1495-1517	NAP		g1293655	880	347	1.00E-94	41	73	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
19979	ENU03773	ANI61C6810: 6538..8040	32-60	1473-1492	NAP		g138595	57	41	0.02	26	8	Vitellogenin II precursor (major vitellogenin) [contains: lipovitellin I (LVI); phosvitin (PV); lipovitellin II (LVII); YGP40] ; vitellogenin II precursor - chicken ; (X13607)
19980	ENU03774	ANI61C5895: 2179..672	43-63	1474-1504	NAP		g2497105	546	166	4.00E-40	38	97	vitellogenin [Gallus gallus] "hypothetical 43.7 KD protein in OST6-PSP2 intergenic region ; probable membrane protein YML018c - yeast (Saccharomyces cerevisiae) ; (Z46659) unknown orf, len: 393, CAL: 0.13 [Saccharomyces cerevisiae] "
19981	ENU03775	ANI61C9701: 1300..2803	65-84	1501-1526	NAP		g2133295	664	187	2.00E-73	38	96	maackiain detoxification protein 1 - fungus (Nectria haematococca) ; (U35892) predicted flavin-containing mono-oxygenase [Nectria haematococca]
19982	ENU03776	ANI61C3368: 5624..4118	22-41	1467-1486	NAP		g417337		77	3.00E-13			nuclear polyadenylated RNA-binding protein NAB2 ; RNA-binding protein NAB2 - yeast (Saccharomyces cerevisiae) ; (L10288) RNA-binding protein [Saccharomyces cerevisiae] ; (Z72644) ORF YGL122c [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
19983	ENU03777	ANI61C7316: 3717..2210	28-47	1463-1493	NAP		g2132651	161	2.00E-45				probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae); (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
19984	ENU03778	ANI61C4256: 52-71	28-47	1497-1517	NAP		g2143220	1826	681	0	79	93	(Y13338) cellular serine proteinase [Aspergillus fumigatus]
19985	ENU03779	2933..1425	22-53	1458-1489	NAP		g3328946	155	80	4.00E-14	34	30	(AE001323) S13 Ribosomal Protein [Chlamydia trachomatis]
19986	ENU03780	528..1019	22-48	1472-1492	NAP		g2132374	501	205	5.00E-52	34	57	p-aminobenzoate synthase (EC 4.1.3.-) - yeast (Saccharomyces cerevisiae); (Z71648) ORF YNR033w [Saccharomyces cerevisiae]
19987	ENU03781	ANI61C1036 47-65	47-65	1499-1520	NAP		g4502041	818	147	1.00E-75	44	83	"aldehyde dehydrogenase 6; aldehyde dehydrogenase 6; aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 6 precursor, salivary - human; (U07919) aldehyde dehydrogenase 6 [Homo sapiens]"
19988	ENU03782	ANI61C1098 26-51	26-51	1483-1503	NAP		g152650	54	0.000000				(M95300) csgA [Stigmatella aurantiaca]
19989	ENU03783	1:2404..3923	71-90	1525-1549	NAP		g1470090	243	64	0.000000	30	72	(U62028) negative acting factor [Fusarium solani f. sp. pisi]
19990	ENU03784	1616..95	68-88	1520-1547	NAP		g729186	474	194	2.00E-51	38	52	serine/threonine-protein kinase COT-1; probable protein kinase cot-1 (EC 2.7.1.-) - Neurospora crassa
19991	ENU03785	ANI61C9152: 61-80	61-80	1522-1541	NAP		g2133315	914	330	2.00E-89	45	94	"met-10+ protein - Neurospora crassa; (L40806) Restriction enzyme inactivation of met-10 complementation in this region. Sequence similarity to S. cerevisiae chromosome VIII cosmid 9205, accession no. U10556 CDS residues 22627-24126 [Neurospora crassa]; met-10 gene [Neurospora crassa]"
19992	ENU03786	ANI61C800:1 22-56	22-56	1476-1502	NAP		g1708060	1088	179	e-107	53	94	"glutathione reductase (GR) (GRASE); glutathione reductase (NADPH) (EC 1.6.4.2) - yeast (Saccharomyces cerevisiae); (U43281) Grlp, Lpg17p [Saccharomyces cerevisiae]"
19993	ENU03787	ANI61C6075: 72-91	72-91	1535-1554	NAP		g2118296	1531	550	e-159	69	87	glutathione reductase (NADPH) (EC 1.6.4.2) - yeast (Saccharomyces cerevisiae); (U43281) Grlp, Lpg17p [Saccharomyces cerevisiae]"

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19994	ENU03788	ANI61C357:2 251..726	27-47	1491-1510	NAP		g4160574	528	127	3.00E-49	33	83	(AL035226) major facilitator superfamily protein
19995	ENU03789	ANI61C7020: 49-69 6795..5263	49-69	1520-1539	NAP		g1351917	422	68	8.00E-20	41	24	[Schizosaccharomyces pombe] probable amidase ; amidase (EC 3.5.1.4) - yeast (Saccharomyces cerevisiae) ; (Z49701) Amdyp [Saccharomyces cerevisiae]
19996	ENU03790	ANI61C7125: 24-53 1703..166	24-53	1484-1519	NAP		g2826168	67	57	0.000000	45	10	(AB010714) salicylate hydroxylase [Pseudomonas putida]
19997	ENU03791	ANI61C3681: 22-53 2420..2906	22-53	1496-1518	NAP		g3157928	455	152	4.00E-45	38	96	"(AC002131) Similar to fumarylacetoacetate hydrolase, gb L41670 from Emericella nidulans. [Arabidopsis thaliana] "
19998	ENU03792	ANI61C3681: 24-55 2420..2906	24-55	1498-1520	NAP		g3157928	455	152	4.00E-45	38	96	"(AC002131) Similar to fumarylacetoacetate hydrolase, gb L41670 from Emericella nidulans. [Arabidopsis thaliana] "
19999	ENU03793	ANI61C59:17 23-42 35..3274	23-42	1501-1520	NAP		g2492825	374	141	7.00E-41	32	88	"N-carbamyl-L-amino acid amidohydrolase ; N-carbamyl-L-amino acid amidohydrolase (EC 3.5.-.-) - Bacillus stearothermophilus (strain NS1122A) ; (S67784) N-carbamyl-L-amino acid amidohydrolase [Bacillus stearothermophilus, NS1122A, Peptide, 409 aa] [Bacillus stearothermophilus] "
20000	ENU03794	ANI61C7924: 50-69 618..2163	50-69	1529-1553	NAP		g121146	766	162	5.00E-80	45	94	geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (Dimethylallyltransferase / geranyltransferase / farnesyltransferase ; geranylgeranyl pyrophosphate synthetase - Neurospora crassa ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]
20001	ENU03795	ANI61C2480: 24-43 4201..5746	24-43	1502-1527	NAP		g3738166	561	172	4.00E-50	41	97	"(AL031856) STAM-like protein, VHS domain containing, putative signal transducing adaptor [Schizosaccharomyces pombe] "

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20002	ENU03796	ANI61C3788: 2095..548	72-96	1544-1577	NAP		g1351102	1128	342	4.00E-93	65	57	putative agmatinase precursor (agmatine ureohydrolase) (AUH); (Z68166) unknown
20003	ENU03797	ANI61C7597: 45-64 1548..1	45-64	1527-1550	NAP		g549620	349	122	7.00E-27	33	85	[Schizosaccharomyces pombe] hypothetical 46.5 KD protein in MRS4-DYN1 intergenic region; hypothetical protein YKR053c - yeast (Saccharomyces cerevisiae); (Z28278) ORF YKR053c [Saccharomyces cerevisiae]
20004	ENU03798	ANI61C9849: 24-54 2809..4358	24-54	1513-1531	NAP		g3122249	687	296	3.00E-79	41	97	"D-hydantoinase (dihydropyrimidinase) (DHPASE); dihydropyrimidinase (EC 3.5.2.2) - Bacillus stearothermophilus; (S73773) hydantoinase [Bacillus stearothermophilus, NS1122A, Peptide, 471 aa] [Bacillus stearothermophilus]; hydantoinase [Bacillus stearothermophilus]"
20005	ENU03799	ANI61C1077 8:549..2098	24-43	1512-1531	NAP		g2239243	1343	374	e-103	64	82	(Z97211) probable inosine-5'-monophosphate dehydrogenase [Schizosaccharomyces pombe]
20006	ENU03800	ANI61C1086 6:956..2507	42-62	1521-1551	NAP		g3024434	1475	344	e-151	69	99	26S protease regulatory subunit 6A homolog (TAT-binding protein homolog 1) (TBP-1); (D88663) Tat binding protein 1 [Brassica rapa]
20007	ENU03801	ANI61C821:4 ..1563	25-48	1520-1542	NAP		g1351702	608	149	2.00E-62	35	84	hypothetical 61.1 KD protein C11D3:05 in chromosome I; (Z68166) unknown [Schizosaccharomyces pombe]
20008	ENU03802	ANI61C5992: 47-66 2851..4414	47-66	1547-1568	NAP		g118498	1272	437	e-142	54	96	"aldehyde dehydrogenase (ALDDH); aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) - Emericella nidulans; (M16197) aldehyde dehydrogenase [Emericella nidulans]; dehydrogenase,aldehyde [Emericella nidulans]"
20009	ENU03803	ANI61C5357: 57-76 587..2151	57-76	1560-1579	NAP		g135407	1608	455	e-156	73	94	tubulin alpha-2 chain; tubulin alpha-2 chain - Emericella nidulans (AI031543) stxbp-unc-18-sec1 family protein [Schizosaccharomyces pombe]
20010	ENU03804	ANI61C1612: 22-57 3035..1470	22-57	1522-1545	NAP		g3581893	1005	336	e-112	51	70	

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20011	ENU03805	ANI61C2135: 1917..345	32-52	1543-1562	NAP		g2493387	804	261	1.00E-93	43	96	probable sterigmatocystin biosynthesis p450 monooxygenase STCS (cytochrome P450 59) ; (U34740) putative p450 monooxygenase [Emericella nidulans] (AF130355) Pad-1 [Neurospora crassa]
20012	ENU03806	ANI61C486:1 35-58 932..359	35-58	1537-1566	NAP		g4530579	1474	483	e-151	71	79	"(AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda] "
20013	ENU03807	ANI61C1046 26-46 1:4647..6221	26-46	1532-1558	NAP		g2245570	437	89	1.00E-36	32	63	PRL1/PRL2-like protein ; (AB004535)
20014	ENU03808	ANI61C385:3 45-64 898..2323	45-64	1558-1578	NAP		g3122623	1340	511	e-144	56	98	PRL1 [Schizosaccharomyces pombe]
20015	ENU03809	ANI61C4744: 22-47 844..2420	22-47	1534-1556	NAP		g2370467	1132	441	e-123	49	75	(Z98951) hypothetical protein [Schizosaccharomyces pombe] ; (AL031546) putative dna-binding protein [Schizosaccharomyces pombe]
20016	ENU03810	ANI61C1035 70-89 6:1872..2880	70-89	1583-1606	NAP		g1171477	1118	724	0	72	95	(D49827) alpha-mannosidase [Aspergillus phoenicis]
20017	ENU03811	ANI61C5378: 22-52 1679..1447	22-52	1540-1559	NAP		g2497056	557	202	5.00E-51	44	35	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
20018	ENU03812	ANI61C9607: 25-46 84..1664	25-46	1544-1563	NAP		g2105061	180	85	2.00E-15	30	40	(Z95436) hypothetical protein Rv3633 [Mycobacterium tuberculosis]
20019	ENU03813	ANI61C1014 36-55 5:1689..1205	36-55	1552-1574	NAP		g3219948	474	123	4.00E-43	33	96	hypothetical 54.2 KD TRP-ASP repeats containing protein C29A4.08C in chromosome I ; (Z97210) beta-transducin [Schizosaccharomyces pombe]
20020	ENU03814	ANI61C1559: 64-82 2644..1063	64-82	1585-1604	NAP		g2851498	1058	386	e-109	49	90	serine/threonine-protein kinase PRP4 ; (L10739) serine/threonine kinase [Schizosaccharomyces pombe] ; (AL031532) mRNA splicing-associated serine-threonine protein kinase [Schizosaccharomyces pombe]
20021	ENU03815	ANI61C7:410 25-46 1..5688	25-46	1548-1570	NAP		g1723245	419	131	1.00E-29	28	89	hypothetical 51.9 KD protein C27F1.04C in chromosome I ; (Z69368) unknown [Schizosaccharomyces pombe]

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20022	ENU03816	ANI61C318:8	22-41	1548-1572	NAP		g1063421	412	95	5.00E-28	27	89	(L48797) toxin pump [Cochliobolus carbonum]
20023	ENU03817	ANI61C7785: 53-72	53-72	1583-1604	NAP		g4507707	330	144	1.00E-33	37	60	thiosulfate sulfurtransferase (rhodanese); 3-mercapotpyruvate sulfurtransferase (MST); thiosulfate sulfurtransferase (EC 2.8.1.1) - human; (X59434) rhodanese [Homo sapiens]
20024	ENU03818	ANI61C1069	33-52	1557-1585	NAP		g2833225	1329	275	e-113	60	85	Nucleolar protein NOP5; hypothetical protein YOR310c - yeast (Saccharomyces cerevisiae); (X90565) orf 06108 [Saccharomyces cerevisiae]; (Z75217) ORF YOR310c [Saccharomyces cerevisiae]; (AF056070) nucleolar protein Nop5p [Saccharomyces cerevisiae]; putative transporter YGR260W; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae); (Z73044) ORF YGR260w [Saccharomyces cerevisiae]; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
20025	ENU03819	ANI61C7618: 34-54	34-54	1570-1589	NAP		g1723769	363	82	3.00E-15	29	81	putative transporter YGR260W; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae); (Z73044) ORF YGR260w [Saccharomyces cerevisiae]; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
20026	ENU03820	ANI61C6527: 22-48	22-48	1557-1579	NAP		g2414603	443	89	3.00E-31	38	99	aminoalcoholphosphotransferase [Schizosaccharomyces pombe]
20027	ENU03821	ANI61C30:82	23-47	1561-1580	NAP		g3668171	2167	531	e-150	69	41	(AB006052) RNA polymerase I second-largest subunit [Neurospora crassa]
20028	ENU03822	ANI61C1185: 69-88	69-88	1599-1629	NAP		g3219963	1564	235	e-135	53	78	"putative GTP-binding protein C1B3.04C; (Z98598) putative gtp binding protein, gtpase; Elongation factor Tu family [Schizosaccharomyces pombe]"
20029	ENU03823	ANI61C1894: 36-64	36-64	1566-1598	NAP		g3650387	510	170	3.00E-41	35	20	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe]
20030	ENU03824	ANI61C1794: 22-49	22-49	1570-1594	NAP		g1870209	1025	324	e-102	42	94	(AC000133) ORF [Emmericella nidulans]
20031	ENU03825	ANI61C7709: 43-64	43-64	1594-1618	NAP		g4507375	255	65	8.00E-19	30	84	tubulin-specific chaperone e; (U61232) cofactor E [Homo sapiens]
20032	ENU03826	ANI61C4819: 62-82	62-82	1609-1637	NAP		g3766367	1267	338	e-125	52	97	(AL031907) trp-asp repeat containing protein [Schizosaccharomyces pombe]

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20033	ENU03827	ANI61C6841: 4850..6468	26-47	1581-1602	NAP		g3702646	681	280	2.00E-74	33	98	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
20034	ENU03828	ANI61C9043: 22-45 645..2268	22-45	1584-1603	NAP		g1346290	750	282	2.00E-80	40	82	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
20035	ENU03829	ANI61C3809: 48-76 3146..4771	48-76	1603-1631	NAP		g2956784	549	228	1.00E-58	44	79	(AL022103) hypothetical protein [Schizosaccharomyces pombe]
20036	ENU03830	ANI61C896:1 34-54 3..1638	34-54	1592-1617	NAP		g114555	2077	439	0	86	83	"ATP synthase beta chain, mitochondrial precursor ; H+-transporting ATP synthase (EC 3.6.1.34) beta chain - Neurospora crassa ; (X53720) F(1)-ATPase beta-subunit precursor (519 AA) [Neurospora crassa] ; (M84192) mitochondrial ATPase beta-subunit [Neurospora crassa]"
20037	ENU03831	ANI61C1139 22-53 6:500..2128	22-53	1588-1608	NAP		g1346290	456	125	3.00E-50	31	88	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
20038	ENU03832	ANI61C6331: 59-78 7851..6217	59-78	1630-1651	NAP		g126694	225	103	4.00E-21	27	62	Maltose permease MAL6T (maltose transport protein MAL6T) ; maltose transport protein MAL61 - yeast (Saccharomyces cerevisiae) ; (X17391)
20039	ENU03833	ANI61C4568: 37-56 2950..1316	37-56	1598-1629	NAP		g2495096	629	250	2.00E-65	39	98	maltose permease [Saccharomyces cerevisiae] ; (M27823) maltose permease [Saccharomyces carlsbergensis] glutathione synthetase (glutathione synthase) (GSH synthetase) (GSH-S) ; hypothetical protein YOL049w - yeast (Saccharomyces cerevisiae) ; (Z74791)
20040	ENU03834	ANI61C1188: 72-91 4935..6572	72-91	1645-1667	NAP		g4049539	85	57	0.000000	34	18	ORF YOL049w [Saccharomyces cerevisiae] ; (Y13804) Glutathione synthetase [Saccharomyces cerevisiae] (AL034564) hypothetical protein [Schizosaccharomyces pombe]
20041	ENU03835	ANI61C3095: 61-80 1688..3330	61-80	1636-1656	NAP		g2267601	723	233	1.00E-74	34	93	(AF009417) cytochrome P450 [Myrothecium roridum]

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20042	ENU03836	ANI61C9933: 1111..2751	28-47	1607-1626	NAP		g127289	1692	458	0	73	99	mitochondrial processing peptidase beta subunit precursor (beta-MPP) (ubiquinol-cytochrome C reductase complex CORE protein I) ; mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - Neurospora crassa ; (M20928) processing enhancing protein precursor [Neurospora crassa] (AL031179) hypothetical protein [Schizosaccharomyces pombe] aldehyde dehydrogenase (ALDDH) ; (M32351) aldehyde dehydrogenase [Aspergillus niger] probable membrane protein YLL031c - yeast (Saccharomyces cerevisiae) ; (Z73136) ORF YLL031c [Saccharomyces cerevisiae] (Z98529) mating and morphogenesis protein Sed1p. [Schizosaccharomyces pombe] putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe] Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] potential transcriptional adaptor ; probable transcriptional adaptor ADA2 - yeast (Saccharomyces cerevisiae) ; (M95396) ADA2 [Saccharomyces cerevisiae] ; (U33007) Ada2p: probable transcriptional adaptor; YDR448W; CAI: 0.12 [Saccharomyces cerevisiae] (AL021815) hypothetical protein [Schizosaccharomyces pombe] ; [Schizosaccharomyces pombe] (AL035675) adducin N terminal domain protein [Schizosaccharomyces pombe]
20043	ENU03837	ANI61C2470: 52-71	52-71	1632-1651	NAP		g3395585	735	129	5.00E-65	49	86	
20044	ENU03838	ANI61C1647: 72-94	72-94	1651-1672	NAP		g1169291	1259	277	e-116	54	96	
20045	ENU03839	ANI61C349:3 22-48	22-48	1594-1622	NAP		g2132652	1240	222	7.00E-57	34	41	
20046	ENU03840	ANI61C6338: 23-47	23-47	1606-1625	NAP		g2330697	400	52	0.000000 2	24	43	
20047	ENU03841	ANI61C9837: 69-89	69-89	1649-1675	NAP		g1351714	588	146	2.00E-60	33	94	
20048	ENU03842	ANI61C54:20 23-46	23-46	1603-1631	NAP		g3915154	602	156	4.00E-68	33	96	
20049	ENU03843	ANI61C7279: 30-60	30-60	1621-1641	NAP		g399006	844	232	3.00E-64	48	98	
20050	ENU03844	ANI61C1109 44-64	44-64	1639-1657	NAP		g2879861		59	1.00E-10			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20051	ENU03845	ANI61C1085 9:1847..3502	46-66	1640-1659	NAP		g2132080	918	230	1.00E-71	37	29	hypothetical protein YOR191w - yeast (Saccharomyces cerevisiae) ; (Z75099) ORF YOR191w [Saccharomyces cerevisiae]
20052	ENU03846	ANI61C1145 2:1..1658	22-50	1616-1637	NAP		g3560233	582	182	5.00E-45	32	54	(AL031530) putative b-zip transcription factor [Schizosaccharomyces pombe]
20053	ENU03847	ANI61C8860: 40-61 105..700	40-61	1638-1657	NAP		g3184114	344	61	0.000000	34	17	(AL023780) hypothetical protein [Schizosaccharomyces pombe]
20054	ENU03848	ANI61C3943: 50-69 1430..1779	50-69	1647-1668	NAP		g3874345	84	48	0.0001			(Z81035) predicted using Genefinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes from...
20055	ENU03849	ANI61C6208: 51-70 1216..2876	51-70	1650-1669	NAP		g4502169	673	189	4.00E-69	34	95	unknown ; (U50939) amyloid precursor protein-binding protein 1 [Homo sapiens] ; (AC004638) amyloid precursor protein-binding protein 1 (APP-B1) [Homo sapiens]
20056	ENU03850	ANI61C9150: 23-44 851..2511	23-44	1606-1641	NAP		g1870209	2694	1027	0	94	99	(AC000133) ORF [Emericella nidulans]
20057	ENU03851	ANI61C1229: 23-44 6807..8467	23-44	1606-1641	NAP		g1870209	2917	1107	0	99	99	(AC000133) ORF [Emericella nidulans]
20058	ENU03852	ANI61C6693: 24-47 4549..2888	24-47	1621-1642	NAP		g3702646		66	2.00E-29			(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
20059	ENU03853	ANI61C5910: 67-95 3284..3411	67-95	1665-1686	NAP		g4493738		35	1.3			"(AL034358) predicted using hexExon; L4830.1, Hypothetical protein, len: 1107 [Leishmania major]"
20060	ENU03854	ANI61C5282: 42-69 3179..1518	42-69	1641-1661	NAP		g3258635	526	218	3.00E-60	32	97	(AF041049) 4-coumarate:CoA ligase [Populus tremuloides]
20061	ENU03855	ANI61C1045 22-47 8:6523..6683	22-47	1621-1643	NAP		g1255728	1081	195	1.00E-94	56	96	(U33265) complement fixation antigen [Coccidioides immitis] ; (U51271) complement-fixation antigen [Coccidioides immitis]

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20062	ENU03856	ANI61C1000: 23-48 4222..2557		1619-1645	NAP		g2498883	821	363	2.00E-99	43	50	Spliceosome associated protein 145 (SAP 145) (SF3B150) ; (U41371) spliceosome associated protein [Homo sapiens]
20063	ENU03857	ANI61C4380: 38-59 1178..2844		1643-1662	NAP		g2791647	700	168	3.00E-78	41	90	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis] (Z99120) yuII [Bacillus subtilis]
20064	ENU03858	ANI61C6812: 25-44 2103..437		1623-1650	NAP		g2635698	234	74	3.00E-25	37	49	"vacuolar ATP synthase catalytic subunit A (V-ATPase 67 KD subunit) ; H+-transporting ATPase (EC 3.6.1.35), vacuolar, 67K chain - Neurospora crassa ; (J03955) vacuolar ATPase vma-1 [Neurospora crassa] "
20065	ENU03859	ANI61C6552: 60-79 1967..299		1666-1686	NAP		g137461	2306	363	0	80	80	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous] hypothetical ABC transporter ATP-binding protein YHES ; (U18997) ORF_o637 [Escherichia coli] ; (AE000411) putative ATP-binding component of a transport system [Escherichia coli]
20066	ENU03860	ANI61C5299: 61-81 1205..2876		1671-1690	NAP		g2804298	813	261	2.00E-88	38	94	(AL033385) cadmium resistance protein [Schizosaccharomyces pombe]
20067	ENU03861	ANI61C4054: 31-50 1151..2824		1644-1662	NAP		g1176239	470	207	2.00E-52	36	62	(M35237) argininosuccinate synthetase (ARG1; E.C. 6.8.4.5) [Saccharomyces cerevisiae]
20068	ENU03862	ANI61C7785: 27-47 3418..5091		1639-1658	NAP		g3850071	823	260	3.00E-74	48	56	alg2 protein ; (U40857) AIG2 [Arabidopsis thaliana]
20069	ENU03863	ANI61C9135: 40-59 2422..4097		1654-1673	NAP		g171085	1225	276	e-121	66	96	hypothetical protein YDL201w - yeast (Saccharomyces cerevisiae) ; (X99000) ORF D1075 [Saccharomyces cerevisiae] ; (Z74249) ORF YDL201w [Saccharomyces cerevisiae]
20070	ENU03864	ANI61C1100: 22-48 2732..1056		1623-1656	NAP		g1703220	57	38	0.2	30	38	Major facilitator superfamily protein [Schizosaccharomyces pombe]
20071	ENU03865	ANI61C6528: 23-43 30..1710		1641-1660	NAP		g2131358	588	166	3.00E-40	52	28	
20072	ENU03866	ANI61C1117: 22-54 5555..7234		1638-1659	NAP		g3560142	651	167	2.00E-40	31	83	

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20073	ENU03867	ANI61C8874: 2557..877	49-76	1667-1687	NAP		g1170324	1662	422	e-170	56	64	Heavy metal tolerance protein precursor ; vacuolar membrane protein HMT1 - fission yeast (Schizosaccharomyces pombe) ; (Z14055) HMT1 [Schizosaccharomyces pombe] "ankyrin, erythrocyte - mouse ; (X69063) erythroid ankyrin [Mus musculus] " (AJ223630) homocitrate synthase [Penicillium chrysogenum] "hypothetical 23.6 KD protein C23C11.13C in chromosome I ; (Z98559) SPAC23C11.13c; len:206aa; similar eg. to YJR133W, Y19B_yeast, P47165, hypothetical 23.7 kd protein, (209aa), fasta scores, opt:737, E(0;0, (59.0% identity in 200 aa overlap) [Schizosaccharomyces pombe] " [AL035076) putative carboxylesterase-lipase family member [Schizosaccharomyces pombe] (AF010145) hexose transporter [Aspergillus parasiticus] unknown ; (U50939) amyloid precursor protein-binding protein 1 [Homo sapiens] ; (AC004638) amyloid precursor protein-binding protein 1 (APP-B1) [Homo sapiens] (AB003102) 26S proteasome subunit p44.5 [Homo sapiens] (Z50044) similar to phenylalanyl-tRNA synthetase; cDNA EST EMBL:T01401 comes from this gene; cDNA EST yk303c5.3 comes from this gene; cDNA EST yk452d5.3 comes from this gene; cDNA EST yk...
20074	ENU03868	ANI61C9789: 22-55 3347..5030	22-55	1630-1663	NAP		g543187		46	0.000003			
20075	ENU03869	ANI61C5161: 22-52 880..2565	22-52	1645-1664	NAP		g4165570	1971	551	0	86	99	
20076	ENU03870	ANI61C6798: 25-45 3320..5007	25-45	1650-1670	NAP		g3183352	490	104	2.00E-32	64	26	
20077	ENU03871	ANI61C2287: 26-54 340..2028	26-54	1652-1672	NAP		g4107289	569	237	1.00E-61	35	96	
20078	ENU03872	ANI61C903:1 23-43 894..206	23-43	1650-1669	NAP		g2306977	1793	432	e-176	72	98	
20079	ENU03873	ANI61C6208: 25-54 1181..2876	25-54	1659-1678	NAP		g4502169	673	189	5.00E-72	35	97	
20080	ENU03874	ANI61C7715: 60-84 3303..1604	60-84	1698-1717	NAP		g1945609	951	328	5.00E-89	55	65	
20081	ENU03875	ANI61C5156: 22-55 3261..1560	22-55	1648-1681	NAP		g3876233	1161	223	e-112	48	83	

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20082	ENU03876	ANI61C5447: 30-49 2892..1180		1682-1701	NAP		g2493011	1294	434	e-145	48	33	probable calcium-transporting ATPase 8 ; probable membrane protein YMR162c - yeast (Saccharomyces cerevisiae) ; (Z49705) unknown [Saccharomyces cerevisiae] (U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]
20083	ENU03877	ANI61C7051: 34-63 2926..1213		1686-1705	NAP		g1778093	334	134	4.00E-40	27	89	"isocitrate dehydrogenase [NAD], mitochondrial subunit 2 precursor (isocitric dehydrogenase) (NAD+-specific ICDH) ; isocitrate dehydrogenase (NAD+) (EC 1.1.1.41) chain IDH2 precursor - yeast (Saccharomyces cerevisiae) ; (M74131) isocitrate dehydrogenase kinase/phosphatase [Saccharomyces cerevisiae] ; (X94335) YOR3326w [Saccharomyces cerevisiae] ; (Z75043) ORF YOR136w [Saccharomyces cerevisiae] "
20084	ENU03878	ANI61C1717: 55-76 86..183		1708-1728	NAP		g124159	1022	205	e-107			(Y17243) cytochrome P450 [Gibberella fujikuroi]
20085	ENU03879	ANI61C5779: 22-54 1281..2998		1677-1696	NAP		g4127832	513	163	2.00E-51	29	97	Recessive suppressor of secretory defect ; RSD1 protein - yeast (Saccharomyces cerevisiae) ; (X75951) RSD1 (SAC1) [Saccharomyces cerevisiae] ; (Z28212) ORF YKL212w [Saccharomyces cerevisiae] ; (X51672) recessive suppressor of secretory defect [Saccharomyces cerevisiae] ; RSD1 gene [Saccharomyces cerevisiae]
20086	ENU03880	ANI61C2392: 28-48 100..1817		1683-1702	NAP		g417726	667	179	7.00E-71			putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
20087	ENU03881	ANI61C9372: 22-56 155..1872		1666-1697	NAP		g1723769	297	92	8.00E-18	27	88	

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20088	ENU03882	ANI61C54:20 34..2093	22-51	1663-1698	NAP		g3915154	602	156	1.00E-67	33	99	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20089	ENU03883	ANI50C2738 9_1:83..1802	24-46	1682-1701	NAP		g114303		300	e-125	47	53	Calcium-transporting ATPase 3 ; Ca2+-transporting ATPase (EC 3.6.1.38) - fission yeast (Schizosaccharomyces pombe) ; (J05634) Ca-2+-ATPase (cta3) [Schizosaccharomyces pombe] ; (AL021816) calcium-transporting atpase 3 [Schizosaccharomyces pombe]
20090	ENU03884	ANI61C6494: 1725..3	48-67	1706-1726	NAP		g125349	591	277	2.00E-73	40	46	Carboxypeptidase KEX1 precursor (carboxypeptidase D) ; KEX1 protein precursor - yeast (Saccharomyces cerevisiae) ; (M17231) carboxypeptidase B-like peptide [Saccharomyces cerevisiae] ; (Z72725) ORF YGL203c [Saccharomyces cerevisiae]

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20091	ENU03885	ANI61C1084 3:757..2477	33-52	1689-1711	NAP		g2914624	152	9.00E-39				"Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl[cyclo-7[(2r)-(N-Valyl) Amino]-2-(Hydroxyl-(1s)-1-Methoxycarbonyl-2-Phenylethoxy) Phosphinyloxy-Ethyl]-1-Naphthaleneacetamide] Sodium Sa... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl (2s)-[1-(((N-Formyl)-L-Valyl)amino-2-(2-Naphthyl)ethyl) Hydroxyphosphinyloxy]-3-Phenylpropanoate, Sodium Salt Hydrolase, Penicillopepsin,... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Inhibitor: Methyl (2s)-[1-Valyl)aminomethyl) Hydroxyphosphinyloxy]-3-Phenylpropanoate, Sodium Salt Hydrolase, Penicillopepsin... ; Acid Proteinase (Penicillopepsin) (E.C.3.4.23.20) Complex With Phosphonate Macrocyclic Inhibitor: Methyl[cyclo-7[(2r)-(N-Valyl)amino)-2-(Hydroxyl-(1s)-1-Methoxycarbonyl-2-Phenylethoxy) Phosphinyloxy-Ethyl]-1-Naphthaleneacetamid..."
20092	ENU03886	ANI61C7717: 3275..4997	61-80	1722-1741	NAP		g548494	1662	539	0	61	94	Phosphoglucumutase 2 (glucose phosphomutase 2) (PGM 2) ; phosphoglucumutase (EC 5.4.2.2) PGM2 - yeast (Saccharomyces cerevisiae) ; (X74823) phosphoglucumutase [Saccharomyces cerevisiae] ; (U09499) phosphoglucumutase [Saccharomyces cerevisiae] ; (Z49702) Pgm2p [Saccharomyces cerevisiae]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20093	ENU03887	ANI61C6918: 22-49 338..2061	22-49	1683-1703	NAP		g4154078	253	122	7.00E-27	29	55	(AL035161) putative efflux protein [Streptomyces coelicolor]
20094	ENU03888	ANI61C593:6 71-90 2..1786	71-90	1723-1753	NAP		g731613	558	196	3.00E-49	32	88	hypothetical 60.6 KD protein in CBP2-SSBR1 intergenic region; hypothetical protein YHL036w - yeast (Saccharomyces cerevisiae); (U11583) Small region of weak similarity to ectopic retrovirus receptor [Saccharomyces cerevisiae]
20095	ENU03889	ANI61C1065: 55-79 2137..413	55-79	1718-1737	NAP		g4218005	95	59	0.000000			(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
20096	ENU03890	ANI61C3446: 72-92 82..1810	72-92	1730-1756	NAP		g585356	268	61	1.00E-15	32	40	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase); kduD protein - Erwinia chrysanthemi; (X62073) 2-keto-3-deoxygluconate oxydoreductase [Erwinia chrysanthemi]
20097	ENU03891	ANI61C8444: 22-54 1125..2855	22-54	1691-1710	NAP		g4160583	626	273	2.00E-72	47	58	(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]
20098	ENU03892	ANI61C1118 69-89 7:1981..250	69-89	1738-1758	NAP		g3876093	650	148	5.00E-43	40	77	(Z69635) cDNA EST yk472e10.5 comes from this gene; cDNA EST yk473c9.5 comes from this gene; cDNA EST yk472e10.3 comes from this gene [Caenorhabditis elegans]
20099	ENU03893	ANI61C6296: 65-84 2207..2685	65-84	1741-1760	NAP		g1711561	535	59	1.00E-12	34	37	Sugar transporter STL1; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae); (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20100	ENU03894	ANI61C1948: 23-52 6..1744	23-52	1695-1719	NAP		g2250699	289	128	1.00E-28	36	16	(AB001517) PWP2 protein [Homo sapiens]
20101	ENU03895	ANI61C7713: 23-43 3728..1986	23-43	1703-1722	NAP		g2293058	324	94	4.00E-21	33	93	(AJ000318) putative RNA-binding protein [Schizosaccharomyces pombe]; (AL022304) putative rna-binding protein. [Schizosaccharomyces pombe]
20102	ENU03896	ANI61C884:1 50-70 177..2919	50-70	1727-1750	NAP		g2388969	162	76	5.00E-13	30	50	(Z98979) hypothetical protein [Schizosaccharomyces pombe]

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20103	ENU03897	ANI61C6290: 2282..538	66-85	1748-1768	NAP		g4103070	597	277	2.00E-73	45	37	(AF020705) protein kinase homolog [Schizosaccharomyces pombe]
20104	ENU03898	ANI61C8572: 24-44		1710-1729	NAP		g2388980	1225	233	5.00E-84	40	62	(Z98980) hypothetical protein [Schizosaccharomyces pombe]
20105	ENU03899	ANI61C1026 71-106 0:301..2051		1757-1778	NAP		g2132053	568	237	1.00E-61	46	49	hypothetical protein YOR091w - yeast (Saccharomyces cerevisiae) ; (X94335) YOR3160w [Saccharomyces cerevisiae] ; (Z74999) ORF YOR091w [Saccharomyces cerevisiae]
20106	ENU03900	ANI61C9080: 43-62		1726-1751	NAP		g2258125	399	87	2.00E-33	27	97	(Z83828) AmMst-1 [Amanita muscaria]
20107	ENU03901	5119..3369 ANI61C9442: 39-58 1885..129		1734-1753	NAP		g3881018	389	210	3.00E-53	34	79	(AL032621) similar to Acyl-CoA dehydrogenase; cDNA EST EMBL:D75425 comes from this gene; cDNA EST EMBL:M89392 comes from this gene; cDNA EST EMBL:M89303 comes from this gene; cDNA EST EMBL:D27766 comes from this gene; cDNA EST ...
20108	ENU03902	ANI61C498:4 65-84 226..2469		1751-1780	NAP		g3915154	868	304	1.00E-81	39	96	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20109	ENU03903	ANI61C382:6 55-74 514..4757		1744-1770	NAP		g2131246	1035	247	e-119	49	70	EMP70 protein precursor - yeast (Saccharomyces cerevisiae) ; (U53880) Emp70p: P24A protein [Saccharomyces cerevisiae] ; (Z73255) ORF YLR083c [Saccharomyces cerevisiae]
20110	ENU03904	ANI61C2254: 29-48 2069..3837		1736-1755	NAP		g3953471	288	146	3.00E-34	32	35	(AC002328) F22O2.16 [Arabidopsis thaliana]
20111	ENU03905	ANI61C9764: 41-60 4110..2337		1745-1772	NAP		g2132443	124	75	2.00E-12	30	21	probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae) ; (Z74192) ORF YDL144c [Saccharomyces cerevisiae]

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20112	ENU03906	ANI61C9185: 6127..4354	45-65	1753-1776	NAP		g121855	1258	176	2.00E-87			"Exoglucanase II precursor (exocellobiohydrolase II) (CBHII) (1,4-beta-cellobiohydrolase); cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II precursor - fungus (Trichoderma reesei); cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus (Trichoderma viride); (M16190) cellobiohydrolase II [Trichoderma reesei]; cellobiohydrolase II [Trichoderma reesei] "
20113	ENU03907	ANI61C1113 1:3625..4360	50-71	1763-1782	NAP		g543928	697	162	6.00E-59	38	87	Adenylyl cyclase-associated protein (CAP); adenylyl cyclase-associated protein cap - fission yeast (Schizosaccharomyces pombe); (L16577) adenylyl cyclase-associated protein [Schizosaccharomyces pombe] formyltetrahydrofolate DEformylase (formyl-FH(4) hydrolase); formyltetrahydrofolate deformylase (EC 3.5.1.10) - Corynebacterium sp.; (U23955) 10-formyltetrahydrofolate hydrolase [Corynebacterium sp.] (AF067947) contains similarity to NADH oxidase [Caenorhabditis elegans]
20114	ENU03908	ANI61C9049: 33-52 12..1788	33-52	1743-1767	NAP		g2500006	708	289	4.00E-77	52	56	(Z50108) esterase [Streptomyces lividans]
20115	ENU03909	ANI61C1144 71-91 2:3154..2530	71-91	1781-1805	NAP		g3193204	256	65	0.000000	36	19	hypothetical 75.2 KD protein in ACS1-GCV3 intergenic region; probable membrane protein YAL048c - yeast (Saccharomyces cerevisiae); (U12980) Yal048cp [Saccharomyces cerevisiae] (AL034433) hypothetical protein [Schizosaccharomyces pombe] (AF103949) cytochrome P450 alkane hydroxylase [Debaryomyces hansenii] probable membrane protein YLR004c - yeast (Saccharomyces cerevisiae); (Z73176) ORF YLR004c [Saccharomyces cerevisiae]
20116	ENU03910	ANI61C203:2 46-74 141..365	46-74	1756-1780	NAP		g908888	95	55	0.000002	31	27	
20117	ENU03911	ANI61C352:2 45-64 500..4277	45-64	1759-1780	NAP		g731284	1337	475	e-133	47	80	
20118	ENU03912	ANI61C2376: 44-71 3593..1814	44-71	1755-1781	NAP		g4007753	513	166	2.00E-53	33	81	
20119	ENU03913	ANI61C6098: 72-95 2210..429	72-95	1790-1811	NAP		g4557164	805	233	5.00E-83	45	74	
20120	ENU03914	ANI61C1044 44-64 1:1964..182	44-64	1749-1784	NAP		g2132659	404	94	4.00E-29	32	77	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20121	ENU03915	ANI61C1119: 4762..2977	69-88	1793-1812	NAP	g2342601	g2851586	2120	161	1.00E-38	36	5	(X89442) peptide synthetase [Metarhizium anisopliae] repressible alkaline phosphatase precursor ; alkaline phosphatase (EC 3.1.3.1) - yeast (Saccharomyces cerevisiae) ; (U33050) Pho8p: repressible alkaline phosphatase; CAI: 0.16 [Saccharomyces cerevisiae] ; quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans] (AC000133) ORF [Emericella nidulans] hypothetical 45.2 KD GTP-binding protein in TRX1-RTA1 intergenic region ; probable membrane protein YGR210c - yeast (Saccharomyces cerevisiae) ; (Z49133) unknown [Saccharomyces cerevisiae] ; (U40843) ORFS7; Method: conceptual translation supplied by author. [Saccharomyces cerevisiae] ; (Z72995) ORF YGR210c [Saccharomyces cerevisiae] fatty acid amide hydrolase ; (U82535) fatty acid amide hydrolase [Homo sapiens] ; (AF098019) fatty acid amide hydrolase [Homo sapiens] (AL035216) component of chaperonin-containing T-complex (zeta subunit) [Schizosaccharomyces pombe] SEL-10 protein ; (Z79757) Similarity to Candida CDC4 gene (TR:E234056); cDNA EST EMBL:D27699 comes from this gene; cDNA EST EMBL:D27698 comes from this gene; cDNA EST EMBL:D32793 comes from this gene; cDNA EST EMBL:D33271 comes from this gene;
20122	ENU03916	ANI61C9379: 27-47	2592..804	1751-1770	NAP			1085	300	2.00E-84	48	94	
20123	ENU03917	ANI61C8749: 70-89	2659..867	1788-1819	NAP		g131768		118	1.00E-53			
20124	ENU03918	ANI61C1159: 35-68	6201..4408	1751-1786	NAP	g1870209	g1176059	2185	195	2.00E-77	84	61	
20125	ENU03919	ANI61C1488: 24-43	815..2612	1744-1779	NAP			1059	157	e-105			
20126	ENU03920	ANI61C8242: 27-52	2420..623	1763-1782	NAP	g4557575		453	105	2.00E-33	36	87	
20127	ENU03921	ANI61C6145: 58-81	2678..878	1797-1816	NAP	g4160347		1694	549	e-180	69	95	
20128	ENU03922	ANI61C8452: 56-75	35..1841	1790-1820	NAP	g3915881		467	210	2.00E-53	38	30	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20129	ENU03923	ANI61C1699: 22-47 1845..35	1771-1790	1771-1790	NAP	g2983324	578	201	9.00E-51	43	52		(AE000705) hypothetical protein [Aquilifex acolicus]
20130	ENU03924	ANI61C1046 23-49 8:2683..868	1777-1796	1777-1796	NAP	g1084975	522	130	6.00E-68	38	76		"endo-beta-1,6-glucanase - fungus (Trichoderma harzianum) ; (X79197) glucan endo-1,6-beta-glucosidase [Trichoderma harzianum] "
20131	ENU03925	ANI61C7744: 60-79 2111..295	1807-1834	1807-1834	NAP	g2995342	890	206	3.00E-94	52	69		(AL022244) hypothetical protein [Schizosaccharomyces pombe]
20132	ENU03926	ANI61C9735: 61-90 2573..757	1804-1835	1804-1835	NAP	g2495263	2565	473	e-177	75	43		3-hydroxy-3-methylglutaryl-coenzyme A reductase (HMG-CoA reductase) ; (X94307) HMG-CoA-reductase [Gibberella fujikuroi]
20133	ENU03927	ANI61C8580: 22-41 752..2581	1790-1809	1790-1809	NAP	g2956763	936	300	4.00E-87	46	71		(AL022104) kinase-binding protein 1. [Schizosaccharomyces pombe]
20134	ENU03928	ANI61C3143: 28-47 6798..4967	1798-1817	1798-1817	NAP	g127562	437	152	7.00E-36	43	56		hydroxymethylglutaryl-CoA lyase (HMG-CoA lyase) (HL) (3-hydroxy-3-methylglutarate-CoA lyase) ; hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) - Pseudomonas sp ; (M31807) HMG-CoA-lyase (mvaB) [Pseudomonas mevalonii] ; (M24016) HMG-CoA lyase (EC 4.1.3.4) [Pseudomonas mevalonii]
20135	ENU03929	ANI61C7424: 52-71 5243..3411	1822-1842	1822-1842	NAP	g2981103	75	8.00E-25					(AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe] ; transporter Liz1p (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe]
20136	ENU03930	ANI61C7315: 22-47 1047..1914	1793-1812	1793-1812	NAP	g2388904	144	65	2.00E-12	36	14		[Schizosaccharomyces pombe] (Z98974) hypothetical protein [Schizosaccharomyces pombe]
20137	ENU03931	ANI61C4353: 68-90 44..1879	1838-1861	1838-1861	NAP	g2330711	737	282	7.00E-75	43	65		(Z98597) hypothetical protein [Schizosaccharomyces pombe]
20138	ENU03932	ANI61C9080: 37-56 5157..3319	1804-1833	1804-1833	NAP	g2258125	399	87	2.00E-33	26	99		(Z83828) AmMst-1 [Amanita muscaria]
20139	ENU03933	ANI61C8981: 37-56 5134..3296	1812-1833	1812-1833	NAP	g1711565	2232	493	0	64	78		Oligosaccharyl transferase STT3 subunit ; STT3 protein - yeast (Saccharomyces cerevisiae) ; (Z72544) ORF YGL022w [Saccharomyces cerevisiae]

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20140	ENU03934	ANI61C1122: 5430..3592	32-67	1802-1828	NAP		g730721	751	182	9.00E-45	40	99	SCD2 protein ; (U12539) scd2 [Schizosaccharomyces pombe] ; (Z69730) mating and morphogenesis protein [Schizosaccharomyces pombe] (AJ223327) rAsp f 9 [Aspergillus fumigatus]
20141	ENU03935	ANI61C3398: 22-49	22-49	1794-1818	NAP		g2879890	665	276	3.00E-73	49	97	hypothetical 34.4 KD protein in IDS2-MP12 intergenic region ; hypothetical protein YJL145w - yeast (Saccharomyces cerevisiae) ; (X87371) ORF10 [Saccharomyces cerevisiae] ; (Z49420) ORF YJL145w [Saccharomyces cerevisiae]
20142	ENU03936	ANI61C4813: 25-46	25-46	1804-1823	NAP		g1353018	177	103	3.00E-21	33	29	Acetamidase ; amdS protein - Emericella nidulans ; (M16371) acetamidase enzyme [Emericella nidulans]
20143	ENU03937	ANI61C1056 62-85	62-85	1839-1861	NAP		g113701	469	98	8.00E-26	40	68	(U84350) hypothetical hydroxylase a [Amycolatopsis orientalis] (AL035259) conserved hypothetical protein [Schizosaccharomyces pombe] "D14846) endo alpha-1,4 polygalactosaminidase precursor [Pseudomonas sp.]" (AL031786) putative atp dependent ma helicase [Schizosaccharomyces pombe] hypothetical 64.5 KD protein in COX4-GTS1 intergenic region ; probable membrane protein YGL186c - yeast (Saccharomyces cerevisiae) ; (X91489) putative purine-cytosine transport protein [Saccharomyces cerevisiae] ; (Z72708) ORF YGL186c [Saccharomyces cerevisiae]
20144	ENU03938	ANI61C1054 41-60	41-60	1807-1842	NAP		g1872509	256	98	3.00E-19	31	67	hypothetical protein 1 - Pseudomonas cepacia ; (U19883) unknown [Burkholderia cepacia]
20145	ENU03939	ANI61C7623: 33-52	33-52	1809-1836	NAP		g4176557	522	132	2.00E-44	30	73	
20146	ENU03940	ANI61C61:28 69-91	69-91	1854-1876	NAP		g286165	397	191	1.00E-47	41	41	
20147	ENU03941	ANI61C7855: 40-59	40-59	1833-1858	NAP		g3687476	907	161	6.00E-65	42	91	
20148	ENU03942	ANI61C7388: 46-64	46-64	1845-1865	NAP		g1723945	480	144	4.00E-37	32	87	
20149	ENU03943	ANI61C6750: 22-50	22-50	1824-1843	NAP		g2120652		126	5.00E-28	45	42	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20150	ENU03944	ANI61C5845: 867..1270	53-72	1853-1879	NAP		g731893	815	286	3.00E-76	38	97	putative transporter YIL166C; putable membrane protein YIL166c - yeast (Saccharomyces cerevisiae); (Z46921) unknown [Saccharomyces cerevisiae]
20151	ENU03945	ANI61C1049 5:420..2292	22-55	1833-1852	NAP		g1709915	2011	695	0	72	95	phosphoribosylaminimidazolecarboxamide formyltransferase 2 (AICAR transformylase) / IMP cyclohydrolase (inosinase) (IMP synthetase) (ATIC); hypothetical protein YMR120c - yeast (Saccharomyces cerevisiae); (Z49273) unknown [Saccharomyces cerevisiae]
20152	ENU03946	ANI61C9731: 2136..4011	32-52	1843-1864	NAP		g2145376	505	218	1.00E-55	47	33	"(Y09476) YisK [Bacillus subtilis]; (Z99109) similar to 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase [Bacillus subtilis]" (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
20153	ENU03947	ANI61C916:2 201..324	64-82	1866-1899	NAP		g3560142	669	131	9.00E-60	32	95	[Schizosaccharomyces pombe] (AL034490) putative PHD-type zinc finger [Schizosaccharomyces pombe] (Z98602) hypothetical WW domain-containing protein [Schizosaccharomyces pombe]
20154	ENU03948	ANI61C1096 3:673..2552	41-63	1858-1878	NAP		g4008555	305	104	4.00E-32	28	95	(AL023860) short chain dehydrogenase [Schizosaccharomyces pombe]
20155	ENU03949	ANI61C8717: 198..2079	49-70	1865-1887	NAP		g2330816	792	205	3.00E-75	35	64	hypothetical 65.3 KD protein in MAD1-SCY1 intergenic region; probable membrane protein YGL084c - yeast (Saccharomyces cerevisiae); (Z72606) ORF YGL084c [Saccharomyces cerevisiae]
20156	ENU03950	ANI61C532:4 68..1024	32-62	1852-1872	NAP		g3218393	261	125	1.00E-27	35	32	quinase permease (quinase transporter); quinase transport protein - Emericella nidulans; (X13525) quinase permease [Emericella nidulans]
20157	ENU03951	ANI61C9167: 2721..834	22-51	1838-1867	NAP		g1723878	1097	374	e-111	47	92	
20158	ENU03952	ANI61C8749: 2731..841	22-49	1848-1869	NAP		g131768		118	1.00E-53			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20159	ENU03953	ANI61C7362: 2297..402	44-63	1877-1897	NAP		g140371	516	206	2.00E-56	32	95	"hypothetical 58.8 KD protein in GLK1-SRO9 intergenic region ; hypothetical protein YCL038c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL038c, len:528 [Saccharomyces cerevisiae] "
20160	ENU03954	ANI61C1642: 22-48		1848-1877	NAP		g2822399	320	84	1.00E-33	43	37	(AF016485) ORF H1434 [Halobacterium sp. NRC-1] transcription factor TAU 131 KD subunit (TFIIC 131 KD subunit) ; transcription factor IIC chain TFC4 - yeast (Saccharomyces cerevisiae) ; (L12722) transcription factor IIIB 131kDa subunit [Saccharomyces cerevisiae] ; (Z72832) ORF YGR047c [Saccharomyces cerevisiae]
20161	ENU03955	ANI61C1137 40-61		1878-1897	NAP		g464876	363	82	4.00E-31			putative prolyl-TRNA synthetase YHR020W (proline--TRNA ligase (PRORS) ; multifunctional amino acid--tRNA ligase homolog - yeast (Saccharomyces cerevisiae) ; (U10399) Yhr020wp [Saccharomyces cerevisiae] (X05204) arom polypeptide [Emericella nidulans] (AF121000) oxidoreductase protein homolog Oxi [Corynebacterium glutamicum] DNA replication licensing factor MCM6 (P105MCM) ; (D84557) HsMcm6 [Homo sapiens] NEMPA protein precursor ; (U62332) NEMPA [Emericella nidulans] (Z99163) very hypothetical protein [Schizosaccharomyces pombe] (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe] (AL023518) hypothetical protein [Schizosaccharomyces pombe]
20162	ENU03956	ANI61C888:2 24-52		1866-1885	NAP		g731640	1216	392	e-134	58	49	
20163	ENU03957	ANI61C4369: 24-45		1866-1888	NAP		g3834343	3235	888	0	99	38	
20164	ENU03958	ANI61C4856: 45-66		1885-1909	NAP		g4583402	259	55	1.00E-19	32	55	
20165	ENU03959	ANI61C8873: 23-51		1869-1888	NAP		g2497824	1471	324	e-127	47	72	
20166	ENU03960	ANI61C3272: 31-50		1873-1898	NAP		g2499479	2644	481	e-135	97	96	
20167	ENU03961	ANI61C1676: 48-67		1898-1917	NAP		g4584706	300	53	4.00E-10	36	25	
20168	ENU03962	ANI61C2883: 22-45		1874-1893	NAP		g3738200	918	207	4.00E-96	35	65	
20169	ENU03963	ANI61C5338: 69-88		1922-1941	NAP		g3130053	967	277	7.00E-97	45	80	

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20170	ENU03964	ANI61C1051 7:2578..663	54-79	1908-1927	NAP		g3879809	172	85	1.00E-15			(Z47356) similar to protein kinase C substrate; cDNA EST EMBL:M75788 comes from this gene; cDNA EST EMBL:D71530 comes from this gene; cDNA EST EMBL:C08471 comes from this gene; cDNA EST yk427a3.3 comes from this gene; cDNA EST ...; (Z47358) similar to protein kinase C substrate; cDNA EST EMBL:M75788 comes from this gene; cDNA EST EMBL:D71530 comes from this gene; cDNA EST EMBL:C08471 comes from this gene; cDNA EST yk427a3.3 comes from this gene; cDNA EST ... comes from this gene; cDNA EST ... "(AL035085) t-complex protein 1, alpha subunit homolog; chaperonin family [Schizosaccharomyces pombe]" (D45893) acr-2 [Neurospora crassa]
20171	ENU03965	ANI61C8625: 4894..2977	63-82	1919-1938	NAP		g4107478	1900	541	0	73	98	tubulin alpha-2 chain ; tubulin alpha-2 chain - Emericella nidulans
20172	ENU03966	ANI61C1025 8:241..2165	58-78	1910-1940	NAP		g1754596	129	92	1.00E-17	25	72	(AL035259) putative utp--glucose-1-phosphate uridylyltransferase [Schizosaccharomyces pombe]
20173	ENU03967	ANI61C3731: 62-81	62-81	1927-1946	NAP		g135407	1617	592	e-168	97	67	[Schizosaccharomyces pombe] alternatively spliced form (AL009146) [Drosophila melanogaster]
20174	ENU03968	ANI61C7229: 2862..936	50-69	1912-1934	NAP		g4176544	1741	691	0	68	81	(AL031786) hypothetical protein [Schizosaccharomyces pombe]
20175	ENU03969	ANI61C1097 8:9619..11546	22-45	1878-1908	NAP		g2827482		41	0.027			L-amino acid oxidase precursor (LAO) ; L-amino-acid oxidase (EC 1.4.3.2) precursor - Neurospora crassa
20176	ENU03970	ANI61C9827: 1002..2933	22-44	1890-1909	NAP		g3687484	193	79	9.00E-14	38	22	hypothetical protein YDR425w - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr425wp; CAI: 0.15 [Saccharomyces cerevisiae]
20177	ENU03971	ANI61C1125: 1551..3485	29-48	1902-1921	NAP		g129307	885	126	5.00E-55	52	22	Retrovirus-related pol polyprotein from transposon TNT 1-94 [contains: protease ; reverse transcriptase ; endonuclease] ; hypothetical protein - common tobacco ; (X13777) ORF [Nicotiana tabacum]
20178	ENU03972	ANI61C8860: 1235..3176	68-87	1947-1966	NAP		g2131481	271	116	5.00E-25	34	43	
20179	ENU03973	ANI61C3512: 34..159	55-90	1926-1955	NAP		g130582		77	4.00E-13			

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20180	ENU03974	ANI61C9440: 37-58		1908-1938	NAP		g2257503	484	195	1.00E-53	42	52	(AB004535) BEM46 protein [Schizosaccharomyces pombe]
20181	ENU03975	ANI61C4271: 38-57		1919-1939	NAP		g2896767	656	157	8.00E-78	42	51	(AL021899) hypothetical protein Rv2030c [Mycobacterium tuberculosis]
20182	ENU03976	ANI61C8421: 68-90		1942-1969	NAP		g2492615	280	68	2.00E-10	35	26	acetate kinase (acetokinase) ; (X89084) acetate kinase [Corynebacterium glutamicum]
20183	ENU03977	ANI61C3682: 22-45		1900-1926	NAP		g1408257	222	88	2.00E-16	32	16	(U60989) putative transposase [Magnaporthe grisea]
20184	ENU03978	ANI61C4018: 22-51		1896-1926	NAP		g231361	332	167	2.00E-40	38	62	1-aminocyclopropane-1-carboxylate deaminase (ACC deaminase) ; (M73488) 1-aminocyclopropane-1-carboxylate deaminase [Pseudomonas sp.]
20185	ENU03979	ANI61C7081: 22-48		1903-1928	NAP		g2622063	272	99	2.00E-28	32	48	(AE000870) conserved protein [Methanobacterium thermoautotrophicum]
20186	ENU03980	ANI61C1105 22-44		1906-1935	NAP		g1542908		96	1.00E-18			(Z80108) lipI [Mycobacterium tuberculosis]
20187	ENU03981	ANI61C9507: 54-73		1948-1970	NAP		g586354	353	136	4.00E-31	28	88	putative 60.3 KD transcriptional regulatory protein in PRP5-THI2 intergenic region ; probable regulatory protein - yeast (Saccharomyces cerevisiae) ; (Z36108) ORF YBR239c [Saccharomyces cerevisiae]
20188	ENU03982	ANI61C7071: 56-77		1954-1973	NAP		g3281851	707	94	2.00E-18	43	26	(AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]
20189	ENU03983	ANI61C1040 71-95		1979-1999	NAP		g3075511	968	385	e-106	47	82	(AF059534) severin kinase [Dictyostelium discoideum]
20190	ENU03984	ANI61C9829: 35-67		1946-1967	NAP		g4249357	275	92	2.00E-28	31	40	(U22463) T-2 toxin biosynthesis protein; TRI7 [Fusarium sporotrichioides]
20191	ENU03985	ANI61C7972: 40-62		1955-1974	NAP		g2116732	277	68	2.00E-10	34	55	(D85129) bphC [Pseudomonas stutzeri]

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20192	ENU03986	ANI61C6593: 5081..3101	42-61	1956-1980	NAP		g117619	500	230	2.00E-59	28	67	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
20193	ENU03987	ANI61C6331: 53-82	53-82	1981-2001	NAP		g3130051	1240	311	e-132	52	86	(AL023518) conserved hypothetical protein [Schizosaccharomyces pombe] probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae] hypothetical 41.3 KD protein C26F1.12C in chromosome I ; (Z73100) unknown [Schizosaccharomyces pombe] "(S76267) Snq2 homolog=bfr1 [Schizosaccharomyces pombe=fission yeast, Peptide, 1530 aa] [Schizosaccharomyces pombe] "
20194	ENU03988	ANI61C8122: 45-65	45-65	1979-1998	NAP		g2132851	303	122	1.00E-26	29	52	mitochondrial outer membrane protein MMM1 ; mitochondrial outer membrane protein MMM1 - yeast (Saccharomyces cerevisiae) ; (Z73111) ORF YLL006w [Saccharomyces cerevisiae] ; (X91488) L1357/MMM1 protein [Saccharomyces cerevisiae] (AL034567) putative protein [Arabidopsis thaliana] (AL023704) weak similarity to B.subtilis spore outgrowth factor B [Schizosaccharomyces pombe] (AL049609) hypothetical protein [Schizosaccharomyces pombe] [Schizosaccharomyces pombe] (Z97204) hypothetical protein [Schizosaccharomyces pombe]
20195	ENU03989	ANI61C4157: 70-89	70-89	1996-2026	NAP		g1723584	698	234	1.00E-60	48	60	
20196	ENU03990	ANI61C6693: 58-77	58-77	2001-2020	NAP		g913016	651	188	1.00E-46	31	19	
20197	ENU03991	ANI61C7484: 42-61	42-61	1989-2008	NAP		g1709060	437	157	3.00E-37	39	46	
20198	ENU03992	ANI61C1217: 22-45	22-45	1981-2003	NAP		g4049341	402	74	2.00E-37	38	53	
20199	ENU03993	ANI61C314:2 22-47	22-47	1983-2004	NAP		g3169059	1605	207	e-140	57	75	
20200	ENU03994	ANI61C6921: 24-43	24-43	1988-2007	NAP		g4584703	569	214	1.00E-54	29	63	
20201	ENU03995	ANI61C1070 30-49	30-49	1996-2015	NAP		g2226422	2075	744	0	58	97	

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20202	ENU03996	ANI61C9941: 22-51 2745..704		2002-2021	NAP		g401441	1673	263	0	50	85	dolichyl-phosphate-mannose--protein mannosyltransferase 2 ; hypothetical protein YAL023 - yeast (Saccharomyces cerevisiae) ; (L05146) Pmt2p: protein O-D-
20203	ENU03997	ANI61C1146 48-68 2:56..2097		2027-2047	NAP		g4007778	284	166	5.00E-40	30	38	mannosyltransferase [Saccharomyces cerevisiae] ; (L05027) ORF YAL23 [Saccharomyces cerevisiae] (Z69730) similar to RanBP7-importin- beta-Cse1p superfamily
20204	ENU03998	ANI61C6137: 45-68 2940..896		2021-2046	NAP		g3766370	698	129	1.00E-67	39	88	[Schizosaccharomyces pombe] (AL031907) lysyl-trna synthetase [Schizosaccharomyces pombe]
20205	ENU03999	ANI61C3240: 32-52 2321..270		2009-2041	NAP		g2507312	402	141	7.00E-39	56	35	60S ribosomal protein L23A (L25) ; (U44800) ribosomal protein L23a [Puccinia graminis f. sp. avenae] (U89924) protein phosphatase 1 binding protein PTG [Mus musculus] (AL031534) Major facilitator superfamily protein
20206	ENU04000	ANI61C1068 22-54 4:93..2057		2016-2036	NAP		g1888566		73	5.00E-12			[Schizosaccharomyces pombe] (AF015771) putative transcriptional regulator [Magnaporthe grisea] (X97657) serine/threonine kinase [Neurospora crassa]
20207	ENU04001	ANI61C6812: 70-89 2231..4290		2052-2087	NAP		g3560142	479	90	1.00E-37	31	78	hypothetical 143.6 KD protein C26A3.09C in chromosome I ; (Z69240) hypothetical protein [Schizosaccharomyces pombe] "hypothetical zinc metalloproteinase YIL108W ; probable membrane protein YIL108w - yeast (Saccharomyces cerevisiae) ; (Z38125) orf, len: 696, CAI: 0.15 [Saccharomyces cerevisiae] "
20208	ENU04002	ANI50C8879 60-79 1:2468..401		2066-2085	NAP		g2367591		136	5.00E-31	45	71	
20209	ENU04003	ANI61C7903: 36-55 1959..4027		2041-2062	NAP		g1870019	1576	254	e-176	57	97	
20210	ENU04004	ANI61C6374: 39-64 1829..3908		2056-2076	NAP		g1723237	319	103	2.00E-34	38	13	
20211	ENU04005	ANI61C6284: 29-55 4146..6226		2047-2067	NAP		g731856	820	348	9.00E-95	37	92	
20212	ENU04006	ANI61C195:2 67-87 097..16		2080-2106	NAP		g1546072	364	96	2.00E-28	33	14	(U68040) polyketide synthase [Cochliobolus heterostrophus] (AL034490) putative ATP-dependent DNA helicase [Schizosaccharomyces pombe]
20213	ENU04007	ANI61C8249: 28-50 1665..3749		2049-2069	NAP		g4008550	656	154	2.00E-36	34	97	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20214	ENU04008	ANI61C1046 7:3670..1587	22-52	2044-2063	NAP		g2648250		73	7.00E-12			(AE000948) 3-hydroxyacyl-CoA dehydrogenase (hbd-10)
20215	ENU04009	ANI61C8491: 40-59 55..2138	40-59	2062-2081	NAP		g1872502	184	83	5.00E-15	35	29	[Archaeoglobus fulgidus] (U84349) hypothetical hydroxylase a
20216	ENU04010	ANI61C7424: 56-75 1403..3487	56-75	2078-2098	NAP		g2506921	322	66	1.00E-29	42	51	[Amycolatopsis orientalis] "probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613) dioxygenase [Escherichia coli] ; (U73857) dioxygenase [Escherichia coli] ; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli] "
20217	ENU04011	ANI61C1159: 23-44 4526..4419	23-44	2036-2071	NAP		g1870209	2185	353	e-124	84	87	(AC000133) ORF [Emmericella nidulans]
20218	ENU04012	ANI61C378:6 66-85 832..8934	66-85	2098-2126	NAP		g3885836	769	258	1.00E-67	33	91	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
20219	ENU04013	ANI61C5335: 32-52 3871..5977	32-52	2077-2096	NAP		g549736	485	154	2.00E-36	37	52	hypothetical 49.7 KD protein in GIN2-STE3 intergenic region ; hypothetical protein YKL172w - yeast (Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28172) ORF YKL172w [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
20220	ENU04014	ANI61C257:4 29-50 869..2761	29-50	2073-2095	NAP		g586048	1636	431	e-148	54	31	[Saccharomyces cerevisiae] Phosphatidylinositol 4-kinase STT4 (PI4-kinase) (PTDINS-4-kinase) ; probable 1-phosphatidylinositol 4-kinase (EC 2.7.1.67) - yeast (Saccharomyces cerevisiae) ; (D13717) homologous protein to PI3-kinase (STT4) [Saccharomyces cerevisiae] ; (U17247) Sit4p: Phosphatidylinositol-4-kinase [Saccharomyces cerevisiae]
20221	ENU04015	ANI61C8788: 22-55 65..2177	22-55	2067-2092	NAP		g3912968	1229	362	e-128	41	72	alpha-adaptin homolog ; (Y11104) alpha-adaptin [Drosophila melanogaster]
20222	ENU04016	ANI61C6107: 22-48 2158..45	22-48	2067-2093	NAP		g3820614	949	231	e-106	43	84	(AF094516) E1-like protein [Homo sapiens]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20223	ENU04017	ANI61C9256: 2327..214	72-94	2119-2143	NAP		g401172		65	0.000000			Tetracycline resistance protein (transposon TN4351 / TN4400) ; NADP-requiring oxidoreductase - Bacteroides fragilis ; (M37699) tetracycline resistance protein [Transposon Tn4351]
20224	ENU04018	ANI61C6644: 45-64 4295..2181	45-64	2096-2117	NAP		g481285	3041	1143	0	85	98	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger ; (Z26938) NADPH cytochrome P450 oxidoreductase [Aspergillus niger] ; NADPH cytochrome P450 reductase [Aspergillus niger] (AL023777) hypothetical protein [Schizosaccharomyces pombe] (AF094516) E1-like protein [Homo sapiens] phenylalanine ammonia-lyase ; phenylalanine ammonia-lyase (EC 4.3.1.5) - fungus (Rhodosporidium toruloides) (strain CBS14) ; (X51513) phenylalanine ammonia-lyase [Rhodosporidium toruloides] ; (X12702) L-phenylalanine ammonia-lyase [Rhodosporidium toruloides] A-aggutinin attachment subunit precursor ; a-aggutinin core protein AGA1 - yeast (Saccharomyces cerevisiae) ; (M60590) a-aggutinin core subunit [Saccharomyces cerevisiae] ; (Z71659) ORF YNR044w [Saccharomyces cerevisiae]
20225	ENU04019	ANI61C1430: 40-62 5060..2944	40-62	2086-2114	NAP		g3184096	1012	263	e-115	40	98	
20226	ENU04020	ANI61C6107: 30-59 2162..45	30-59	2079-2105	NAP		g3820614	949	231	e-106	43	84	
20227	ENU04021	ANI61C467:4 62-81 1..2175	62-81	2135-2154	NAP		g129593	1039	270	e-115	43	79	
20228	ENU04022	ANI61C6214: 43-62 47..2184	43-62	2113-2137	NAP		g416592		40	0.052			
20229	ENU04023	ANI61C4312: 24-55 3724..1589	24-55	2086-2118	NAP		g585695	208	120	4.00E-26	29	54	pisatin demethylase (cytochrome P450 57A2) ; pisatin demethylase - fungus (Nectria haematococca) ; (X73145) pisatin demethylase [Nectria haematococca]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20230	ENU04024	ANI61C1100 3:1406..3542	22-45	2096-2116	NAP		g731771	453	148	1.00E-47	31	82	"hypothetical 59.7 KD protein in BET1-PAN1 intergenic region ; probable membrane protein YIL001w - yeast (Saccharomyces cerevisiae) ; (Z38062) orf, len: 513, CAI: 0.12 [Saccharomyces cerevisiae]"
20231	ENU04025	ANI61C5348: 29-48 4465..2314	29-48	2115-2138	NAP		g2501339	2759	813	0	80	99	Copper amine oxidase 1 ; (U31869) copper amine oxidase [Aspergillus niger]
20232	ENU04026	ANI61C9151: 37-59 807..2961	37-59	2129-2149	NAP		g2959373	297	137	2.00E-32	34	62	(AL022117) hypothetical protein [Schizosaccharomyces pombe]
20233	ENU04027	ANI61C9700: 70-89 1239..3393	70-89	2161-2182	NAP		g2435522	619	164	9.00E-73	38	72	(AF024504) contains similarity to other AMP-binding enzymes [Arabidopsis thaliana]
20234	ENU04028	ANI61C9533: 54-75 108..2268	54-75	2153-2172	NAP		g2130244	120	46	0.001	39	31	hypothetical protein - fission yeast (Schizosaccharomyces pombe) (fragment)
20235	ENU04029	ANI61C1143 6:4771..6934	58-77	2159-2179	NAP		g4033481	304	148	1.00E-34	33	33	putative tartrate transporter ; (U32375) membrane protein [Agrobacterium vitis]
20236	ENU04030	ANI61C1020 8:5667..3503	29-52	2127-2151	NAP		g4007795	1053	407	e-115	34	55	(AL034463) putative nuclear envelope pore membrane protein [Schizosaccharomyces pombe]
20237	ENU04031	ANI61C8814: 22-57 3337..1159	22-57	2130-2157	NAP		g2226427	1130	318	e-120	44	91	(Z97204) hypothetical protein [Schizosaccharomyces pombe]
20238	ENU04032	ANI61C5857: 23-43 2257..2151	23-43	2139-2158	NAP		g3334847	392	180	2.00E-44	41	30	(AJ007840) Ctr4 protein [Schizosaccharomyces pombe] ; (AL034382) mating-type locus and centromeric silencing protein Ctr4p [Schizosaccharomyces pombe]
20239	ENU04033	ANI61C466:4 28-47 818..6998	28-47	2142-2166	NAP		g2501570	395	137	1.00E-36	35	70	hypothetical 51.4 KD protein in RAR1-SCJ1 intergenic region ; hypothetical protein YMR210w - yeast (Saccharomyces cerevisiae) ; (Z49809) unknown [Saccharomyces cerevisiae]
20240	ENU04034	ANI61C5683: 23-45 2294..114	23-45	2141-2161	NAP		g729091	1165	418	e-130	48	83	cell division control protein 5 ; probable transcription factor cdc5 - fission yeast (Schizosaccharomyces pombe) ; (L19525) Cdc5 [Schizosaccharomyces pombe]

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20241	ENU04035	ANI61C5347: 1539..46	23-58	2164-2183	NAP		g3646451	391	158	1.00E-37	41	44	(AL031603) mRNA cap methyltransferase
20242	ENU04036	ANI61C1073: 32-51	32-51	2174-2200	NAP		g4291	167	87	6.00E-16	41	22	[Schizosaccharomyces pombe] (X00528) URF c-ras (sc-2)
20243	ENU04037	ANI61C9737: 61-80	61-80	2212-2231	NAP		g3184082	1297	494	e-139	39	95	[Saccharomyces cerevisiae] (AL023781) N-terminal acetyltransferase 1
20244	ENU04038	ANI61C4134: 57-76	57-76	2209-2230	NAP		g1709439	951	262	e-102	53	69	[Schizosaccharomyces pombe] 2-oxoisovalerate dehydrogenase alpha subunit precursor (branched-chain alpha-keto acid dehydrogenase component alpha chain (E1)) (BCKDH E1-alpha) ; (L47335) branched chain alpha ketoacid decarboxylase E1a subunit [Mus musculus]
20245	ENU04039	ANI61C4107: 42-61	42-61	2202-2219	NAP		g1703215	400	147	2.00E-34	28	54	general alpha-glucoside permease ; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) ; (Z73074) ORF YGR289c
20246	ENU04040	ANI61C1092: 29-52	29-52	2185-2211	NAP		g131761	59	4.00E-28				[Saccharomyces cerevisiae] quinate permease (quate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
20247	ENU04041	ANI61C1113: 64-83	64-83	2256-2275	NAP		g416866	1065	273	1.00E-92	65	53	Cyanide hydratase (formamide hydrolyase) ; cyanide hydratase (EC 4.2.1.66) - imperfect fungus (Gloeocercospora sorghi) ; (M99044) cyanide hydratase [Gloeocercospora sorghi]
20248	ENU04042	ANI61C1109: 22-51	22-51	2227-2246	NAP		g2276360	848	330	3.00E-89	36	98	(Z97992) N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein [Schizosaccharomyces pombe]
20249	ENU04043	ANI61C1047: 41-63	41-63	2247-2266	NAP		g3929362	396	113	2.00E-30	32	80	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVI]

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20250	ENU04044	ANI61C5969: 32-51 3987..1712	32-51	2247-2266	NAP		g731746	119	52	0.000000	30	38	hypothetical 42.4 KD protein in ENO2-STB5 intergenic region ; hypothetical protein YHR176w - yeast (Saccharomyces cerevisiae) ; (U00027) Yhr176wp [Saccharomyces cerevisiae] Anthranilate synthase component II (contains: glutamine amidotransferase; indole-3-glycerol phosphate synthase (IGPS); N-(5'-phosphoribosyl)anthranilate isomerase (PRAI) ; anthranilate synthase multifunctional protein - Emericella nidulans
20251	ENU04045	ANI61C6532: 46-65 3329..1053	46-65	2260-2281	NAP		g136287	3886	1273	0	99	98	2 [Aspergillus fumigatus] ; (U62936) multidrug resistance protein 2 [Aspergillus fumigatus]
20252	ENU04046	ANI61C2678: 42-62 273..2553	42-62	2261-2280	NAP		g2673955	755	192	8.00E-48	67	13	hypothetical 104.5 KD protein C26A3.10 in chromosome I ; (Z69240) putative zinc finger protein [Schizosaccharomyces pombe]
20253	ENU04047	ANI61C2605: 63-89 2520..233	63-89	2282-2308	NAP		g1723238	578	193	4.00E-48	31	72	D-lactate dehydrogenase (cytochrome) precursor (D-lactate ferricytochrome C oxidoreductase) (D-LCR) ; D-lactate dehydrogenase (cytochrome) (EC 1.1.2.4) - yeast (Saccharomyces cerevisiae) ; (Z67750) D-lactate dehydrogenase [Saccharomyces cerevisiae] ; (Z74222) ORF YDL174c [Saccharomyces cerevisiae]
20254	ENU04048	ANI61C9553: 23-51 2365..4652	23-51	2243-2268	NAP		g2506961	640	139	7.00E-50	41	75	(AF059202) ACAT related gene product 1 [Homo sapiens]
20255	ENU04049	ANI61C1074 65-84 7:1744..4039	65-84	2297-2318	NAP		g3746533	379	175	1.00E-42	34	46	(U68040) polyketide synthase [Cochliobolus heterostrophus]
20256	ENU04050	ANI61C6708: 58-88 2595..4897	58-88	2298-2317	NAP		g1546072	1290	169	9.00E-41	35	10	fatty acid amide hydrolase ; (U82535) fatty acid amide hydrolase [Homo sapiens] ; (AF098019) fatty acid amide hydrolase [Homo sapiens]
20257	ENU04051	ANI61C8242: 24-55 2932..623	24-55	2272-2291	NAP		g4557575	453	105	3.00E-33	35	71	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20258	ENU04052	ANI61C153:2 547..236	39-61	2285- 2308	NAP		g1168266	1199	316	3.00E-85	45	96	alpha-L-arabinofuranosidase A precursor (arabinosidase A) (ABF A); (L29005) alpha-L-arabinofuranosidase [Aspergillus niger]
20259	ENU04053	ANI61C6248: 35-57 8568..6252		2280- 2309	NAP		g3023956	1360	344	1.00E-93	38	42	Vegetatible incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]
20260	ENU04054	ANI50C2773 46-66 4_1:2361..39		2308- 2326	NAP		g548630		349	e-128	46	92	peptide transporter PTR2 (peptide permease PTR2) ; peptide transport protein PTR2 - yeast (Saccharomyces cerevisiae) ; (X73541) ORF YKR413 [Saccharomyces cerevisiae] ; (Z28318) ORF YKR093w [Saccharomyces cerevisiae]
20261	ENU04055	ANI61C8136: 61-83 285..2616		2331- 2350	NAP		g3123199	953	354	e-102	40	94	CUT9 protein ; anaphase control protein cut9 - fission yeast (Schizosaccharomyces pombe) ; (Z98533) cut9 protein; possible anaphase control
20262	ENU04056	ANI61C1097 38-61 6:4140..3035		2314- 2337	NAP		g1076205	86	45	0.003	26	26	[Schizosaccharomyces pombe] ; cut9 gene [Schizosaccharomyces pombe] "hypothetical protein WP6 - Chlamydomonas eugametos ; (L29028) amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .. 109, 128 .. 130, 132 .. 134, 158 .. 160, 163 .. 165; amino acid feature: Rod protein domain, aa 169 .. 340; amino acid feature: globular pro...
20263	ENU04057	ANI61C498:3 35-55 824..5910		2313- 2334	NAP		g3915154	868	115	1.00E-24	43	16	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20264	ENU04058	ANI61C9423: 3560..5906	64-84	2343-2368	NAP		g4506957	412	152	1.00E-35	57	30	unknown ; clathrin coat assembly protein AP19 (clathrin coat associated protein AP19) (GOLGI adaptor AP-1 19 KD adaptor) (HA1 19 KD subunit) (clathrin assembly protein complex 1 small chain) ; (AB015320) sigma1B subunit of AP-1 clathrin adaptor complex [Homo sapiens] putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emmericella nidulans] hypothetical 39.0 KD protein in DAL5-THI11 intergenic region ; hypothetical protein YJR154w - yeast (Saccharomyces cerevisiae) ; (Z49654) ORF YJR154w [Saccharomyces cerevisiae]
20265	ENU04059	ANI61C3730: 4255..1906	34-53	2306-2341	NAP		g2498971	725	173	3.00E-65	39	75	SUGAR transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20266	ENU04060	ANI61C753:4 859..2507	22-51	2313-2332	NAP		g1352945	188	63	2.00E-19	28	49	"hypothetical 58.5 KD protein C12G12.14 in chromosome I ; hypothetical protein SPAC12G12.14 - fission yeast (Schizosaccharomyces pombe) ; (Z66568) SPAC12G12.14, unknown, len: 510, some similarity to PIR:A24907 hypothetical protein 1 (chromosome 4 centromere) - yeast [Schizosaccharomyces pombe] "
20267	ENU04061	ANI61C9176: 4403..4737	27-53	2320-2340	NAP		g1711561	261	62	7.00E-22	29	67	(D73369) pyranose oxidase [Coriolus versicolor]
20268	ENU04062	ANI61C5315: 697..3059	70-89	2370-2390	NAP		g1351637	581	168	5.00E-57	39	74	"(AF005035) alpha 1,2-mannosidase [Spodoptera frugiperda] "
20269	ENU04063	ANI61C9185: 10946..7334	24-49	2323-2348	NAP		g1845549	555	192	8.00E-48	38	57	hypothetical 38.5 KD protein C3H8.04 in chromosome I ; (Z69086) unknown [Schizosaccharomyces pombe]
20270	ENU04064	ANI61C1046 1:3851..6221	63-81	2365-2391	NAP		g2245570	437	89	2.00E-36	33	43	
20271	ENU04065	ANI61C1113 1:6189..8561	22-57	2333-2352	NAP		g1723215	162	94	4.00E-18	36	24	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20272	ENU04066	ANI61C9602: 22-50 3318..5702	22-50	2345-2364	NAP		g3915154	334	156	5.00E-37	26	75	Trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (<i>Fusarium sporotrichioides</i>) ; (<i>U22462</i>) trichodiene oxygenase [<i>Fusarium sporotrichioides</i>] (<i>U96968</i>) alcohol oxidase [<i>Pichia pastoris</i>] (<i>Y15277</i>) cytochrome P450 monooxygenase [<i>Gibberella fujikuroi</i>] (<i>AF092565</i>) splicing factor Prp8 [<i>Homo sapiens</i>] probable serine/threonine-protein kinase YJL057C ; probable membrane protein YJL057c - yeast (<i>Saccharomyces cerevisiae</i>) ; (<i>Z49332</i>) ORF YJL057c [<i>Saccharomyces cerevisiae</i>] (<i>AF091342</i>) neurofilament-M subunit [<i>Bos taurus</i>] putative ATP-dependent RNA helicase C12C2.06 ; (<i>Z54140</i>) probable ATP-dependent RNA helicase [<i>Schizosaccharomyces pombe</i>] Nucleoporin NUP100/NSP100 (nuclear pore protein NUP100/NSP100) ; nuclear pore complex protein NUP100 - yeast (<i>Saccharomyces cerevisiae</i>) ; (<i>Z15035</i>) nuclear pore complex protein NUP100 [<i>Saccharomyces cerevisiae</i>] ; (<i>X75780</i>) B959 [<i>Saccharomyces cerevisiae</i>] ; (<i>Z28068</i>) ORF YKL068w [<i>Saccharomyces cerevisiae</i>] ; nuclear pore complex protein NUP100 [<i>Saccharomyces cerevisiae</i>]
20273	ENU04067	ANI61C4610: 47-66 2569..4956	47-66	2366-2393	NAP		g2104963	2260	330	e-177	68	98	
20274	ENU04068	ANI61C1053 49-84 2:625..3014	49-84	2377-2396	NAP		g3549879	649	256	5.00E-67	46	27	
20275	ENU04069	ANI61C1031 42-62 8:8701..11091	42-62	2362-2390	NAP		g3661610	9138	1158	0	73	33	
20276	ENU04070	ANI61C7390: 28-49 2167..4558	28-49	2356-2377	NAP		g1346384	293	166	6.00E-40	30	32	
20277	ENU04071	ANI61C1117 36-55 9:1892..4301	36-55	2384-2405	NAP		g3641350	132	63	0.000000 007			
20278	ENU04072	ANI61C8270: 22-47 819..3231	22-47	2372-2391	NAP		g1175426	889	150	2.00E-66	56	39	
20279	ENU04073	ANI61C6479: 22-56 1..2453	22-56	2413-2432	NAP		g400320	296	85	2.00E-15			

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20280	ENU04074	ANI61C6479: 22-56 1..2453	22-56	2413-2432	NAP		g400320	296	85	2.00E-15			Nucleoporin NUP100/NSP100 (nuclear pore protein NUP100/NSP100); nuclear pore complex protein NUP100 - yeast (Saccharomyces cerevisiae); (Z15035) nuclear pore complex protein NUP100 [Saccharomyces cerevisiae]; (X75780) B959 [Saccharomyces cerevisiae]; (Z28068) ORF YKL068w [Saccharomyces cerevisiae]; nuclear pore complex protein NUP100 [Saccharomyces cerevisiae] probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae); (Z75214) ORF YOR306c [Saccharomyces cerevisiae] (U51927) SpiR [Salmonella typhimurium] Sugar transporter STL1; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae); (U33057) Stl1p; plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20281	ENU04075	ANI61C1047 6:1454..3919	22-54	2426-2445	NAP		g2132942	206	122	5.00E-27	25	50	
20282	ENU04076	ANI61C1016 4:5..2474	26-45	2434-2453	NAP		g1498305	233	96	8.00E-19	26	43	
20283	ENU04077	ANI61C9107: 72-95 51..2531	72-95	2486-2509	NAP		g1711561	718	180	8.00E-54	38	46	
20284	ENU04078	ANI61C9639: 27-52 8538..6053	27-52	2438-2469	NAP		g731864	383	176	4.00E-43	25	67	hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region; probable membrane protein YIL120w - yeast (Saccharomyces cerevisiae); (Z46833) unknown [Saccharomyces cerevisiae]
20285	ENU04079	ANI61C3499: 22-43 2054..2552	22-43	2464-2483	NAP		g1166378	271	132	1.00E-29	36	15	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
20286	ENU04080	ANI61C8896: 44-63 2766..231	44-63	2515-2534	NAP		g1723232	404	89	2.00E-16	27	86	hypothetical 90.6 KD protein C1D4.10 in chromosome I; (Z69239) unknown [Schizosaccharomyces pombe]
20287	ENU04081	ANI61C6543: 38-59 5355..2821	38-59	2508-2530	NAP		g2414650	346	95	2.00E-31	66	34	(Z99296) 60s ribosomal protein L32 [Schizosaccharomyces pombe]
20288	ENU04082	ANI61C1047 9:1434..3975	32-51	2503-2531	NAP		g3929362	396	113	2.00E-30	31	75	pisatin demethylase (cytochrome P450 57A1); pisatin demethylase - fungus (Nectria haematococca); (L20976) pisatin demethylase [Nectria haematococca mpVI]

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20289	ENU04083	ANI61C6741: 22-50 2948..5519		2532-2551	NAP		g115642	412	134	1.00E-36	37	85	acid protease precursor ; acid proteinase (EC 3.4.23.-) PEP1 precursor - yeast (Saccharomycopsis fibuligera) ; (D00313) open reading frame of PEP1 (putative secretable acid protease) [Saccharomycopsis fibuligera] ; acid protease PEP1 [Saccharomycopsis fibuligera]
20290	ENU04084	ANI61C7542: 72-93 3960..1378		2580-2610	NAP		g2293233		159	6.00E-38			(AF008220) YtcI [Bacillus subtilis] ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
20291	ENU04085	ANI50C1102 52-71 5_1:441..3023		2566-2592	NAP		g1175420		386	e-106	43	64	hypothetical 63.9 KD protein C12C2.03C in chromosome II ; (Z54140) putative oxidoreductase [Schizosaccharomyces pombe]
20292	ENU04086	ANI61C1043 67-86 9:2596..13		2576-2608	NAP		g2388966	188	105	1.00E-21	32	15	(Z98979) putative phosphatidylserine decarboxylase proenzyme
20293	ENU04087	ANI61C9480: 23-49 57..2646		2550-2569	NAP		g3915964	1332	319	e-145	37	84	[Schizosaccharomyces pombe] hypothetical 112.2 KD protein in TIF35-NPL3 intergenic region (ORF1) ; hypothetical protein YDR430c - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr430cp; CAI: 0.15 [Saccharomyces cerevisiae]
20294	ENU04088	ANI61C9498: 22-47 3043..442		2554-2581	NAP		g117619	371	90	5.00E-33	27	81	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
20295	ENU04089	ANI61C9516: 23-42 3271..656		2571-2596	NAP		g2330659	2225	816	0	53	67	(Z98595) putative snf2 family helicase [Schizosaccharomyces pombe]

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20296	ENU04090	ANI61C5840: 5..2659	26-48	2618-2637	NAP		g115208	2843	555	0			"C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) (methy)ENETetrahydrofolate dehydrogenase / methenyltetrahydrofolate cyclohydrolase / formyltetrahydrofolate synthetase ; methyl/enetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) - yeast (Saccharomyces cerevisiae) ; (M12878) C-1-tetrahydrofolate synthase [Saccharomyces cerevisiae] ; (Z49133) C-1-tetrahydrofolate synthase [Saccharomyces cerevisiae] ; (Z72989) ORF YGR204w [Saccharomyces cerevisiae]"
20297	ENU04091	ANI61C8143: 98..2760	23-43	2617-2643	NAP		g125935	553	138	1.00E-60	33	54	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] DHP1 protein ; dhp1 protein - fission yeast (Schizosaccharomyces pombe) ; (D17752) Dhp1 protein [Schizosaccharomyces pombe] ; (Z69240) dna exoribonuclease [Schizosaccharomyces pombe] mitotic control protein DIS3 ; mitotic control protein dis3+ - fission yeast (Schizosaccharomyces pombe) ; (M74094) mitotic control protein [Schizosaccharomyces pombe] ; (AL031743) mitotic control protein dis3. [Schizosaccharomyces pombe]
20298	ENU04092	ANI61C1129: 45-64 443..3125	45-64	2666-2685	NAP		g729332	1949	350	0	47	82	Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20299	ENU04093	ANI61C1106 70-93 6:4260..1572	70-93	2684-2715	NAP		g585053	2427	562	0	56	86	U58946) transposase [Aspergillus awamori]
20300	ENU04094	ANI61C9176: 40-58 1414..4115	40-58	2680-2699	NAP		g1711561	261	62	9.00E-22	29	58	
20301	ENU04095	ANI61C9979: 24-45 1144..1080	24-45	2671-2695	NAP		g1805251	367	188	1.00E-46	30	60	

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20302	ENU04096	ANI61C6593; 41-62 3013..2451		2708-2732	NAP		g117619	500	230	3.00E-59	26	75	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
20303	ENU04097	ANI61C3011; 22-55 670..3453		2744-2763	NAP		g131761	449	163	5.00E-49	28	71	quinate permease (quinate transporter) ; quinate transport protein - Neurospora crassa ; (X14603) quinate transporter [Neurospora crassa]
20304	ENU04098	ANI61C1560; 31-53 2550..5335		2751-2774	NAP		g1168802	578	275	1.00E-72	37	56	Carboxypeptidase S precursor (YSCS) (GLY-X carboxypeptidase) ; Gly-X carboxypeptidase (EC 3.4.17.4) precursor - yeast (Saccharomyces cerevisiae) ; (X63068) carboxypeptidase yscS [Saccharomyces cerevisiae] ; (Z49447) ORF YJL172w [Saccharomyces cerevisiae]
20305	ENU04099	ANI61C3679; 29-50 5645..2857		2749-2775	NAP		g4512618	665	252	2.00E-93	28	63	(AC004793) Strong similarity to gi3600044 T12H20.12 protease homolog from Arabidopsis thaliana BAC gb AF080119 and is a member of the reverse transcriptase family PF 00078.
20306	ENU04100	ANI61C1146 4:4675..1884		2802-2820	NAP		g1711561	592	282	8.00E-75	37	57	Sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Stl1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20307	ENU04101	ANI61C9791; 32-58 10551..7746		2776-2795	NAP		g1402634	288	155	1.00E-36	32	29	(D83125) secretory component [Sarcophaga peregrina]
20308	ENU04102	ANI61C8214; 56-77 2948..121		2824-2843	NAP		g104311	2172	541	0	54	87	"Ca2+-transporting ATPase (EC 3.6.1.38), fast skeletal muscle - edible frog ; (X63009) fast skeletal muscle Ca-ATPase [Rana esculenta] ; Ca ATPase [Rana esculenta]"
20309	ENU04103	ANI61C241;3 468..636		2836-2857	NAP		g1723448		37	0.0003			hypothetical protein C56F8.17C in chromosome I ; (Z69728) unknown [Schizosaccharomyces pombe]

Seq num	Seq id	Contig Source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20310	ENU04104	ANI61C230:1 39-58 34..2683		2815-2834	NAP		g1166378	924	442	e-123	33	84	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "
20311	ENU04105	ANI61C7266: 46-65 2194..1294		2830-2855	NAP		g422615	277	125	1.00E-27	21	26	"myosin heavy chain form B, nonmuscle - African clawed frog ; (L09740) nonmuscle myosin heavy chain b [Xenopus laevis] "
20312	ENU04106	ANI61C716:3 68-97 383..520		2867-2888	NAP		g4580007	3063	1016	0	61	91	(D87259) poly(A)+ RNA transport protein Prt3p [Schizosaccharomyces pombe]
20313	ENU04107	ANI61C8701: 22-52 1942..4824		2834-2862	NAP		g3150139	720	131	6.00E-78	36	57	(AL023594) amino-acid permease [Schizosaccharomyces pombe]
20314	ENU04108	ANI61C7618: 22-45 1455..4387		2882-2911	NAP		g1710803	714	145	2.00E-33	42	21	Retroadaptation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae) ; (X94357) ORF Nrf588; EMBL:SCRTG2X;M97691; PIR:B44344;B44344 [Saccharomyces cerevisiae] ; (M97691) Rtg2p [Saccharomyces cerevisiae] ; (Z72774) ORF YGL252c [Saccharomyces cerevisiae]
20315	ENU04109	ANI61C9:204 45-65 4..2959		2919-2938	NAP		g125935	459	108	8.00E-43	30	45	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis]
20316	ENU04110	ANI61C8661: 72-91 394..3332		2947-2968	NAP		g4263786	850	225	1.00E-99	37	74	"(AC006068) putative acyl coenzyme A oxidase, peroxisomal component [Arabidopsis thaliana] "
20317	ENU04111	ANI61C1760: 69-89 2948..9		2948-2966	NAP		g2808634	1017	211	3.00E-60	45	49	[Aspergillus niger] transcriptional activator (AJ001909)
20318	ENU04112	ANI61C8623: 41-60 795..3765		2949-2968	NAP		g3913798	1430	348	e-115	59	41	"Exoglucanase I precursor (exocellobiohydrolase I) (1,4-beta-cellobiohydrolase I) (beta-glucanase) ; (AB002821) cellobiohydrolase I [Aspergillus aculeatus] "
20319	ENU04113	ANI61C7699: 22-45 3947..974		2923-2953	NAP		g1723974	1511	564	e-160	50	74	"hypothetical 75.4 KD protein in HAP2-ADE5,6 intergenic region ; hypothetical protein YGL236c - yeast (Saccharomyces cerevisiae) ; (Z72758) ORF YGL236c [Saccharomyces cerevisiae] "

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20320	ENU04114	ANI61C4655: 3399..423	38-57	2952-2971	NAP		g730723	1444	604	e-171	67	38	CAMP-dependent protein kinase SCH9 ; probable protein kinase SCH9 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (U00029) Sch9p: cAMP-dependent protein kinase [Saccharomyces cerevisiae]
20321	ENU04115	ANI61C9768: 28-61 3378..6362	28-61	2936-2971	NAP		g118901	2303	426	0	45	63	DNA polymerase zeta catalytic subunit ; DNA-directed DNA polymerase (EC 2.7.7.7) REV3 - yeast (Saccharomyces cerevisiae) ; (M29683) DNA polymerase (pot.); putative [Saccharomyces cerevisiae] ; (Z73523) ORF YPL167c [Saccharomyces cerevisiae] ; (X96770) P2535 protein [Saccharomyces cerevisiae]
20322	ENU04116	ANI61C8537: 45-64 5851..8841	45-64	2973-2992	NAP		g549755	360	89	2.00E-26	27	50	"Carboxylic acid transporter protein homolog ; hypothetical protein YKL217w - yeast (Saccharomyces cerevisiae) ; (X75951) ORF3, A616 [Saccharomyces cerevisiae] ; (Z28217) ORF YKL217w [Saccharomyces cerevisiae] ; (U24155) carboxylic acid transporter protein homolog [Saccharomyces cerevisiae] "
20323	ENU04117	ANI61C6226: 33-64 4891..7889	33-64	2970-2989	NAP		g728850		43	0.009			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, sta1, len: 1367, CAL: 0.3, AMYH_ yeast P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus] "
20324	ENU04118	ANI61C7076: 62-81 1853..2796	62-81	944-963	NAP		g2132846	495	156	2.00E-37	29	58	probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]

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20325	ENU04119	ANI61C1070 5:1016..72	63-86	944-965	NAP		g120777	1144	373	e-103	57	64	"Succinate-semialdehyde dehydrogenase (NADP+) (SSDH) ; (M88334) succinic semialdehyde dehydrogenase [Escherichia coli] ; (AE000351) succinate-semialdehyde dehydrogenase, NADP-dependent activity [Escherichia coli] "
20326	ENU04120	ANI61C4798; 41-62 1015..1960	41-62	924-944	NAP		g2388907	606	65	6.00E-10	29	22	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
20327	ENU04121	ANI61C1948; 25-46 2166..3111	25-46	908-928	NAP		g4127832	475	171	6.00E-42	37	57	(Y17243) cytochrome P450 [Gibberella fujikuroi]
20328	ENU04122	ANI61C681.2 58-80 529..1579	58-80	946-965	NAP		g119216	1224	322	3.00E-87	65	63	"Elongation factor TU, mitochondrial precursor ; translation elongation factor Tu precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z75095) ORF YOR187w [Saccharomyces cerevisiae] "
20329	ENU04123	ANI61C6816; 48-70 1106..155	48-70	938-957	NAP		g4079649	162	63	7.00E-18	32	21	(U78168) cAMP-regulated guanine nucleotide exchange factor I [Homo sapiens]
20330	ENU04124	ANI61C1101 66-85 6:2127..1172	66-85	957-979	NAP		g1351683	341	139	2.00E-32	35	55	hypothetical 53.9 KD protein C1F5.08C in chromosome I ; (Z68136) unknown [Schizosaccharomyces pombe]
20331	ENU04125	ANI61C1047; 38-57 1301..343	38-57	934-954	NAP		g3122248	669	233	1.00E-60	40	67	D-hydantoinase (dihydropyrimidinase) (DHPASE) ; (X91070) D-hydantoinase [Agrobacterium radiobacter]
20332	ENU04126	ANI61C6326; 22-49 1017..54	22-49	917-943	NAP		g3647336	439	102	3.00E-44	52	46	(AL031644) hypothetical protein [Schizosaccharomyces pombe]
20333	ENU04127	ANI61C1037 36-66 9:6723..5760	36-66	938-957	NAP		g1352875	801	66	1.00E-22	33	19	hypothetical 154.9 KD protein in CPR7-PET191 intergenic region ; hypothetical protein YJR033c - yeast (Saccharomyces cerevisiae) ; (Z49533) ORF YJR033c [Saccharomyces cerevisiae]
20334	ENU04128	ANI61C9715; 42-61 101..1066	42-61	946-965	NAP		g1794292	1171	353	1.00E-96	55	65	(U77983) WD-domain protein [Schizosaccharomyces pombe]
20335	ENU04129	ANI61C627.4 69-93 53..1427	69-93	981-1001	NAP		g2133298	552	233	1.00E-60	49	82	"chitinase, 33k, precursor - fungus (Trichoderma harzianum) ; (X80006) chitinase [Trichoderma harzianum] "

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20336	ENU04130	ANI61C9947: 1228..252	43-62	942-977	NAP		g3915154	647	154	1.00E-36	34	57	Trichodiene oxygenase (cytochrome P450 58); trichodiene oxygenase 4 - fungus (<i>Fusarium sporotrichioides</i>); (U22462) trichodiene oxygenase [<i>Fusarium sporotrichioides</i>] (U24215) p-cumic aldehyde dehydrogenase [<i>Pseudomonas putida</i>] hypothetical 42.9 KD protein in ILV2-ADE17 intergenic region; hypothetical protein YMR114c - yeast (<i>Saccharomyces cerevisiae</i>); (Z49702) unknown [<i>Saccharomyces cerevisiae</i>] (Y16399) multidrug resistance protein [<i>Candida albicans</i>] (Y16399) multidrug resistance protein [<i>Candida albicans</i>] Proline iminopeptidase (prolyl aminopeptidase); prolyl aminopeptidase (EC 3.4.11.5) - <i>Aeromonas sobria</i> ; (D30714) prolyl aminopeptidase [<i>Aeromonas sobria</i>] (AC006570) putative polypeptide [<i>Arabidopsis thaliana</i>] "Exopolysaccharuronase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase); (L48982) exo-alpha 1,4-polygalacturonase [<i>Cochliobolus carbonum</i>]" (AL021841) amiB [<i>Mycobacterium tuberculosis</i>] (AL031739) beta transducin [<i>Schizosaccharomyces pombe</i>] hypothetical 58.0 KD protein C2C6.08 in chromosome I; (AL031324) hypothetical protein [<i>Schizosaccharomyces pombe</i>] (AL031154) putative transmembrane transporter [<i>Schizosaccharomyces pombe</i>]
20337	ENU04131	ANI61C942:4 22-40	22-40	942-964	NAP		g2228233	336	130	1.00E-29	40	27	
20338	ENU04132	ANI61C7124: 56-74	56-74	980-1001	NAP		g2497154	337	133	2.00E-30	35	73	
20339	ENU04133	ANI61C8753: 72-94	72-94	997-1020	NAP		g3378550	84	84	1.00E-15			
20340	ENU04134	ANI61C8753: 72-94	72-94	997-1020	NAP		g3378550	84	84	1.00E-15			
20341	ENU04135	ANI61C1583: 42-61	42-61	974-999	NAP		g1730576	316	90	3.00E-17	35	58	
20342	ENU04136	ANI61C8605: 63-90	63-90	997-1023	NAP		g4432807	477	89	5.00E-36	32	20	
20343	ENU04137	ANI61C1048 50-69	50-69	989-1012	NAP		g2499717	430	86	3.00E-16	34	25	
20344	ENU04138	ANI61C7225: 28-47	28-47	976-996	NAP		g2894215	427	139	4.00E-34	37	71	
20345	ENU04139	ANI61C3186: 23-43	23-43	961-992	NAP		g3650407	435	115	7.00E-25	43	59	
20346	ENU04140	ANI61C5164: 41-59	41-59	989-1010	NAP		g3183406	846	274	6.00E-73	49	57	
20347	ENU04141	ANI61C9636: 22-50	22-50	971-993	NAP		g3367790	723	100	1.00E-31	49	60	

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20348	ENU04142	ANI61C91116: 45-67 6791..7805		997-1017	NAP		g1293655	778	109	4.00E-46	40	47	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
20349	ENU04143	ANI61C6687: 24-46 43..1057		977-996	NAP		g2226429	826	260	2.00E-78	47	53	(Z97204) putative vacuolar protein sorting-associated protein. [Schizosaccharomyces pombe]
20350	ENU04144	ANI61S22225: 56-75 1..148		1010-1029	NAP		g3810866		108	6.00E-30	50	94	(AL032681) putative hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe]
20351	ENU04145	ANI61C9501: 34-53 1018..1		987-1009	NAP		g2132474	1332	518	e-146	74	55	probable membrane protein YDR091c - yeast (Saccharomyces cerevisiae) ; (Z50111) unknown [Saccharomyces cerevisiae]
20352	ENU04146	ANI61C164:3 42-64 980..2962		998-1018	NAP		g114971	1677	276	2.00E-73	45	37	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucosidase) ; beta-glucosidase (EC 3.2.1.21) precursor - yeast (Kluyveromyces marxianus var. marxianus) ; (X05918) beta-glucosidase (AA 1 - 845) [Kluyveromyces marxianus]
20353	ENU04147	ANI61C9646: 30-50 1062..39		990-1011	NAP		g4538856	247	111	6.00E-24	35	49	(AJ223758) 54 kDa vacuolar H(+)-ATPase subunit [Sus scrofa]
20354	ENU04148	ANI61C8673: 23-47 19..1049		980-1011	NAP		g3183238	529	181	7.00E-54	36	46	hypothetical 81.2 KD protein C3D6.13C in chromosome II ; (Z95620) putative thioredoxin [Schizosaccharomyces pombe]
20355	ENU04149	ANI61C8886: 71-90 233..1264		1037-1060	NAP		g1084944	742	319	3.00E-86	59	32	hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]

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20356	ENU04150	ANI61C7428: 41..1073	62-81	1030-1051	NAP		g125401	163	94	2.00E-18			choline kinase ; choline kinase (EC 2.7.1.32) - yeast (Saccharomyces cerevisiae) ; (J04454) choline kinase [Saccharomyces cerevisiae] ; (X91258) choline kinase [Saccharomyces cerevisiae] ; (U53881) Cki1p: choline kinase [Saccharomyces cerevisiae] ; (Z73305) ORF YLR133w [Saccharomyces cerevisiae]
20357	ENU04151	ANI61C1035 47-67 8:1425..2461	47-67	1016-1041	NAP		g3334221	1166	203	3.00E-90	60	74	4-hydroxyphenylpyruvate dioxygenase (4HPPD) (HPD) ; (AF038152) 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]
20358	ENU04152	ANI61C3101: 22-54 575..1609	22-54	999-1018	NAP		g3023999	1801	210	e-108	85	55	"Isocitrate dehydrogenase (NADP), mitochondrial precursor (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP) ; (AB000261) NADP-dependent isocitrate dehydrogenase precursor [Aspergillus niger] "
20359	ENU04153	ANI61C7048: 70-89 60..1108	70-89	1055-1076	NAP		g3378447	462	153	6.00E-48	39	73	(AF079317) unknown [Sphingomonas aromaticivorans]
20360	ENU04154	ANI61C299:1 40-59 359..311	40-59	1020-1046	NAP		g2408044	108	56	0.000000	22	43	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
20361	ENU04155	ANI61C1017 22-50 2:10..1066	22-50	1014-1035	NAP		g2673947	994	346	1.00E-98	67	23	(U62931) multidrug resistance protein 1 [Aspergillus flavus] ; (U62932) multidrug resistance protein 1 [Aspergillus flavus]
20362	ENU04156	ANI61C9779: 70-97 2017..959	70-97	1062-1086	NAP		g465668	930	235	3.00E-61	42	22	"ubiquitin fusion degradation protein 4 (UB fusion protein 4) ; hypothetical protein YKL010c - yeast (Saccharomyces cerevisiae) ; (S53418) orf YKL162 [Saccharomyces cerevisiae=yeast, Peptide, 1483 aa] [Saccharomyces cerevisiae] ; (Z28010) ORF YKL010c [Saccharomyces cerevisiae] "

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20363	ENU04157	ANI61C4566: 1873..809	33-58	1034-1054	NAP		g3041656	717	110	1.00E-43	43	62	NADPH:adrenodoxin oxidoreductase precursor (adrenodoxin reductase) (ferredoxin-NADP(+) reductase); (J03826) adrenodoxin reductase precursor species 1 [Homo sapiens] alcohol dehydrogenase (NADP(+)) (aldehyde reductase); alcohol dehydrogenase (NADP+) (EC 1.1.1.2) - human; (J04794) aldehyde reductase (EC 1.1.1.2) [Homo sapiens]; (AF036683) aldehyde reductase [Homo sapiens]
20364	ENU04158	ANI61C269:9 22-47 58..2023	22-47	1017-1045	NAP		g113600	99	41	0.000000 2	29	89	
20365	ENU04159	ANI61C7606: 60-79 2390..1323	60-79	1065-1084	NAP		g3411013	450	175	6.00E-43	33	35	(AF000232) protein mannosyltransferase 1 [Candida albicans]
20366	ENU04160	ANI61C1879: 29-54 1257..2325	29-54	1037-1055	NAP		g3702635	532	184	1.00E-45	35	79	(AL031825) hypothetical protein [Schizosaccharomyces pombe]
20367	ENU04161	ANI61C4366: 23-44 1466..396	23-44	1032-1051	NAP		g3434965	1013	316	2.00E-85	54	66	(AB002530) mus-23 [Neurospora crassa]
20368	ENU04162	ANI61C1061 71-90 3:3032..1957	71-90	1083-1102	NAP		g3850152	564	184	3.00E-54	36	76	(AL033396) hypothetical protein [Candida albicans]
20369	ENU04163	ANI61C7489: 22-46 2110..1036	22-46	1035-1054	NAP		g1363755	931	244	7.00E-64	50	26	hypothetical protein YLR410w - yeast (Saccharomyces cerevisiae); (U20162) Ylr410wp [Saccharomyces cerevisiae] (AF028783) proteasome regulatory subunit 12 [Hypocrea jecorina]
20370	ENU04164	ANI61C2606: 31-50 2026..951	31-50	1042-1063	NAP		g2599117	1269	189	e-125	80	93	(AL034381) conserved hypothetical PFAM UPF0031 containing protein [Schizosaccharomyces pombe]
20371	ENU04165	ANI61C8172: 64-83 1317..243	64-83	1077-1096	NAP		g3947854	481	148	2.00E-38	50	76	(Y16834) hexose transporter [Candida albicans]
20372	ENU04166	ANI61C4401: 67-86 135..1211	67-86	1081-1101	NAP		g3336839	290	81	3.00E-28	30	57	(Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi]
20373	ENU04167	ANI61C2761: 54-73 1270..194	54-73	1067-1088	NAP		g3549891	364	102	7.00E-42	32	61	gamma-Butyrobetaine Hydroxylase; (AF082868) gamma butyrobetaine hydroxylase [Homo sapiens]
20374	ENU04168	ANI61C1042 22-51 5:576..1655	22-51	1040-1059	NAP		g4502369	324	156	3.00E-37	30	89	

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20375	ENU04169	ANI61C7010: 21..1103	42-61	1052-1080	NAP		g1176483	500	129	2.00E-33	45	45	hypothetical 70.2 KD protein in GSH1-CHS6 intergenic region ; hypothetical protein YJL100w - yeast (Saccharomyces cerevisiae) ; (X85021) orf 12 [Saccharomyces cerevisiae] ; (Z49375) ORF YJL100w [Saccharomyces cerevisiae] (AL049522) hypothetical DNAJ domain protein [Schizosaccharomyces pombe] probable membrane protein YDR282c - yeast (Saccharomyces cerevisiae) ; (U51030) Ydr282cp [Saccharomyces cerevisiae] (AL033389) aminotransferase [Schizosaccharomyces pombe] "Exopolygalacturonase precursor (EXOPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) ; (X99795) exopolygalacturonase [Aspergillus tubingensis] " probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae] (AL023554) dna topoisomerase iii. [Schizosaccharomyces pombe] (Y12819) putative RNA helicase (DEAD box) [Danio rerio]
20376	ENU04170	ANI61C1082: 7:471..1551	25-48	1033-1063	NAP		g4539596	179	102	2.00E-22	28	44	
20377	ENU04171	ANI61C5138: 172..1252	25-43	1041-1063	NAP		g2132490	228	100	3.00E-24	41	29	
20378	ENU04172	ANI61C22:30 69-92 60..4145	69-92	1096-1115	NAP		g3850081	987	294	7.00E-79	50	67	
20379	ENU04173	ANI61C9101: 60-78 1688..597	60-78	1090-1109	NAP		g2499716	564	97	2.00E-52	38	68	
20380	ENU04174	ANI61C5379: 22-49 58..1149	22-49	1051-1071	NAP		g2132942	348	145	7.00E-34	29	66	
20381	ENU04175	ANI61C2460: 25-51 2020..3114	25-51	1053-1077	NAP		g4388617	1412	259	7.00E-80	49	52	
20382	ENU04176	ANI61C1138 59-83 2:1354..2459	59-83	1103-1122	NAP		g2558533	596	94	2.00E-29	39	42	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20383	ENU04177	ANI61C9581: 61-80 49..1156		1106-1125	NAP		g3876562	194	88	1.00E-16	28	37	(Z81074) Similarity to Soybean 3-methylcrotonyl-CoA carboxylase (TR:Q42777); cDNA EST EMBL:M75819 comes from this gene; cDNA EST EMBL:M89099 comes from this gene; cDNA EST EMBL:D32737 comes from this gene; cDNA EST EMBL:D32763 ... (D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta] (AL031854) hypothetical protein [Schizosaccharomyces pombe] hypothetical 70.5 KD protein in AGP3-DAK3 intergenic region ; probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae) ; (D50617) YFL054C [Saccharomyces cerevisiae] ; (D44603) unknown [Saccharomyces cerevisiae]
20384	ENU04178	ANI61C9305: 47-68 3996..5103		1089-1112	NAP		g1020413	363	59	0.000000	22	68	"(AC001229) ESTs gb T45673.gb N37512 come from this gene. [Arabidopsis thaliana] " mitochondrial processing peptidase alpha subunit precursor (alpha-MPP) ; mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - Neurospora crassa (U26160) 43 kDa secreted glycoprotein precursor [Paracoccidioides brasiliensis] ; glycoprotein gp43 [Paracoccidioides brasiliensis] (AL022070) yeast mic1 homolog [Schizosaccharomyces pombe]
20385	ENU04179	ANI61C5766: 65-88 383..1490		1108-1130	NAP		g3738180	216	52	0.000000			"(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe] "
20386	ENU04180	ANI61C5933: 71-90 1169..61		1111-1137	NAP		g1175958	445	194	1.00E-48	35	46	
20387	ENU04181	ANI61C2930: 43-62 888..1997		1080-1110	NAP		g2190550	420	182	3.00E-51	42	95	
20388	ENU04182	ANI61C1100 53-78 4:1280..171		1108-1127	NAP		g127286	1673	316	4.00E-93	62	63	
20389	ENU04183	ANI61C1104 48-68 1:3384..2267		1099-1123	NAP		g1050956	1043	273	e-104	52	84	
20390	ENU04184	ANI61C9293: 41-61 20..1140		1100-1119	NAP		g2950486	249	111	7.00E-24	30	33	
20391	ENU04185	ANI61C1010 35-54 9:1151..28		1095-1114	NAP		g1749480	332	96	4.00E-19	35	77	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20392	ENU04186	ANI61C1135 8:1723..2848	22-57	1086-1105	NAP		g4008554	53	0.000003				putative tyrosine kinase (AL034490) [Schizosaccharomyces pombe]
20393	ENU04187	ANI61C5254: 2305..3434	59-78	1127-1146	NAP		g731688	641	107	2.00E-35	32	37	hypothetical 104.0 KD protein in HXT5-NRK1 intergenic region ; hypothetical protein YHR098c - yeast [Saccharomyces cerevisiae] ; (U00060) Yhr098cp [Saccharomyces cerevisiae] ; (AJ009784) Sfb3 [Saccharomyces cerevisiae]
20394	ENU04188	ANI61C2574: 23-42 83..1213	23-42	1091-1111	NAP		g2894293	380	93	3.00E-18	32	62	hypothetical protein [Schizosaccharomyces pombe]
20395	ENU04189	ANI61C7640: 37-56 1168..34	37-56	1109-1129	NAP		g1711561	495	165	3.00E-47	34	57	sugar transporter STL1 ; sugar transport protein STP1 - yeast [Saccharomyces cerevisiae] ; (U33057) Std1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20396	ENU04190	ANI61C1134: 63-82 2191..1719	63-82	1131-1157	NAP		g3256111	38	0.13				(AL024456) 1-evidence=predicted by motif; 1-match_accession=PROSITE:PS00017; 1-match_description=ATP/GTP-binding site motif A (P-loop).; 1-method=ppsearch;; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS...
20397	ENU04191	ANI61C8073: 46-74 4595..5734	46-74	1122-1143	NAP		g2842688	558	77	2.00E-13	26	21	hypothetical 70.6 KD protein CIF8.03C in chromosome I ; (Z81312) unknown [Schizosaccharomyces pombe]
20398	ENU04192	ANI61C6332: 29-56 3210..2068	29-56	1102-1129	NAP		g549755	690	156	2.00E-37	39	27	"carboxylic acid transporter protein homolog ; hypothetical protein YKL217w - yeast [Saccharomyces cerevisiae] ; (X75951) ORF3, A616 [Saccharomyces cerevisiae] ; (Z28217) ORF YKL217w [Saccharomyces cerevisiae] ; (U24155) carboxylic acid transporter protein homolog [Saccharomyces cerevisiae] "

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20399	ENU04193	ANI61C4155: 22-42 111..1254	22-42	1104-1123	NAP	g2497126	96	64	0.000000	002	26	54	actin-like protein ARP9 ; probable membrane protein YMR033w - yeast (Saccharomyces cerevisiae) ; (Z49213) unknown [Saccharomyces cerevisiae]
20400	ENU04194	ANI61C2929: 27-47 1303..2447	27-47	1110-1129	NAP	g140489	735	142	2.00E-68				"GNS1 protein ; probable membrane protein YCR034w - yeast (Saccharomyces cerevisiae) ; (X56909) YCR521 [Saccharomyces cerevisiae] ; (S78624) YCR521 [Saccharomyces cerevisiae]=yeast, Peptide, 347 aa [Saccharomyces cerevisiae] ; (X59720) YCR034w, len:347 [Saccharomyces cerevisiae] ; (AF012655) v-snare bypass mutant [Saccharomyces cerevisiae] "
20401	ENU04195	ANI61C7783: 22-52 496..1642	22-52	1105-1126	NAP	g3150261	85	1.00E-15					(AL023634) protein kinase dsk1 [Schizosaccharomyces pombe]
20402	ENU04196	ANI61C6885: 72-91 1175..24	72-91	1154-1181	NAP	g729862	157	72	4.00E-16	32	32		sexual differentiation process protein ISP7 ; isp7 protein - fission yeast (Schizosaccharomyces pombe) ; (D14064) ORF [Schizosaccharomyces pombe]
20403	ENU04197	ANI61C4087: 25-44 316..1468	25-44	1099-1134	NAP	g2506349	449	109	8.00E-46	33	67		potassium-activated aldehyde dehydrogenase precursor ; probable aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) YOR374w - yeast (Saccharomyces cerevisiae) ; (Z75282) ORF YOR374w [Saccharomyces cerevisiae]
20404	ENU04198	ANI50C1851 _1:10..1152	46-65	1128-1155	NAP	g3850128	120	2.00E-26	34	76			(AL033391) COQ3 homologue [Candida albicans]
20405	ENU04199	ANI61C1123 1:3476..4627	25-44	1110-1134	NAP	g2950465	216	85	7.00E-16				(AL022071) fructosyl amine [Schizosaccharomyces pombe]
20406	ENU04200	ANI61C1724: 39-60 554..1712	39-60	1136-1155	NAP	g3183342	350	109	2.00E-41	33	83		hypothetical 44.5 KD protein C14C4.09 in chromosome I ; (Z98596) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20407	ENU04201	ANI61C5929: 1346..188	56-75	1153-1172	NAP		g3929399	2005	438	0	99	67	proline-specific permease (proline transport protein) ; (X79797) proline permease [Emericella nidulans]
20408	ENU04202	ANI61C9268: 22-52 4133..2971	22-52	1124-1142	NAP		g3043726	505	176	2.00E-43	45	22	(AB011173) KIAA0601 protein [Homo sapiens]
20409	ENU04203	ANI61C6430: 22-43 8426..7264	22-43	1115-1142	NAP		g3560143	77	55	0.000000	35	10	(AL031534) putative vacuolar protein sorting-associated protein [Schizosaccharomyces pombe]
20410	ENU04204	ANI61C9220: 22-49 2429..1263	22-49	1123-1146	NAP		g2500937	1219	221	5.00E-96	48	62	probable glucose transporter RCO-3 ; (U54768) RCO3 [Neurospora crassa]
20411	ENU04205	ANI61C9825: 44-63 23..1190	44-63	1139-1169	NAP		g3367585	164	90	3.00E-17	33	44	(AL031135) putative polygalacturonase [Arabidopsis thaliana]
20412	ENU04206	ANI61C3276: 28-47 3347..2173	28-47	1141-1160	NAP		g3687231	208	114	1.00E-24	31	51	(AC005169) hypothetical protein [Arabidopsis thaliana]
20413	ENU04207	ANI61C2648: 54-73 1339..165	54-73	1166-1186	NAP		g1077378	522	179	2.00E-44	35	39	probable membrane protein YLR222c - yeast (Saccharomyces cerevisiae) ; (U19027) Ylr222cp [Saccharomyces cerevisiae]
20414	ENU04208	ANI61C5015: 24-43 1300..122	24-43	1124-1159	NAP		g517205	261	134	1.00E-30	31	59	(U09352) 67 kDa Myosin-crossreactive streptococcal antigen [Streptococcus pyogenes]
20415	ENU04209	ANI61C7035: 59-78 40..1217	59-78	1167-1194	NAP		g2808776	242	125	6.00E-28	33	62	(AL021411) putative oxidoreductase [Streptomyces coelicolor]
20416	ENU04210	ANI61C5367: 22-47 1331..151	22-47	1131-1160	NAP		g3560020	520	210	1.00E-53	38	40	(AL031515) putative secreted cellulase [Streptomyces coelicolor]
20417	ENU04211	ANI61C3671: 55-74 1222..34	55-74	1177-1200	NAP		g2498968	112	50	0.000000	30	57	putative sterigmatocystin biosynthesis peroxidase STCC ; (U34740) putative peroxidase [Emericella nidulans]
20418	ENU04212	ANI61C1123: 47-67 2:1473..284	47-67	1173-1193	NAP		g1174727	199	52	7.00E-14	38	37	thiamin pyrophosphokinase (TPK) (thiamin kinase) ; thiamin pyrophosphokinase (EC 2.7.6.2) - fission yeast (Schizosaccharomyces pombe) ; (X84417) thiamin pyrophosphokinase [Schizosaccharomyces pombe] ; (Z98533) thiamin pyrophosphokinase [Schizosaccharomyces pombe]

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20419	ENU04213	ANI61C1041	22-48	1141-	NAP		g2384693	91	48	5.00E-10	28	51	(AF013216) unknown [Myxococcus xanthus]
20420	ENU04214	ANI61C3678: 1:4698..5891	22-43	1173	NAP		g3819705	726	187	6.00E-62	37	53	(AL032824) syntaxin binding protein 1; sec1 family secretor y protein [Schizosaccharomyces pombe]
20421	ENU04215	ANI61C2667: 1224..20	54-76	1184	NAP		g2289244		37	0.000005			(U97107) membrane glycoprotein CIG30 [Mus musculus]
20422	ENU04216	ANI61C1041	56-75	1201-	NAP		g4490992	312	122	4.00E-27	37	76	(AL035707) putative salicylate hydroxylase [Streptomyces coelicolor]
20423	ENU04217	ANI61C1191: 0:1220..8	22-54	1226	NAP		g417358	260	113	5.00E-37	30	56	ADA3 protein (NGG1 protein) ; NGG1 protein - yeast (Saccharomyces cerevisiae) ; (L12137) NGG1 [Saccharomyces cerevisiae] ; (Z46727) Ngg1p [Saccharomyces cerevisiae]
20424	ENU04218	ANI61C1120	31-51	1185-	NAP		g558311	1277	332	e-121	66	93	(L35487) mannanase [Aspergillus aculeatus]
20425	ENU04219	0:2052..833	22-55	1207	NAP		g731415	1049	317	7.00E-86	56	29	probable calcium-transporting ATPase 6 ; hypothetical protein YEL031w - yeast (Saccharomyces cerevisiae) ; (U18530) P-type ATPase; YEL031W [Saccharomyces cerevisiae]
20426	ENU04220	ANI61C433:3	22-45	1174-	NAP		g731893	922	217	2.00E-62	39	67	putative transporter YIL166C ; probable membrane protein YIL166c - yeast (Saccharomyces cerevisiae) ; (Z46921) unknown [Saccharomyces cerevisiae]
20427	ENU04221	ANI61C9916: 6626..5397	59-87	1211-	NAP		g2388995	159	66	7.00E-13	27	30	(Z98981) hypothetical protein [Schizosaccharomyces pombe]
20428	ENU04222	ANI61C5847: 598..1838	28-52	1246	NAP		g2497199	514	152	5.00E-48	33	77	hypothetical 50.5 KD protein in RNA1-RNT1 intergenic region ; probable membrane protein YMR238w - yeast (Saccharomyces cerevisiae) ; (Z49939) unknown [Saccharomyces cerevisiae] (AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
20429	ENU04223	ANI61C8210: 1498..256	22-40	1203-	NAP		g4104775		46	0.0005			(AJ001261) NIPSNAP2 protein [Mus musculus]
20430	ENU04224	ANI61C6527: 5092..6335	59-79	1222	NAP		g2769258	367	53	3.00E-12	26	55	

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20431	ENU04225	ANI61C9146: 31-52 831..739	31-52	1219-1238	NAP		g4585875	169	48	0.000000	32	89	Unknown protein [Arabidopsis thaliana]
20432	ENU04226	ANI61C8955: 33-52 198..1453	33-52	1225-1246	NAP		g1175374	1122	433	e-120	57	75	hypothetical 57.8 KD protein C2F7.11 in chromosome I; hypothetical protein SPAC2F7.11 - fission yeast (Schizosaccharomyces pombe); (Z50142) unknown [Schizosaccharomyces pombe]; (AF079876) Nrd1p [Schizosaccharomyces pombe] (AF014950) chitinase A [Stenotrophomonas maltophilia] (AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe] proline-specific permease (proline transport protein); (X79797) proline permease [Emmericella nidulans] (AL022244) hypothetical protein [Schizosaccharomyces pombe] (M82963) hexose transporter [Saccharomyces cerevisiae] hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae); (U10400) Ysc84p [Saccharomyces cerevisiae] (AJ235272) SCO2 protein precursor (sco2) [Rickettsia prowazekii] "(AF031228) D-arabinono-1,4-lactone oxidase; L-galactono-gamma-lactone oxidase [Candida albicans] "
20433	ENU04227	ANI61C5197: 22-50 4347..3086	22-50	1222-1241	NAP		g2429326	89	62	2.00E-15	30	36	
20434	ENU04228	ANI61C1024 32-55 3:2189..3452	32-55	1225-1253	NAP		g3560142	716	173	2.00E-42	33	64	
20435	ENU04229	ANI61C1120 61-80 3:1271..2534	61-80	1263-1282	NAP		g3929399	1125	380	e-104	48	76	
20436	ENU04230	ANI61C9721: 42-61 1288..21	42-61	1245-1266	NAP		g2995339	1134	337	e-109	56	46	
20437	ENU04231	ANI61C7513: 41-61 2858..1583	41-61	1248-1274	NAP		g171741	395	164	1.00E-39	25	74	
20438	ENU04232	ANI61C352:1 72-92 358..78	72-92	1290-1309	NAP		g626598	707	247	7.00E-72	43	83	
20439	ENU04233	ANI61C1051 26-49 1:667..1942	26-49	1248-1267	NAP		g3861132	225	97	3.00E-19	29	60	
20440	ENU04234	ANI61C6078: 23-47 3729..5017	23-47	1247-1269	NAP		g4090945	619	307	1.00E-82	38	76	
20441	ENU04235	ANI61C3595: 60-79 1111..2400	60-79	1284-1307	NAP		g2493356	309	125	5.00E-28	47	39	transcription factor btf3 homolog; (U29488) similar to human transcription factor BTF3 and to S. cerevisiae GAL4 DNA-binding enhancer protein [Caenorhabditis elegans]

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20442	ENU04236	ANI61C1023 2:469..1761	23-48	1252-1273	NAP		g1352621	1338	303	e-115	64	83	dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex precursor (E2) (PDC-E2) (MRP3) ; dihydrolipoamide acetyltransferase homolog - Neurospora crassa ; (J04432) ribosomal protein [Neurospora crassa] (AL031545) hypothetical protein [Schizosaccharomyces pombe] (AF091042) putative cercosporin transporter [Cercospora kikuchii] (U78597) kinesin light chain [Plectonema boryanum] (Z97052) hypothetical protein [Schizosaccharomyces pombe] (Z97052) hypothetical protein [Schizosaccharomyces pombe] (S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger] "
20443	ENU04237	ANI61C5788: 22-46 4310..3016	22-46	1247-1274	NAP		g3581917	200	86	6.00E-16	40	65	
20444	ENU04238	ANI61C8008: 22-48 882..2188	22-48	1268-1286	NAP		g3885836	584	113	5.00E-62	37	62	
20445	ENU04239	ANI61C132:1 38-61 038..1569	38-61	1284-1303	NAP		g2645229	430	163	3.00E-39	37	40	
20446	ENU04240	ANI61C7007: 23-52 94..1402	23-52	1257-1289	NAP		g2213548	432	181	8.00E-45	33	70	
20447	ENU04241	ANI61C7007: 23-52 94..1402	23-52	1257-1289	NAP		g2213548	432	181	8.00E-45	33	70	
20448	ENU04242	ANI61C194:2 53-76 083..757	53-76	1317-1337	NAP		g1911486	269	81	1.00E-14	41	47	"(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger] "
20449	ENU04243	ANI61C756:1 71-91 778..449	71-91	1336-1358	NAP		g544049	263	78	1.00E-13			"3',5'-cyclic-nucleotide phosphodiesterase (PDEASE) ; probable 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) pde1 - fission yeast (Schizosaccharomyces pombe) ; (S64907) Dictyostelium discoideum phosphodiesterase homolog [Schizosaccharomyces pombe=fission yeast, Peptide, 346 aa] [Schizosaccharomyces pombe] ; (AL031545) 3',5'-cyclic-nucleotide phosphodiesterase [Schizosaccharomyces pombe] ; pde1 gene [Schizosaccharomyces pombe] "

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20450	ENU04244	ANI61C2416: 3066..1734	22-45	1293-1312	NAP		g400276	531	142	2.00E-53			"mitochondrial peptide chain release factor 1 precursor (MRF-1) ; translation releasing factor RF-1, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X60381) mitochondrial release factor 1 [Saccharomyces cerevisiae] ; (Z72665) ORF YGL143c [Saccharomyces cerevisiae] ; (X99960) YGL143c [Saccharomyces cerevisiae]"
20451	ENU04245	ANI61C1065 4:1589..257	22-43	1290-1312	NAP		g1346290	339	87	2.00E-35	29	63	high-affinity glucose transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
20452	ENU04246	ANI61C5171: 68-90 554..1892	68-90	1345-1364	NAP		g1072485	442	166	4.00E-40	31	79	hypothetical protein YER060w - yeast (Saccharomyces cerevisiae)
20453	ENU04247	ANI61C3347: 42-64 1086..2431	42-64	1326-1345	NAP		g2104457	666	244	1.00E-68	46	92	(Z95397) unknown [Schizosaccharomyces pombe]
20454	ENU04248	ANI61C1024 72-96 4:3131..1786	72-96	1351-1375	NAP		g416864		103	3.00E-21			cycloheximide resistance protein ; (M64932) cyclohexamide resistance protein [Candida maltosa]
20455	ENU04249	ANI61C2921: 38-57 1350..1	38-57	1321-1345	NAP		g731676	349	85	8.00E-16	38	84	hypothetical 44.9 KD protein in ERG7-NMD2 intergenic region ; hypothetical protein YHR075c - yeast (Saccharomyces cerevisiae) ; (U10556) Yhr075cp [Saccharomyces cerevisiae]
20456	ENU04250	ANI61C6844: 68-89 1816..464	68-89	1345-1378	NAP		g2501342	1085	409	e-113	54	68	Peroxisomal targeting signal receptor (peroxisomal protein PAY32) (peroxin-5) (PTS1 receptor) ; (U28155) Pay32p [Yarrowia lipolytica] ; Pay32 gene [Yarrowia lipolytica]
20457	ENU04251	ANI61C2078: 44-63 2042..688	44-63	1333-1356	NAP		g1723275	544	189	4.00E-47	35	80	Hypothetical 55.6 KD protein C13F4.15C in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (AL031322) putative diphthamide biosynthesis protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20458	ENU04252	ANI61C2445: 48-71 1772..411	56-73	1348-1367	NAP		g3915154	523	198	6.00E-50	34	76	trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20459	ENU04253	ANI61C6612: 56-73 1528..162	22-47	1361-1380	NAP		g3560246	806	327	9.00E-89	45	90	(AL031532) putative acetylornithine aminotransferase precursor [Schizosaccharomyces pombe]
20460	ENU04254	ANI61C6742: 22-47 685..2056	25-46	1336-1357	NAP		g729376	787	201	1.00E-50	31	61	urea active transporter ; urea transport protein - yeast (Saccharomyces cerevisiae) ; (U11582) No definition line found [Saccharomyces cerevisiae]
20461	ENU04255	ANI61C211:3 25-46 451..2076	36-56	1347-1371	NAP		g2132005	271	59	4.00E-11	29	49	hypothetical protein YOL057w - yeast (Saccharomyces cerevisiae) ; (Z74799) ORF YOL057w [Saccharomyces cerevisiae]
20462	ENU04256	ANI61C1019 36-56 6:1027..2404	24-44	1341-1363	NAP		g2132942	525	189	4.00E-47	33	79	probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
20463	ENU04257	ANI61C3867: 24-44 3780..2398	26-48	1348-1367	NAP		g3287945	447	140	1.00E-34	36	22	hypothetical 123.7 KD protein C14C4.02 in chromosome I
20464	ENU04258	ANI61C6734: 26-48 2085..3468	22-50	1347-1366	NAP		g3560227	558	158	2.00E-65	39	83	(AL031530) hypothetical protein [Schizosaccharomyces pombe]
20465	ENU04259	ANI61C5197: 22-50 4347..2961	22-54	1347-1368	NAP		g2429326	89	69	1.00E-17	31	38	(AF014950) chitinase A [Stenotrophomonas maltophilia]
20466	ENU04260	ANI61C9460: 22-54 60..1448	22-56	1337-1368	NAP		g4185142	795	314	9.00E-85	41	37	(AC005724) putative DNA repair and recombination protein of the SNF2 family [Arabidopsis thaliana]
20467	ENU04261	ANI61C9182: 22-56 704..2092			NAP		g436464	179	71	2.00E-11	24	89	(Z29098) transposase (putative) [Drosophila hydei]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20468	ENU04262	ANI61C1082 7:1859..3253	22-51	1356-1374	NAP		g1351640	1327	354	6.00E-97	55	78	hypothetical 62.7 KD protein C8A4.06 in chromosome I ; hypothetical protein SPAC8A4.06 - fission yeast (Schizosaccharomyces pombe) ; (Z66569) unknown [Schizosaccharomyces pombe] ; (AL032824) putative chromatin binding snw family nuclear pr otein. [Schizosaccharomyces pombe]
20469	ENU04263	ANI61C5930: 8907..8658	22-51	1356-1375	NAP		g1805251	1103	150	2.00E-35	40	29	(U58946) transposase [Aspergillus awamori]
20470	ENU04264	ANI50C2449 7_1:46..1451	48-68	1383-1411	NAP		g140464		195	2.00E-88	48	48	"hypothetical 107.9 KD protein in POL4-SRD1 intergenic region ; probable membrane protein YCR017c - yeast (Saccharomyces cerevisiae) ; (X59720) YCR017c, len:953 [Saccharomyces cerevisiae] "
20471	ENU04265	ANI61C3644: 5962..6753	54-73	1396-1418	NAP		g2645229	494	153	2.00E-36	37	57	(U78597) kinesin light chain [Plectonema boryanum]
20472	ENU04266	ANI61C1085 7:4172..2761	68-91	1415-1437	NAP		g17006485	1827	277	1.00E-73	55	52	dynammin-related protein DNM1 ; dynammin-related protein DNM1 - yeast (Saccharomyces cerevisiae) ; (Z73106) ORF YLL001w [Saccharomyces cerevisiae] ; (X91488) L1381/DNM1 protein [Saccharomyces cerevisiae]
20473	ENU04267	ANI61C1059 2:83..1499	22-43	1371-1396	NAP		g4049645	1538	484	e-136	64	82	(AF052515) eburicol 14alpha demethylase; CYP51; cytochrome P450 sterol 14-demethylase [Erysiphe graminis f. sp. hordei]
20474	ENU04268	ANI61C7107: 373..1797	53-83	1408-1434	NAP		g1711638	1372	128	e-105	51	39	"putative leucyl-TRNA synthetase, cytoplasmic (leucine--TRNA ligase) (LEURS) ; (Z73100) unknown [Schizosaccharomyces pombe] "

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20475	ENU04269	ANI61C8415: 72-91 4439...3005		1445-1464	NAP		g121146	602	209	2.00E-67	48	59	geranylgeranyl pyrophosphate synthetase (GGPP synthetase) (dimethylallyltransferase / geranyltranstransferase / farnesyltranstransferase ; geranylgeranyl pyrophosphate synthetase - Neurospora crassa ; (U20940) geranylgeranyl pyrophosphate synthetase [Neurospora crassa]
20476	ENU04270	ANI61C2838: 44-64 2795..1360		1411-1439	NAP		g3182996	539	78	1.00E-30	42	92	translation initiation factor EIF-2B beta subunit (EIF-2B GDP-GTP exchange factor) (S20115) ; (U40756) S20i15 [Fugu rubripes]
20477	ENU04271	ANI61C7391: 38-59 1464..23		1416-1436	NAP		g448379	681	155	5.00E-52	41	82	lignostilbene dioxygenase [Sphingomonas paucimobilis]
20478	ENU04272	ANI61C1048 44-63 4:4216..2772		1423-1446	NAP		g422215	825	290	8.00E-94	43	89	alpha-amylase (EC 3.2.1.1) precursor - Aspergillus oryzae
20479	ENU04273	ANI61C1029 52-71 1:1462..1059		1441-1460	NAP		g1351676	992	330	e-101	52	87	probable peptidyl-prolyl cis-trans isomerase C21E11.05C ; hypothetical protein SPAC21E11.05c - fission yeast (Schizosaccharomyces pombe) ; (Z67999) peptidyl-prolyl cis-trans isomerase [Schizosaccharomyces pombe]
20480	ENU04274	ANI61C8002: 69-88 3866..2408		1463-1485	NAP		g3758890	2466	656	0	65	65	(Y14317) catalase/peroxidase [Streptomyces reticuli]
20481	ENU04275	ANI61C6047: 52-71 2779..1320		1447-1469	NAP		g1709501	414	181	1.00E-44	30	97	putative dolichyl-diphosphooligosaccharide--protein glycosyltransferase alpha subunit precursor (oligosaccharyl transferase alpha subunit) ; (Z69368) unknown [Schizosaccharomyces pombe]
20482	ENU04276	ANI61C1060: 23-42 2378..917		1417-1441	NAP		g2879870		59	0.000000 06			(AL021816) hypothetical protein [Schizosaccharomyces pombe]
20483	ENU04277	ANI61C5186: 23-51 843..2305		1420-1443	NAP		g3746666	281	101	3.00E-23	36	98	(AF076848) trihydroxytoluene oxygenase [Burkholderia cepacia]

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20484	ENU04278	ANI61C9834: 1721..252	72-93	1480-1499	NAP		g2621739	892	308	6.00E-83	46	74	(AE000845) long-chain-fatty-acid-CoA ligase [Methanobacterium thermoautotrophicum]
20485	ENU04279	ANI61C5211: 65-85 2167..697	65-85	1474-1493	NAP		g4007751	485	125	6.00E-28	36	62	(Z99126) putative chromatin assembly factor subunit [Schizosaccharomyces pombe]
20486	ENU04280	ANI61C8457: 48-68 5120..3641	48-68	1458-1485	NAP		g731422	724	110	4.00E-30	43	33	hypothetical 70.6 KD protein in HXT8-CAN1 intergenic region ; hypothetical protein YEL065w - yeast (Saccharomyces cerevisiae) ; (U18795)
20487	ENU04281	ANI61C1136 8:1532..53	22-41	1440-1459	NAP		g731864	438	154	1.00E-36	29	79	Yel065wp [Saccharomyces cerevisiae] hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YIL120w - yeast (Saccharomyces cerevisiae) ; (Z46833)
20488	ENU04282	ANI61C1015 36-55 7:1793..3273	36-55	1455-1474	NAP		g118507	771	236	2.00E-79	41	96	unknown [Saccharomyces cerevisiae] "aldehyde dehydrogenase, dimeric nadp-preferring (class 3) (tumor-associated aldehyde dehydrogenase) (HTC-ALDH) ; aldehyde dehydrogenase (NADP+) (EC 1.2.1.4) 3, tumor-associated - rat ; (J03637) aldehyde dehydrogenase [Rattus norvegicus] "
20489	ENU04283	ANI61C6871: 22-47 1566..83	22-47	1442-1462	NAP		g112800	524	130	3.00E-55	39	73	4-coumarate--CoA ligase 1 (4CL) ; 4-coumarate--CoA ligase (EC 6.2.1.12) (clone pc4CL-1) - parsley ; (X13324)
20490	ENU04284	ANI61C3461: 30-49 3057..1569	30-49	1442-1476	NAP		g2605934	2542	914	0	98	94	4-coumarate:CoA ligase Pc4Cl-1 (AA 1-544) [Petroselinum crispum] (AF029885) putative homoserine O-acetyltransferase [Emmericella nidulans]
20491	ENU04285	ANI61C7333: 71-90 1582..92	71-90	1500-1519	NAP		g493580	1781	287	e-111	58	57	(U09580) beta-D-glucoside glucosylhydrolase [Trichoderma reesei]
20492	ENU04286	ANI50C7209 23-47 _6:34..1525	23-47	1453-1472	NAP		g2257513		147	4.00E-52	31	66	(AB004535) hypothetical 105.9 KD protein in AAC3-RFC5 intergenic region. [Schizosaccharomyces pombe]
20493	ENU04287	ANI50C7209 23-47 _6:34..1525	23-47	1453-1472	NAP		g2257513		147	4.00E-52	31	66	(AB004535) hypothetical 105.9 KD protein in AAC3-RFC5 intergenic region. [Schizosaccharomyces pombe]

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20494	ENU04288	ANI61C1125 0:2104..609	23-50	1456-1476	NAP		g730942	744	134	1.00E-47			probable thiamin biosynthetic bifunctional enzyme [contains: thiamin-phosphate pyrophosphorylase (TMP pyrophosphorylase) (TMP-PPASE); hydroxyethylthiazole kinase (4-methyl-5-beta-hydroxyethylthiazole kinase) (THZ kinase) ... ; thi4 protein - fission yeast (Schizosaccharomyces pombe) ; (X78824) thi4 [Schizosaccharomyces pombe] ; (Z98977) thiamin biosynthetic bifunctional enzyme [Schizosaccharomyces pombe] hypothetical 70.4 KD protein C4G9.04C in chromosome I ; (Z69727) hypothetical protein [Schizosaccharomyces pombe] (AL022019) glucosyltransferase [Schizosaccharomyces pombe] (AL031261) hypothetical protein [Schizosaccharomyces pombe] trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (D38414) ORF2 [Bombyx mori] amino acid permease 2 ; (AF053231) amino acid permease [Neurospora crassa] dihydroxy-acid dehydratase (EC 4.2.1.9) - Methanococcus jannaschii ; (U67568) dihydroxy-acid dehydratase (ilvD) [Methanococcus jannaschii] (M16076) low temperature essential protein [Saccharomyces cerevisiae]
20495	ENU04289	ANI61C1139: 4872..3372	22-44	1450-1480	NAP		g1723423	602	92	2.00E-33	27	70	
20496	ENU04290	ANI61C1055 0:1129..2623	27-46	1468-1487	NAP		g2924503	979	306	3.00E-82	44	84	
20497	ENU04291	ANI61C5108: 15..1521	36-56	1481-1500	NAP		g3417417	357	116	1.00E-34	36	59	
20498	ENU04292	ANI61C901:4 642..3126	22-41	1477-1496	NAP		g3915154	728	173	2.00E-73	39	84	
20499	ENU04293	ANI61C9197: 1602..84	25-46	1481-1501	NAP		g1549144		70	3.00E-11			
20500	ENU04294	ANI61C1903: 3547..2027	60-79	1504-1538	NAP		g3929337	271	114	1.00E-24	25	44	
20501	ENU04295	ANI61C8936: 218..1739	43-63	1502-1522	NAP		g2127851	616	136	6.00E-44	34	82	
20502	ENU04296	ANI61C1103 3:3840..5366	44-68	1508-1527	NAP		g171850	350	152	5.00E-36	31	65	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20503	ENU04297	ANI61C3982: 1171..2702	37-57	1500-1525	NAP		g544017	624	268	7.00E-71	35	90	protein kinase CHK1 (checkpoint kinase CHK1) ; protein kinase chk1 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe) ; (L13742) protein kinase [Schizosaccharomyces pombe] ; (U37421) protein kinase [Schizosaccharomyces pombe] ; (AL034564) protein kinase chk1 [Schizosaccharomyces pombe] (AF027687) GTPase activating protein homolog [Cochliobolus heterotrophus] (AL033389) aminotransferase [Schizosaccharomyces pombe]
20504	ENU04298	ANI61C8369: 1620..81	48-67	1518-1544	NAP		g2598189	899	123	1.00E-39	47	60	peroxisome biosynthesis protein PAS1 (peroxin-1) ; PAS1 protein - yeast (Pichia pastoris) ; (Z36987) PAS1 [Pichia pastoris]
20505	ENU04299	ANI61C2578: 4121..5669	22-57	1507-1526	NAP		g3850081	962	293	6.00E-84	45	97	serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) ; serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) ; (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] ; (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe]
20506	ENU04300	ANI61C1144 4:1677..128	63-86	1551-1570	NAP		g1172019	1098	345	4.00E-94	50	37	(AL023704) putative translocation elongation factor-Tu family [Schizosaccharomyces pombe]
20507	ENU04301	ANI61C1100 4:8033..9596	59-77	1561-1580	NAP		g1346422	1720	624	e-178	62	84	"(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe] "
20508	ENU04302	ANI61C1042 7:4705..3139	64-87	1558-1588	NAP		g3169065	1046	181	e-108	52	44	(AB018331) KIAA0788 protein [Homo sapiens]
20509	ENU04303	ANI61C8276: 48..1626	40-59	1554-1573	NAP		g1749480	431	154	1.00E-36	61	16	(AF042379) spindle pole body protein spe97 homolog GCP2 [Homo sapiens]
20510	ENU04304	ANI61C4319: 4290..5870	63-82	1582-1601	NAP		g3882297	2494	460	e-128	48	37	
20511	ENU04305	ANI61C8432: 2298..709	67-95	1577-1612	NAP		g2801701	575	134	2.00E-48	32	49	

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20512	ENU04306	ANI61C3797: 237..1828	31-54	1549-1580	NAP		g2132851	204	82	1.00E-14	24	87	probable membrane protein YOL137w - yeast (Saccharomyces cerevisiae) ; (Z74879) ORF YOL137w [Saccharomyces cerevisiae] ; (X95465) ORF [Saccharomyces cerevisiae] sugar transporter STL1 ; sugar transport protein STP1 - yeast (Saccharomyces cerevisiae) ; (U33057) Std1p: plasma membrane sugar transporter; CAI: 0.19 [Saccharomyces cerevisiae]
20513	ENU04307	ANI61C9558: 4822..3228	22-47	1555-1574	NAP		g1711561	506	199	5.00E-50	30	85	
20514	ENU04308	ANI61C8986: 99..1693	23-44	1556-1579	NAP		g4007794	111	69	1.00E-10	28	41	(AL034463) hypothetical protein [Schizosaccharomyces pombe]
20515	ENU04309	ANI61C5894: 1725..125	26-46	1565-1584	NAP		g1351684	1064	314	e-109	43	13	hypothetical 420.8 KD protein C1F5.11C in chromosome I ; (Z68136) unknown [Schizosaccharomyces pombe]
20516	ENU04310	ANI61C1677: 1762..1704	40-59	1589-1609	NAP		g2506776	993	410	e-113	42	79	"translation initiation factor IF-2, mitochondrial precursor (IF-2MT) ; translation initiation factor IF-2, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z74765) ORF YOL023w [Saccharomyces cerevisiae] "
20517	ENU04311	ANI61C8887: 227..1875	70-90	1642-1676	NAP		g1723769	177	61	0.000000	27	41	putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
20518	ENU04312	ANI61C1038: 7:2377..735	26-45	1608-1635	NAP		g3560201	423	153	2.00E-36	34	45	(AL031528) pseudouridine synthase [Schizosaccharomyces pombe]
20519	ENU04313	ANI61C9601: 4936..3281	48-70	1642-1661	NAP		g2408051	1465	271	e-119	45	57	(Z99164) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20520	ENU04314	ANI61C6953: 1015..2681	22-44	1625-1645	NAP		g1175369	331	126	4.00E-28	32	83	hypothetical DNA polymerase beta-like protein C2F7.06C ; hypothetical protein SPAC2F7.06c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe] (L25310) beta-mannase [Trichoderma reesei]
20521	ENU04315	ANI61C2457: 68-86	169-1692	1641-1660	NAP		g506848	771	327	2.00E-88	47	66	"5-aminolevulinic acid synthase, mitochondrial precursor (delta-aminolevulinic synthase) (delta-Ala synthetase) ; 5-aminolevulinic synthase (EC 2.3.1.37) precursor - Emericella nidulans ; (X64170) 5-aminolevulinic acid synthase [Emericella nidulans] "
20522	ENU04316	ANI50C4730 _1:12..1681	33-52	1641-1660	NAP		g585244	1033	0	99	99	82	hypothetical 76.8 KD protein in chromosome II ; (AF064207) putative histone deacetylase [Schizosaccharomyces pombe]
20523	ENU04317	ANI61C1190: 15284..13607	33-54	1645-1667	NAP		g3023933	1040	73	8.00E-31	42	55	putative urea active transporter [Schizosaccharomyces pombe]
20524	ENU04318	ANI61C8043: 4994..3314	70-93	1678-1708	NAP		g4106690	758	220	3.00E-56	41	48	(AL021816) hypothetical protein [Schizosaccharomyces pombe]
20525	ENU04319	ANI61C7218: 69-93	69-93	1699-1722	NAP		g2879870	1686	182	5.00E-45	35	48	(AE000703) N-methylhydantoinase A [Aquifex aeolicus]
20526	ENU04320	ANI61C8090: 40-61	40-61	1670-1695	NAP		g2983296	794	309	4.00E-83	36	82	(Y15277) cytochrome P450 monooxygenase [Gibberella fujikuroi]
20527	ENU04321	ANI61C1567: 39-70	39-70	1682-1701	NAP		g3549879	742	292	4.00E-78	39	91	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976)
20528	ENU04322	ANI61C3019: 22-55	22-55	1663-1688	NAP		g3929362	432	197	3.00E-49	32	72	pisatin demethylase [Nectria haematococca mpVI]
20529	ENU04323	ANI61C8724: 22-47	22-47	1677-1698	NAP		g2688966	537	139	2.00E-55	26	90	(AF027979) carnitine acetyl transferase [Magnaporthe grisea]

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20530	ENU04324	ANI61C379:2 693..966	38-57	1700-1721	NAP		g2497193	785	170	2.00E-60	36	69	hypothetical 56.2 KD protein in ERG8-UBP8 intergenic region ; probable membrane protein YMR221c - yeast (<i>Saccharomyces cerevisiae</i>) ; (Z49939)
20531	ENU04325	ANI61C1536: 15..1749	35-55	1708-1727	NAP		g3650401	278	137	2.00E-31	27	52	unknown [<i>Saccharomyces cerevisiae</i>] (AL031739) zinc finger protein
20532	ENU04326	ANI61C8724: 3923..5671	22-51	1707-1728	NAP		g2688966	537	139	2.00E-55	26	90	[<i>Schizosaccharomyces pombe</i>] (AF027979) carnitine acetyl transferase [Magnaporthe grisea]
20533	ENU04327	ANI61C1070: 530..2304	63-83	1776-1795	NAP		g4033486	274	82	5.00E-23	31	40	putative tartrate transporter ; (U25634) putative tartrate transporter; inducible by tartrate; Method: conceptual translation supplied by author. [<i>Agrobacterium vitis</i>] ; ttuB gene
20534	ENU04328	ANI61C8868: 6159..4379	22-52	1725-1756	NAP		g2144167	1713	362	e-143	55	71	[<i>Agrobacterium vitis</i>] beta-glucosidase (EC 3.2.1.21) - yeast (<i>Candida molischiana</i>) ; (U16259)
20535	ENU04329	ANI61C9692: 4164..2329	58-77	1836-1855	NAP		g3924850	252	109	8.00E-23	32	27	beta-glucosidase [<i>Pichia capsulata</i>] "(Z81586) predicted using Genefinder; similar to Alcohol/other dehydrogenases, short chain type
20536	ENU04330	ANI61C7957: 4466..2619	67-87	1853-1872	NAP		g4502497	149	69	2.00E-19	32	59	[<i>Caenorhabditis elegans</i>] "chromosome 22 open reading frame 1 ; (U84894) 239AB [<i>Homo sapiens</i>] regulatory protein GAL4 ; regulatory protein GAL4 - yeast (<i>Saccharomyces cerevisiae</i>) ; (K01486) GAL4 protein
20537	ENU04331	ANI61C7791: 716..2576	23-46	1819-1841	NAP		g1169823	61	61	0.000000			[<i>Saccharomyces cerevisiae</i>] ; (Z67751) GAL4 [<i>Saccharomyces cerevisiae</i>] ; (Z73604) ORF YPL248c
20538	ENU04332	ANI61C1004 0:1927..66	70-92	1867-1889	NAP		g1872514	513	120	3.00E-26	37	33	[<i>Saccharomyces cerevisiae</i>] (U84404) E6-associated protein E6-AP/ubiquitin-protein ligase [<i>Homo sapiens</i>] ; (AF016708) E6-AP ubiquitin-protein ligase [<i>Homo sapiens</i>]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20539	ENU04333	ANI61C7032: 22-54 1524..3386		1823-1842	NAP		g466152	446	173	9.00E-48	35	44	hypothetical 76.2 KD protein ZK632.7 in chromosome III ; hypothetical protein ZK632.7 - Caenorhabditis elegans ; (Z22181) cDNA EST CEESN66F comes from this gene; cDNA EST yk395c9.5 comes from this gene [Caenorhabditis elegans]
20540	ENU04334	ANI61C7032: 22-54 1524..3386		1823-1842	NAP		g466152	446	173	9.00E-48	35	44	hypothetical 76.2 KD protein ZK632.7 in chromosome III ; hypothetical protein ZK632.7 - Caenorhabditis elegans ; (Z22181) cDNA EST CEESN66F comes from this gene; cDNA EST yk395c9.5 comes from this gene [Caenorhabditis elegans]
20541	ENU04335	ANI61C6610: 28-47 3603..3426		1847-1880	NAP		g3929362	555	147	2.00E-70	36	98	pisatin demethylase (cytochrome P450 57A1) ; pisatin demethylase - fungus (Nectria haematococca) ; (L20976) pisatin demethylase [Nectria haematococca mpVI]
20542	ENU04336	ANI61C9614: 68-86 47..1956		1915-1934	NAP		g3184088	392	160	8.00E-44	29	76	(AL023781) hypothetical protein [Schizosaccharomyces pombe]
20543	ENU04337	ANI61C7030: 22-48 3655..1743		1873-1892	NAP		g2626826		98	3.00E-19			"(D83967) YfkN [Bacillus subtilis] ; (Z99108) similar to 2',3'-cyclic-nucleotide 2'-phosphodiesterase [Bacillus subtilis] "
20544	ENU04338	ANI61C7115: 71-90 130..2055		1931-1954	NAP		g2133268	97	85	2.00E-15	25	52	DNA-binding protein amdA - Emericella nidulans ; (L28810) regulatory protein [Emericella nidulans]
20545	ENU04339	ANI61C3433: 22-41 1237..3168		1890-1909	NAP		g3925758	182	84	3.00E-15	26	76	(AL034352) hypothetical C2H2-type zinc-finger protein
20546	ENU04340	ANI61C7725: 22-51 2046..107		1900-1919	NAP		g2688313		59	0.00000008			[Schizosaccharomyces pombe] "(AE001146) sensory transduction histidine kinase, putative [Borrelia burgdorferi] "
20547	ENU04341	ANI61C680:3 43-70 6..1995		1932-1960	NAP		g4519181	3365	1236	0	99	63	(AB023911) chitin synthase [Emericella nidulans]
20548	ENU04342	ANI61C6259: 51-72 5140..7105		1955-1974	NAP		g1546072	1439	149	7.00E-35	30	22	(U68040) polyketide synthase [Cochliobolus heterostrophus]

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20549	ENU04343	ANI61C2341: 2086..99	54-74	1979-1999	NAP		g2104457	246	104	8.00E-29	31	45	(Z95397) unknown [Schizosaccharomyces pombe]
20550	ENU04344	ANI61C9697: 45-67 3156..1168		1967-1991	NAP		g399198	603	183	8.00E-73	38	35	cell division control protein 25 ; SKCDC25 protein - yeast (Saccharomyces kluyveri) (fragment) ; (M82964) CDC25 [Saccharomyces kluyveri]
20551	ENU04345	ANI61C4603: 24-44 2740..737		1965-1985	NAP		g3915154	353	83	2.00E-24	33	91	trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20552	ENU04346	ANI61C1932: 35-54 1352..3563		1983-2004	NAP		g1685364	337	113	1.00E-41	33	44	(U78320) chitinase [Entamoeba invadens]
20553	ENU04347	ANI61C9831: 41-60 2452..4478		2004-2023	NAP		g2117303	1418	346	e-155	66	90	(Z95620) n-acetylglucosaminyl-phosphatidylinositol [Schizosaccharomyces pombe]
20554	ENU04348	ANI61C6656: 54-73 3133..1105		2018-2040	NAP		g2506921	161	55	0.000001	32	43	"probable taurine catabolism dioxygenase (sulfate starvation-induced protein 3) (SSI3) ; (D85613) dioxygenase [Escherichia coli] ; (U73857) dioxygenase [Escherichia coli] ; (AE000143) taurine dioxygenase, 2-oxoglutarate-dependent [Escherichia coli] "
20555	ENU04349	ANI61C5227: 22-52 3425..3954		1984-2009	NAP		g728744		53	0.000007			auxin-induced protein PCNT115 ; auxin-induced protein - common tobacco ; (X56267) auxin-induced protein [Nicotiana tabacum]
20556	ENU04350	ANI61C1039 56-77 0:4698..2668		2022-2043	NAP		g4585598		65	2.00E-35			(AL049628) putative exporter [Streptomyces coelicolor]
20557	ENU04351	ANI61C1023 45-64 4:2074..22		2036-2055	NAP		g549758	157	119	6.00E-26	28	36	"ferric reductase transmembrane component 2 precursor ; ferric reductase FRE2 precursor - yeast (Saccharomyces cerevisiae) ; (X75950) ORF5, F711 [Saccharomyces cerevisiae] ; (Z28220) ORF YKL220c [Saccharomyces cerevisiae] ; ORF 5 [Saccharomyces cerevisiae] "

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20558	ENU04352	ANI61C9133: 393..2453	54-73	2053-2073	NAP		g3650375	586	254	2.00E-66	37	55	(AL031740) putative mitochondrial translation system component [Schizosaccharomyces pombe] (X54316) GTP-binding protein [Saccharomyces cerevisiae]
20559	ENU04353	ANI61C2779: 68-89		2079-2099	NAP		g4528		360	0	58	88	probable coatomer gamma subunit (gamma-coat protein) (gamma-COP) ; (Z95396) putative coatomer gamma subunit [Schizosaccharomyces pombe] (U78597) kinesin light chain [Plectonema boryanum]
20560	ENU04354	ANI61C1106 40-59		2054-2073	NAP		g3182972	794	217	e-127	47	68	DNA repair protein RAD50 (153 KD protein) ; RAD50 protein - yeast (Saccharomyces cerevisiae) ; (X14814) 153 kD protein (AA 1 - 1312) [Saccharomyces cerevisiae] ; (X96722) ORF N0872 [Saccharomyces cerevisiae] ; (Z71526) ORF YNL250w [Saccharomyces cerevisiae] (Z83828) AmMst-1 [Amanita muscaria]
20561	ENU04355	ANI61C1103 26-49		2041-2063	NAP		g2645229	442	195	8.00E-49	36	39	(AL021746) phosphatidylserine decarboxylase [Schizosaccharomyces pombe]
20562	ENU04356	ANI61C9409: 23-45		2031-2060	NAP		g131782	956	239	9.00E-89	32	52	trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (AL021816) hypothetical protein [Schizosaccharomyces pombe]
20563	ENU04357	ANI61C439:5 70-89		2092-2112	NAP		g2258125	520	209	1.00E-59	33	95	SpoC1-C1C protein - Emericella nidulans ; (M83571) SpoC1-C1C [Emericella nidulans]
20564	ENU04358	ANI61C8264: 46-67		2074-2109	NAP		g2842521	730	322	6.00E-87	50	100	
20565	ENU04359	ANI61C4603: 26-61		2108-2128	NAP		g3915154	353	83	2.00E-24	33	87	
20566	ENU04360	ANI61C1060: 23-42		2143-2162	NAP		g2879870		59	0.000000			
20567	ENU04361	ANI61C9302: 68-92		2183-2212	NAP		g283343	304	80	1.00E-17	58	16	

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20568	ENU04362	ANI61C1076 9:1972..4306	61-80	2318- 2350	NAP		g1174987	1186	166	3.00E-61	45	20	vacuolar protein sorting-associated protein VPS35 ; vacuolar protein-sorting protein VPS35 - yeast (Saccharomyces cerevisiae) ; (Z49429) ORF YJL154c [Saccharomyces cerevisiae]
20569	ENU04363	ANI61C216:3 135..785	35-55	2322- 2343	NAP		g1352937	48	45	0.002	25	28	hypothetical 39.9 KD protein in HOM6-PMT4 intergenic region ; probable membrane protein YJR141w - yeast (Saccharomyces cerevisiae) ; (Z49641) ORF YJR141w [Saccharomyces cerevisiae]
20570	ENU04364	ANI61C5788: 49-68 2376..22	49-68	2330- 2361	NAP		g3618207	721	320	3.00E-86	33	88	(AL031579) conserved hypothetical protein [Schizosaccharomyces pombe]
20571	ENU04365	ANI61C1001 4:243..2606	66-87	2359- 2385	NAP		g131816	189	64	6.00E-16			DNA repair protein RAD9 ; rad9 protein - fission yeast (Schizosaccharomyces pombe) ; rad9 protein - fission yeast (Schizosaccharomyces pombe) ; (X58231) rad9 protein [Schizosaccharomyces pombe] ; (X64648) rad9 [Schizosaccharomyces pombe] ; (X77276) rad9 [Schizosaccharomyces pombe]
20572	ENU04366	ANI61C9256: 60-80 4444..4770	60-80	2362- 2381	NAP		g3915154		75	2.00E-31			trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides]
20573	ENU04367	ANI61C4216: 58-77 3367..970	58-77	2391- 2410	NAP		g3024061	3393	545	0	85	97	6-phosphofructokinase (phosphofructokinase) (phosphohexokinase) ; (Z79690) phosphofructokinase [Aspergillus niger]
20574	ENU04368	ANI61C1048 2:4278..4010	47-72	2372- 2403	NAP		g1175379	541	111	2.00E-44	44	27	hypothetical 88.2 KD protein C2F7.18C in chromosome I
20575	ENU04369	ANI61C3090: 22-48 650..3116	22-48	2413- 2445	NAP		g1945502	98	82	2.00E-14	34	6	(U13644) F56D2.5 gene product [Caenorhabditis elegans]

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20576	ENU04370	ANI61C9380: 3693..1211	70-89	2490-2510	NAP		g1175371	138	80	5.00E-14	31	22	hypothetical 71.9 KD protein C2F7.08C in chromosome I ; hypothetical protein SPAC2F7.08c - fission yeast (Schizosaccharomyces pombe) ; (Z50142) unknown [Schizosaccharomyces pombe] hypothetical 61.8 KD protein in KGD1-SIM1 intergenic region ; probable membrane protein YIL120w - yeast (Saccharomyces cerevisiae) ; (Z46833) unknown [Saccharomyces cerevisiae] (Z99753) hypothetical protein [Schizosaccharomyces pombe] (AF059906) ubiquitin fusion degradation protein-2 [Schizosaccharomyces pombe] 2-oxoglutarate dehydrogenase E1 component precursor (alpha-ketoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) precursor - yeast (Saccharomyces cerevisiae) ; (Z46833) 2-oxoglutarate dehydrogenase E1 component [Saccharomyces cerevisiae] "transcription initiation factor IIE, alpha subunit (TFIIE-alpha) (transcription factor A large subunit) (factor A 66 KD subunit) ; transcription initiation factor IIE chain TFA1 - yeast (Saccharomyces cerevisiae) ; (Z28028) ORF YKL028w [Saccharomyces cerevisiae] ; (U12825) transcription factor TFIIE, large subunit [Saccharomyces cerevisiae] "
20577	ENU04371	ANI61C9639: 8574..6059	44-75	2490-2516	NAP		g731864	383	176	4.00E-43	25	65	
20578	ENU04372	ANI61C3273: 2642..118	34-53	2497-2517	NAP		g2465152	240	95	2.00E-18	40	13	
20579	ENU04373	ANI61C450:2 701..131	43-64	2552-2571	NAP		g3930517	1333	455	e-127	40	86	
20580	ENU04374	ANI61C9792: 5406..2821	24-45	2547-2566	NAP		g730221	3335	788	0	67	81	
20581	ENU04375	ANI61C1144 2:2530..2683	64-85	2639-2658	NAP		g549038	133	71	1.00E-13			
20582	ENU04376	ANI61C8159: 4169..1515	70-89	2659-2682	NAP		g3882229	85	46	0.001	26	21	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20583	ENU04377	ANI61C4130: 22-41 3177..520	22-41	2608-2637	NAP		g3005592	548	166	7.00E-40	34	27	(AF051911) telomerase reverse transcriptase; mTERT [Mus musculus]; (AF073311) telomerase catalytic subunit [Mus musculus]
20584	ENU04378	ANI61C9698: 56-75 3605..2478	56-75	2651-2671	NAP		g1723845	377	171	3.00E-41	34	45	putative ATP-dependent RNA helicase YGL064C; hypothetical protein YGL064c - yeast (Saccharomyces cerevisiae); (Z72586) ORF YGL064c [Saccharomyces cerevisiae]
20585	ENU04379	ANI61C1132: 72-94 155..2820	72-94	2676-2695	NAP		g3136048	2024	362	5.00E-99	50	64	(AL023592) putative helicase [Schizosaccharomyces pombe]
20586	ENU04380	ANI61C8590: 22-55 1848..4579	22-55	2689-2711	NAP		g4507071	509	229	5.00E-59	33	43	"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3; HIP116 protein - human; (L34673) ATPase [Homo sapiens]"
20587	ENU04381	ANI61C8661: 71-90 50..2869	71-90	2828-2848	NAP		g4263786	850	225	e-100	37	86	"(AC006068) putative acyl coenzyme A oxidase, peroxisomal component [Arabidopsis thaliana]"
20588	ENU04382	ANI61C3919: 51-70 554..3384	51-70	2813-2839	NAP		g4502869	1191	176	e-105	43	64	"chloride channel 3; chloride channel protein 3, long form - human; (X78520) chloride channel 3 [Homo sapiens]"
20589	ENU04383	ANI61C9577: 38-57 3062..68	38-57	2971-2990	NAP		g3116148	1166	196	e-133	37	62	(AL023290) putative ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20590	ENU04384	ANI61C3260: 26-46 1407..2082	26-46	631-655	NAP		g1513174	66	87	9.00E-17	22	43	(U65488) fumocoumarin-inducible cytochrome P450 [Papilio polyxenes]
20591	ENU04385	ANI61C1511: 378..1307			NAP		g2113796	807	196	1.00E-57	59	54	(X94399) cAMP-dependent protein kinase catalytic subunit [Aspergillus niger]
20592	ENU04386	ANI61C6899: 222-240 134..706	222-240	531-552	NAP		g832882	351	116	1.00E-25	57	100	(L42454) EF-hand protein [Schizosaccharomyces pombe]
20593	ENU04387	ANI61C9048: 1..1497			NAP		g3116134	882	219	2.00E-56	42	10	(AL023288) hypothetical protein [Schizosaccharomyces pombe]
20594	ENU04388	ANI61C2436: 35-54 942..1651	35-54	632-651	NAP		g1078673	545	83	3.00E-34	60	22	gamma-adaptin - smut fungus (Ustilago maydis) [Ustilago maydis]
20595	ENU04389	ANI61C4421: 34-60 583..1	34-60	539-561	NAP		g2094863	306	171	3.00E-42	43	19	(Z95334) putative helicase [Schizosaccharomyces pombe]

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20596	ENU04390	ANI61C291:7 480..6857	42-61	578-603	NAP		g2501165	134	79	2.00E-14	32	28	hypothetical 59.6 KD protein in DSK2-CAT8 intergenic region [Saccharomyces cerevisiae]
20597	ENU04391	ANI61C1032 70-88	70-88	516-536	NAP		g2498702	86	70	1.00E-11	37	31	sterigmatocystin 7-O-methyltransferase precursor [Aspergillus parasiticus]
20598	ENU04392	0:4040..4598 ANI61C1073: 71-90 1..662	71-90	579-598	NAP		g3879319	431	177	5.00E-44	44	29	(Z83319) similar to ABC transporters; cDNA EST EMBL:D67233 comes from this gene; cDNA EST
20599	ENU04393	ANI61C5507: 122-139 3945..3369	122-139	442-461	NAP		g2408049	136	46	0.0001	29	8	EMBL:D67486 comes from this gene; cDNA EST yk385d1.5 comes from this gene; cDNA EST yk398a5.5 comes from this gene; cDNA EST yk398a5.3 co... []
20600	ENU04394	ANI61C3342: 114-133 1..470	114-133	372-391	NAP		g731024	295	145	2.00E-34	46	38	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
20601	ENU04395	ANI61C8781: 23-43 1035..1	23-43	728-747	NAP		g729397	616	260	8.00E-69	41	64	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) [Saccharomyces cerevisiae]"
20602	ENU04396	ANI61C5009: 114-133 1..392	114-133	331-358	NAP		g3116140	276	124	2.00E-28	48	38	[elongation factor 1-alpha (EF-1-alpha) (elongation factor TU) (EF-TU) [Sulfolobus solfataricus]
20603	ENU04397	ANI61S1051: 22-44 298..604	22-44	261-280	NAP		g1175960	223	97	9.00E-20	53	43	(AL023288) hypothetical dolichyl-phosphate beta-glucosyltransferase protein [Schizosaccharomyces pombe]
20604	ENU04398	ANI61C8380: 22-47 2017..1526	22-47	394-414	NAP		g1173537	285	140	5.00E-33	42	28	hypothetical 23.9 KD protein in THI5-AGP3 intergenic region [Saccharomyces cerevisiae]
20605	ENU04399	ANI61C5287: 59-86 84..543	59-86	454-479	NAP		g3183344	276	105	2.00E-22	37	22	(U30376) Lipomyces kononenkoae subsp. spenceri martinsiae alpha-amylase [Lipomyces kononenkoae]
20606	ENU04400	ANI61S1675: 1..835			NAP		g786117	180	51	0.00001	24	55	hypothetical 85.4 KD protein C14C4.11 in chromosome I [Schizosaccharomyces pombe]
20607	ENU04401	ANI61C6597: 52-71 10548..9385	52-71	805-829	NAP		g731799	405	129	2.00E-29	38	48	(L41834) nuclear protein [Ensis minor] hypothetical 54.9 KD protein in CBR5-NOT3 intergenic region [Saccharomyces cerevisiae]

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20608	ENU04402	ANI61C9383: 97-116 6240..7174	709-116	709-730	NAP		g586521	303	143	2.00E-33	36	29	hypothetical 86.4 KD protein in PHO5-VPS15 intergenic region [Saccharomyces cerevisiae]
20609	ENU04403	ANI61C1091 24-51 2..1357..1	801-828		NAP		g3261632	498	116	3.00E-28	46	42	(Z79700) accD2 [Mycobacterium tuberculosis]
20610	ENU04404	ANI61C4623: 27-46 1815..1	660-679		NAP		g2499460	1545	267	9.00E-76	54	33	"phosphoenolpyruvate synthase (pyruvate, water dikinase) (PEP synthase) [Synecocystis sp.]"
20611	ENU04405	ANI61C1654: 25-52 1010..1	726-744		NAP		g3172113	1585	522	e-148	97	16	(AB014886) typeII DNA topoisomerase [Emicella nidulans]
20612	ENU04406	ANI61C1070 35-54 7:639..1826	790-811		NAP		g3121791	701	162	2.00E-63	53	23	sodium transport ATPase 5 [Saccharomyces cerevisiae]
20613	ENU04407	ANI61S1450: 850..174			NAP		g3037018	302			36	97	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]
20614	ENU04408	ANI61C5938: 264..1155			NAP		g2624272	56	69	3.00E-11	27	89	(AL008967) hypothetical protein Rv2750 [Mycobacterium tuberculosis]
20615	ENU04409	ANI61C1002 22-48 6:2058..3848	808-829		NAP		g1706177	754	111	6.00E-24	29	27	cutinase transcription factor 1 beta [Fusarium solani f. sp. pisi]
20616	ENU04410	ANI61C3739: 29-48 1..1223	756-781		NAP		g3766365	756	155	3.00E-37	39	23	(AL031907) putative cysteine-rich transcriptional regulator [Schizosaccharomyces pombe]
20617	ENU04411	ANI61S974:9 2..551			NAP		g1709793	151	60	0.000000	29	69	salivary proline-rich protein PO (allele M) (contains: peptide P-D) [Homo sapiens]
20618	ENU04412	ANI61C8633: 25-52 1..2156	802-829		NAP		g3929388	3438	221	e-140	99	35	"neutral trchalase (alpha, alpha-trehalase) (alpha, alpha-trehalose glucosylhydrolase) [Emicella nidulans]"
20619	ENU04413	ANI61C7207: 2146..1628			NAP		g482275	661	266	5.00E-71	79	21	abaA protein - Emicella nidulans [Emicella nidulans]
20620	ENU04414	ANI61C3378: 28-49 1304..1	723-749		NAP		g731689	578	164	7.00E-40	30	7	hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
20621	ENU04415	ANI61C1036 39-58 0:514..1	390-413		NAP		g3273562	425	145	3.00E-34	81	59	(AF036707) RAD6 [Candida albicans]
20622	ENU04416	ANI61C7198: 1588..1082			NAP		g1723597	318	136	1.00E-31	42	32	hypothetical 58.1 KD protein in PET117-CEM1 intergenic region [Saccharomyces cerevisiae]
20623	ENU04417	ANI61C7472: 26-53 1962..1577	310-329		NAP		g112925	127	71	7.00E-12	30	88	41-2 protein antigen precursor [Plasmodium falciparum]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20624	ENU04418	ANI61S4602: 665..1	90-108	530-547	NAP		g465511	359	136	2.00E-31	41	33	hypothetical 73.8 KD protein in SAS3-SEC17 intergenic region [Saccharomyces cerevisiae]
20625	ENU04419	ANI61C3410: 2232..1354	110-137	804-827	NAP		g728828	496	219	3.00E-56	52	49	allantoinase [Saccharomyces cerevisiae]
20626	ENU04420	ANI61C2027: 171-190	347-366		NAP		g2408036	291	117	7.00E-26	35	50	(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
20627	ENU04421	ANI61C7678: 1..578	22-47	429-448	NAP		g423793	75	58	0.000000	35	45	carboxylesterase (EC 3.1.1.1) - Pseudomonas sp. (strain KWI-56) [Pseudomonas sp.]
20628	ENU04422	ANI61C5312: 1..1093	22-48	804-823	NAP		g1321944	224	54	0.000001	26	47	(X97346) FCYX [Saccharomyces cerevisiae]
20629	ENU04423	ANI61S2268: 1..784			NAP		g4218005	263	46	0.0002	27	36	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
20630	ENU04424	ANI61S3044: 1..528	98-117	412-435	NAP		g3980554	227	110	6.00E-24	34	63	"(AC004849) similar to several hypothetical proteins: U70849 (PID:g1572765), U00043 (PID:g470341), Z50070 (PID:g899462), AL033127 (PID:g3821335), and P40034 (PID:g731464) [Homo sapiens]" (AL034490) similar to yeast ngg1-interacting factor 3 [Schizosaccharomyces pombe]
20631	ENU04425	ANI61C3082: 366..833	22-46	459-477	NAP		g4008560	215	88	5.00E-17	57	45	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emeritella nidulans]
20632	ENU04426	ANI61C5001: 1459..1	90-109	717-736	NAP		g1705828	2423	530	e-150	99	26	NADH-cytochrome B5 reductase precursor (P34/P32) [Saccharomyces cerevisiae]
20633	ENU04427	ANI61C8508: 1020..2041	23-50	804-829	NAP		g549725	520	189	2.00E-47			(AF056182) G-protein beta subunit [Emeritella nidulans]
20634	ENU04428	ANI61C1064: 4..1..1254	22-41	805-829	NAP		g3493539	1740	431	e-120	99	69	rad4+/cut5+ product - fission yeast (Schizosaccharomyces pombe) []
20635	ENU04429	ANI61C7169: 755..1	43-62	626-653	NAP		g476807	365	87	8.00E-34	38	51	hypothetical protein YDL087c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
20636	ENU04430	ANI61C7108: 2551..3462	29-56	806-828	NAP		g2131329	388	87	8.00E-35	32	98	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20637	ENU04431	ANI61C1554:1480..1			NAP		g1351183	806	136	2.00E-44	43	38	"tyrosyl-TRNA synthetase, mitochondrial precursor (tyrosine--TRNA ligase) (TYRRS) [Neurospora crassa]"
20638	ENU04432	ANI61C9626:22-41 2931..4989		792-814	NAP		g3702631	2007	406	e-113	68	36	(AL031824) protein transport protein sec23 homolog [Schizosaccharomyces pombe]
20639	ENU04433	ANI61S953:6 14..1	182-204	567-593	NAP		g3647341	556	237	6.00E-62	58	21	(AL031644) RAD16 nucleotide excision repair protein homolog [Schizosaccharomyces pombe]
20640	ENU04434	ANI61C2676:22-47 1204..1		712-739	NAP		g2654106	1074	201	4.00E-51	74	39	(AF034260) protein kinase NRC-2 [Neurospora crassa]
20641	ENU04435	ANI61C4833:1060..1			NAP		g4027860	1541	242	e-125	92	38	(U47540) TamaA [Emericella nidulans]
20642	ENU04436	ANI61C5942:38-57 1632..399		778-797	NAP		g3183172	874	124	2.00E-52	41	56	"probable threonyl-TRNA synthetase, mitochondrial precursor (threonine--TRNA ligase) (THRRS) [Schizosaccharomyces pombe]"
20643	ENU04437	ANI61C528:6 252..8036	22-49	809-828	NAP		g2131739	572	107	1.00E-22	38	36	hypothetical protein YLR002c - yeast [Saccharomyces cerevisiae]
20644	ENU04438	ANI61C7264:22-43 2976..1666		802-829	NAP		g3318897	725	158	4.00E-38	39	36	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum []"
20645	ENU04439	ANI61C1397:80-100 901..1		719-738	NAP		g3834343	1429	468	e-131	95	17	(X05204) arom polypeptide [Emericella nidulans]
20646	ENU04440	ANI61C5143:44-70 718..166	44-70	513-532	NAP		g1620896	620	251	2.00E-66	76	59	(D87956) protein involved in sexual development [Schizosaccharomyces pombe]
20647	ENU04441	ANI61C3620:144-164 1549..1228	144-164	280-301	NAP		g4507229	238	104	2.00E-22	44	20	Succinic semialdehyde dehydrogenase [Homo sapiens]
20648	ENU04442	ANI61C6334:22-44 4081..4982	22-44	722-749	NAP		g448109	216	101	7.00E-21	34	51	6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]
20649	ENU04443	ANI61C3534:27-46 3454..1931	27-46	799-826	NAP		g3722	498	69	3.00E-19	31	39	(X52633) GAP1 protein (AA 1-601) [Saccharomyces cerevisiae]
20650	ENU04444	ANI61C9310:22-47 1086..2744	22-47	726-749	NAP		g114988	2453	480	e-135	95	22	kinesin-like protein BIMC [Emericella nidulans]
20651	ENU04445	ANI61C5922:1467..1			NAP		g3183348	408	136	2.00E-31	35	52	hypothetical 60.1 KD protein C23C11.06C in chromosome I [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20652	ENU04446	ANI61C6611: 121-140 1..516	121-140	409-428	NAP		g3451071	247	80	2.00E-16	45	20	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]
20653	ENU04447	ANI61C6297: 26-49 2531..3687	26-49	711-730	NAP		g3451463	344	113	2.00E-32	34	57	(AL031349) hypothetical protein [Schizosaccharomyces pombe]
20654	ENU04448	ANI61C1107 185-204 1:1..831	185-204	617-641	NAP		g3914212	470	188	5.00E-47	49	19	5-oxoprolinase (5-oxo-L-prolinase) (pyroglutamase) (5-opase) [Rattus norvegicus]
20655	ENU04449	ANI61C181:2 22-49 89..1636	22-49	705-730	NAP		g1805251	198	104	1.00E-21	27	41	(U58946) transposase [Aspergillus awamori]
20656	ENU04450	ANI61C5884: 3718..4724			NAP		g340613	183	38	0.092	27	78	(L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]
20657	ENU04451	ANI61C4283: 27-54 2133..2763	27-54	450-469	NAP		g2330797	199	71	1.00E-17	37	62	(Z98601) zinc finger protein [Schizosaccharomyces pombe]
20658	ENU04452	ANI61C1138: 22-49 12005..10799	22-49	804-829	NAP		g3882339	82	139	2.00E-32	33	18	(AB018352) KIAA0809 protein [Homo sapiens]
20659	ENU04453	ANI61S3751: 36-59 542..1	36-59	467-486	NAP		g4454043	916	333	7.00E-91	97	28	(AL035394) putative receptor kinase [Arabidopsis thaliana]
20660	ENU04454	ANI61C2071: 106-127 781..1	106-127	671-690	NAP		g731805	463	192	2.00E-48	45	26	SYG1 protein [Saccharomyces cerevisiae]
20661	ENU04455	ANI61C2856: 118-138 684..1	118-138	628-655	NAP		g1806628	488	115	1.00E-51	49	50	(U79250) glycerol-3-phosphate dehydrogenase [Homo sapiens]
20662	ENU04456	ANI61C6770: 102-122 1..434	102-122	392-413	NAP		g1708835	188	71	3.00E-12	40	48	"2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (2,5-DDOL dehydrogenase) [Sphingomonas paucimobilis]"
20663	ENU04457	ANI61C2510: 43-62 557..1	43-62	416-437	NAP		g2313520	165	85	5.00E-16	30	45	(AE000557) cyclopropane fatty acid synthase (cfa) [Helicobacter pylori 26695]
20664	ENU04458	ANI61C910:2 458..2116			NAP		g2330815	137	73	7.00E-13	41	36	(Z98602) purine nucleotide binding protein fet5 [Schizosaccharomyces pombe]
20665	ENU04459	ANI61C8051: 44-63 1749..197	44-63	803-826	NAP		g586312	641	80	3.00E-21	33	43	hypothetical 63.4 KD protein in SMY2-RPS101 intergenic region [Saccharomyces cerevisiae]

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20666	ENU04460	ANI61C2836: 653..1378			NAP		g1175939	331	86	1.00E-32	40	58	hypothetical 41.9 KD protein in HAC1-CAK1 intergenic region [Saccharomyces cerevisiae]
20667	ENU04461	ANI61C2759: 1..716	115-134	581-608	NAP		g2492763	395	141	8.00E-38	48	67	hypothetical oxidoreductase in MRPL44-MTF1 intergenic region [Saccharomyces cerevisiae]
20668	ENU04462	ANI61C1083 30-49 5:3653..3984	30-49	282-301	NAP		g1483145	93	36	0.002	29	97	[D64008] Cytochrome b5 [Ascaris suum]
20669	ENU04463	ANI61C1020 29-56 8:1..3278	29-56	804-829	NAP		g1723687	754	129	2.00E-29			hypothetical 140.5 KD protein in CTT1-PRP31 intergenic region [Saccharomyces cerevisiae]
20670	ENU04464	ANI61C4296: 203-222 1465..856	203-222	465-484	NAP		g3242972	416	109	1.00E-23	54	25	(AF069523) heat shock protein Hsp88 [Neurospora crassa]
20671	ENU04465	ANI61C6540: 45-64 1520..2718	45-64	778-797	NAP		g3218400	425	145	2.00E-40	38	75	(AL023860) ser-thr protein kinase [Schizosaccharomyces pombe]
20672	ENU04466	ANI61C4932: 22-46 720..3626	22-46	801-828	NAP		g731882	293	101	9.00E-21			hypothetical 195.1 KD protein in DNA43-UBI1 intergenic region [Saccharomyces cerevisiae]
20673	ENU04467	ANI61C1926: 105-132 1987..1581	105-132	366-386	NAP		g3687497	168	66	2.00E-12	44	67	(AL031788) putative mitochondrial inner membrane protease subunit 2 [Schizosaccharomyces pombe]
20674	ENU04468	ANI61C8052: 22-48 755..2503	22-48	720-744	NAP		g4502323	585	168	6.00E-41	40	17	"ATPase, Cu++ transporting, beta polypeptide (Wilson disease) [Homo sapiens]"
20675	ENU04469	ANI61S1734: 1..854			NAP		g100687	405	37	0.16	41	74	hydroxyproline-rich glycoprotein - rice [Oryza sativa]
20676	ENU04470	ANI61C724:2 22-45 882..1	22-45	807-826	NAP		g2493965	2089	317	5.00E-86	58	20	xanthine dehydrogenase (purine hydroxylase I) [Emericella nidulans]
20677	ENU04471	ANI61C1117 110-129 1:1..795	110-129	683-706	NAP		g2668553	311	89	5.00E-26	33	18	(U62929) multidrug resistance protein 1 [Filobasidiella neoformans]
20678	ENU04472	ANI61C1823: 22-48 1..1738	22-48	748-767	NAP		g2342601	738	137	9.00E-32	29	5	(X89442) peptidase synthetase [Metarhizium anisopliae]
20679	ENU04473	ANI61C5324: 43-62 1589..1	43-62	722-741	NAP		g3043376	1653	240	e-100	75	42	(AJ005258) amyR [Aspergillus oryzae]

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20680	ENU04474	ANI61C6771: 24-44 1090..1		675-697	NAP		g3879362	341	116	1.00E-25	33	52	"(Z81113) similar to DnaJ, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from this gene; cDNA EST yk447h4.5 comes from this gene; cDNA EST yk474e4.5 c... []"
20681	ENU04475	ANI61C1089 9:586..1	215-234	464-484	NAP		g3139137	800	308	7.00E-85	84	22	(AF063864) essential nuclear protein Mcm3p [Schizosaccharomyces pombe]
20682	ENU04476	ANI61S4441: 554..1			NAP		g4835793	148	77	8.00E-14			"(AC007296) Similar to gb U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF00076 RNA recognition motif domains. ESTs gb T44278, gb R65195, gb N65904, gb H37499, gb R90487, gb N95952, gb T4427... []"
20683	ENU04477	ANI61C9025: 37-56 1337..1	792-812		NAP		g3540219	1169	130	6.00E-59	49	22	(D87686) KIAA0017 protein [Homo sapiens]
20684	ENU04478	ANI61S1996: 1..775			NAP		g2135765	221	44	0.00002	35	8	"mucin 2 precursor, intestinal - human (fragments) []"
20685	ENU04479	ANI61C2726: 102-121 601..1	466-486		NAP		g1711467	277	122	2.00E-27	34	43	dibenzothiophene desulfurization enzyme A [Rhodococcus sp.] (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
20686	ENU04480	ANI61S2694: 38-65 450..1	403-429		NAP		g1938424	285	122	1.00E-27	51	13	(AL008967) ltp1 [Mycobacterium tuberculosis]
20687	ENU04481	ANI61C7219: 2951..2457			NAP		g2624312	413	105	1.00E-40	53	40	(AF131877) amino-deoxyarabinohexulose-7-phosphate synthase [Streptomyces collinus]
20688	ENU04482	ANI61S4608: 209-228 431..1	362-386		NAP		g4884833	322	103	7.00E-27			UDP-glucose dehydrogenase [Homo sapiens]
20689	ENU04483	ANI61C9107: 22-45 8199..9462	807-829		NAP		g4507813	185	82	7.00E-15			probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae)
20690	ENU04484	ANI61C4377: 30-51 1961..1330	583-610		NAP		g2132651	309	84	2.00E-26	32	35	[Saccharomyces cerevisiae]
20691	ENU04485	ANI61S591:3 41..767			NAP		g501027	147	31	4.6	33	99	(U01849) ORF2 [Trypanosoma brucei]

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20692	ENU04486	ANI61C7389: 1361..1	22-45	636-663	NAP		g2133317	1829	407	e-113	67	38	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 78K chain precursor - Neurospora crassa [Neurospora crassa] (AL021925) hypothetical protein Rv2263 [Mycobacterium tuberculosis] serine palmitoyltransferase 2 (long chain base biosynthesis protein 2) (SPT 2) [Schizosaccharomyces pombe] actin-like protein ARP5 [Saccharomyces cerevisiae] (Z97210) hypothetical protein [Schizosaccharomyces pombe] beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucosylhydrolase) [Kluyveromyces marxianus] cutinase transcription factor 1 beta [Fusarium solani f. sp. pisi] (Z99112) chromosome segregation SMC protein homolog [Bacillus subtilis]
20693	ENU04487	ANI61C2578: 26-45	26-45	809-829	NAP		g2909569	118	40	0.000003			
20694	ENU04488	ANI61C8776: 26-45	26-45	795-815	NAP		g1346422	1459	317	8.00E-86	60	46	
20695	ENU04489	ANI61C510:1 24-46	24-46	777-796	NAP		g1730738	805	85	2.00E-19	38	35	
20696	ENU04490	ANI61C1122 9:3734..2965			NAP		g2239223	347	77	2.00E-13	40	98	
20697	ENU04491	ANI61C3235: 33-52	33-52	755-780	NAP		g114971	983	96	1.00E-36	34	32	
20698	ENU04492	ANI61C415:2 22-49	22-49	615-642	NAP		g1706177	186	62	1.00E-13	34	21	
20699	ENU04493	ANI61S851:7 19..1			NAP		g2633966	304	102	3.00E-21	35	20	
20700	ENU04494	ANI61C3482: 22-45	22-45	648-669	NAP		g549770	377	79	3.00E-22			
20701	ENU04495	ANI61C7:378 54-73	54-73	804-829	NAP		g121065	548	196	2.00E-49			
20702	ENU04496	ANI61C8363: 41-61	41-61	712-735	NAP		g3820457	817	214	7.00E-55	47	27	
20703	ENU04497	ANI61S1437: 47-66	47-66	307-326	NAP		g3885836	265	96	2.00E-19	39	28	
20704	ENU04498	ANI61C4370: 37-56	37-56	655-679	NAP		g3318897	362	138	7.00E-32	44	31	
20705	ENU04499	ANI61C1120 25-51	25-51	510-529	NAP		g1870215	1027	291	2.00E-78	95	53	

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20706	ENU04500	ANI61C1014 2:1..5159	37-56	718-739	NAP		g2342601	827	286	2.00E-76	53	5	(X89442) peptide synthetase [Metarhizium anisopliae]
20707	ENU04501	ANI61C443:1 .651	26-50	567-586	NAP		g3834343	1013	394	e-109	98	13	(X05204) arom polypeptide [Emicella nidulans]
20708	ENU04502	ANI61C5958: 614..1100	59-78	457-479	NAP		g1293655	410	178	3.00E-44	55	25	(U51327) versicolorin B synthase [Aspergillus parasiticus]
20709	ENU04503	ANI61C7613: 1814..2650	32-51	706-725	NAP		g730506	101	95	7.00E-19	22	63	nuclear division RFT1 protein [Kluyveromyces lactis]
20710	ENU04504	ANI61C1839: 13..658	24-47	592-612	NAP		g3608397	83	68	5.00E-11	32	52	(AF071085) putative dTDP-4-keto-L-rhamnose reductase [Enterococcus faecalis]
20711	ENU04505	ANI61C5791: 587..1	58-84	531-550	NAP		g1293655	292	125	3.00E-28	41	29	(U51327) versicolorin B synthase [Aspergillus parasiticus]
20712	ENU04506	ANI61C262:4 131..2626	54-73	798-820	NAP		g710551	282	76	6.00E-18	29	15	(L40632) ankyrin 3 [Mus musculus]
20713	ENU04507	ANI61C7276: 3527..4344			NAP		g1708836	255	136	2.00E-31	35	98	"2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (2,5-DDOL dehydrogenase) [Sphingomonas paucimobilis]"
20714	ENU04508	ANI61C1144 5:672..1255	61-80	514-538	NAP		g2811058	369	139	1.00E-32	42	51	hypothetical 39.5 KD protein in SIGZ-CSN intergenic region [Bacillus subtilis]
20715	ENU04509	ANI61C1164: 493..1695	22-45	803-829	NAP		g131769	1624	320	7.00E-87	97	70	QUTG protein []
20716	ENU04510	ANI61C1065 4:5634..8953	30-51	719-738	NAP		g3810843	2437	274	5.00E-73	65	25	"(AL032684) putative yeast cell division control protein 68 homolog, putative transcriptional activator [Schizosaccharomyces pombe]"
20717	ENU04511	ANI61S3760: 1..597	26-45	515-534	NAP		g3319372	547	133	1.00E-30	52	17	"(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]"
20718	ENU04512	ANI61C7330: 1..2372	69-88	791-810	NAP		g114967	1244	227	7.00E-59	45	33	beta-glucosidase (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Agrobacterium tumefaciens]
20719	ENU04513	ANI61C8930: 1243..1956	26-45	483-502	NAP		g3395586	234	113	1.00E-24	42	29	(AL031179) similarity to phosphomannomutases [Schizosaccharomyces pombe]

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20720	ENU04514	ANI61C1385: 22-42 1258..1	25-52	704-731	NAP	g2467275	g3850093	138	48	1.00E-33	32	56	(Z99759) serine/threonine-protein kinase [Schizosaccharomyces pombe]
20721	ENU04515	ANI61C1019: 25-52 9:2148..1067	25-52	792-816	NAP	g3850093	g3850093	138	48	0.00006	30	42	(AL033389) putative allantoinase permease [Schizosaccharomyces pombe]
20722	ENU04516	ANI61C1039: 70-89 7:1265..1	70-89	618-637	NAP	g1711561	g1711561	582	126	2.00E-28	39	45	sugar transportR STL1 [Saccharomyces cerevisiae]
20723	ENU04517	ANI61C7331: 24-43 4557..3583	24-43	764-783	NAP	g127568	g127568	298	124	9.00E-28	31	86	interferon-induced GTP-binding protein MX [Perca fluviatilis]
20724	ENU04518	ANI61C8161: 22-46 4359..7310	22-46	721-740	NAP	g731689	g731689	1445	313	9.00E-85	51	7	hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
20725	ENU04519	ANI61C1040: 5:4687..4196			NAP	g12688	g12688	626	182	1.00E-58	89	46	(V00650) URF 1 [Emicella nidulans]
20726	ENU04520	ANI61C9790: 29-56 1..3423	29-56	802-829	NAP	g731871	g731871	1132	153	1.00E-36	32	11	hypothetical 269.9 KD protein in FKH1-MET18 intergenic region [Saccharomyces cerevisiae]
20727	ENU04521	ANI61C1128: 23-43 5:1107..1	23-43	725-747	NAP	g3738194	g3738194	664	153	1.00E-46	42	40	(AL031854) hypothetical protein [Schizosaccharomyces pombe]
20728	ENU04522	ANI61C5443: 27-54 2914..1767	27-54	804-824	NAP	g2342601	g2342601	618	206	2.00E-52	40	5	(X89442) peptide synthetase [Metarhizium anisopliae]
20729	ENU04523	ANI61C1558: 22-48 180..1075	22-48	805-829	NAP	g2388903	g2388903	671	229	2.00E-59	53	49	(Z98974) putative cytochrome p450 [Schizosaccharomyces pombe]
20730	ENU04524	ANI61C6309: 52-71 1351..2378	52-71	770-788	NAP	g3063700	g3063700	160	78	5.00E-15	32	15	(AL022537) putative protein [Arabidopsis thaliana]
20731	ENU04525	ANI61C5366: 22-40 147..1179	22-40	657-676	NAP	g3169096	g3169096	785	204	6.00E-52	46	46	(AL023706) hypothetical protein [Schizosaccharomyces pombe]
20732	ENU04526	ANI61C7102: 72-93 1002..1648	72-93	604-626	NAP	g1942383	g1942383	154	82	3.00E-15	40	31	Human 17-Beta-Hydroxysteroid-Dehydrogenase Type 1 Complexed With 17-Beta-Estradiol []
20733	ENU04527	ANI61S4490: 213-231 153..507	213-231	356-375	NAP	g1244642	g1244642	89	51	0.000005	32	43	(U40374) aminoglycoside 3'-phosphotransferase [Cloning vector pMH30]
20734	ENU04528	ANI61C9993: 27-46 1511..3934	27-46	801-828	NAP	g1175408	g1175408	612	34	0.033			hypothetical 107.3 KD TRP-ASP repeats containing protein C31A2.14 in chromosome I [Schizosaccharomyces pombe]
20735	ENU04529	ANI61C4851: 59-78 1350..2018	59-78	602-626	NAP	g3550602	g3550602	257	118	5.00E-26	36	22	(AJ006710) phosphatidylinositol 3-kinase [Rattus norvegicus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20736	ENU04530	ANI61C3177: 23-48 1..1604	531-55	770-789	NAP		g3914053	2015	426	e-119	76	30	DNA mismatch repair protein MSH2 [Neurospora crassa]
20737	ENU04531	ANI61C1056: 35-55 1..580	531-558		NAP		g2501152	291	134	4.00E-31	48	33	threonine synthase [Schizosaccharomyces pombe]
20738	ENU04532	ANI61S4655: 830..314			NAP		g2131314	127	41	0.000000 009	37	37	hypothetical protein YD8142A.01 - yeast (Saccharomyces cerevisiae) (fragment) []
20739	ENU04533	ANI61C1355: 22-48 500..1	303-324		NAP		g1870215	851	342	9.00E-94	99	46	(AC000133) ORF [Emericella nidulans]
20740	ENU04534	ANI61C5665: 22-48 1..1756	805-824		NAP		g3150253	819	176	9.00E-52	42	24	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
20741	ENU04535	ANI61C3240: 54-73 3384..3956	521-540		NAP		g120625	456	180	7.00E-45	60	100	G10 protein [Xenopus laevis]
20742	ENU04536	ANI61S3332: 47-67 1..306	198-223		NAP		g1706202	269	100	3.00E-21	54	47	cutinase precursor (L1) [Aspergillus oryzae]
20743	ENU04537	ANI61C9348: 122-143 1..380	333-359		NAP		g2911462	398	107	2.00E-37	73	17	(AF046923) serine/threonine protein kinase [Colletotrichum trifolii]
20744	ENU04538	ANI61C4409: 22-49 813..2276	765-784		NAP		g4176523	341	104	6.00E-22	29	45	(AL035263) hypothetical protein [Schizosaccharomyces pombe]
20745	ENU04539	ANI61C9831: 22-44 1646..1	623-642		NAP		g3581903	480	124	9.00E-28	35	38	(AL031545) DEAD box ATP-dependent RNA helicase [Schizosaccharomyces pombe]
20746	ENU04540	ANI61C7608: 37-61 884..1	724-749		NAP		g4102980	121	42	0.005	20	49	(AF019082) virulent strain associated lipoprotein [Borrelia burgdorferi]
20747	ENU04541	ANI61C1617: 22-49 1230..1561	454-479		NAP		g464991	142	80	8.00E-15	40	43	ubiquitin carboxyl-terminal hydrolase YUHI (ubiquitin thioesterase) [Saccharomyces cerevisiae]
20748	ENU04542	ANI61C8017: 39-66 547..1	424-446		NAP		g4758430	256	93	1.00E-24			geranylgeranyl diphosphate synthase [Homo sapiens]
20749	ENU04543	ANI61C4194: 22-45 2114..2587	374-393		NAP		g1168953	76	54	0.000000 7	32	37	citrate lyase beta chain (citrase) (citryl-CoA lyase subunit) [Klebsiella pneumoniae]
20750	ENU04544	ANI61S2295: 1..567			NAP		g100753	167	46	0.000000 06	36	66	hydroxyproline-rich glycoprotein - sorghum [Sorghum bicolor]
20751	ENU04545	ANI61C7450: 23-44 1431..2454	807-829		NAP		g1256839	868	191	4.00E-73	63	52	(U53329) Ran1-like protein kinase [Fusarium solani f. sp. pisi]
20752	ENU04546	ANI61C3751: 68-87 656..219	416-435		NAP		g4902874	112	48	0.00004			"(A1242575) oxide-reductase enzyme, putative [Sinorhizobium meliloti]"

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20753	ENU04547	ANI61C1853: 1..459	25-52	411-438	NAP	g3914278	264	122	1.00E-27	55	34		pectate lyase B precursor [Glomerella cingulata]
20754	ENU04548	ANI61C5321: 22-49	22-49	805-829	NAP	g3183173	591	187	6.00E-48	52	53		"seryl-TRNA synthetase, cytoplasmic (serine--TRNA ligase) (SERRS) [Schizosaccharomyces pombe]"
20755	ENU04549	ANI61C1011: 24-47	24-47	481-499	NAP	g1834342	1043	248	e-106	92	15		(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
20756	ENU04550	ANI61C1045: 1:7120..8069			NAP	g3560208	274	95	7.00E-19	33	34		(AL031536) putative transcription factor of the GCS1-GLO3-SPS18 family [Schizosaccharomyces pombe]
20757	ENU04551	ANI61C2588: 22-49	22-49	628-647	NAP	g130117	815	218	3.00E-79	69	39		phosphate-repressible phosphate permease [Neurospora crassa]
20758	ENU04552	ANI61C5294: 22-46	22-46	498-521	NAP	g2501434	162	103	2.00E-22	30	92		ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) [Schizosaccharomyces pombe]
20759	ENU04553	ANI61C6129: 72-99	72-99	412-431	NAP	g730443	80	47	0.000000	34	70		quinone oxidoreductase (NADPH:quinone reductase) (zeta-crystallin homolog protein) []
20760	ENU04554	ANI61C1614: 56-75	56-75	777-796	NAP	g3646379	1450	199	8.00E-95	75	42		(AJ001540) phenylacetyl-CoA ligase [Penicillium chrysogenum]
20761	ENU04555	ANI61C5779: 71-90	71-90	773-799	NAP	g2443355	723	108	4.00E-23				(AB003395) cnt-Kaurene synthase [Phaeosphaeria sp. L487]
20762	ENU04556	ANI61C1114: 23-42	23-42	788-815	NAP	g2625138	224	116	1.00E-25	34	14		(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]
20763	ENU04557	ANI61C7681: 22-49	22-49	757-780	NAP	g1817584	917	117	8.00E-26	28	19		(Y08991) adaptor protein [Homo sapiens]
20764	ENU04558	ANI61C1919: 221-240	221-240	765-784	NAP	g4165293	962	341	2.00E-99	71	28		(X58824) cdc21 protein [Schizosaccharomyces pombe]
20765	ENU04559	ANI61C1065: 26-45	26-45	767-786	NAP	g1346521	1027	317	8.00E-86	78	62		S-adenosylmethionine synthetase (methionine adenosyltransferase) (ADOMET synthetase) [Neurospora crassa]
20766	ENU04560	ANI61C2670: 101-120	101-120	610-631	NAP	g604369	928	215	6.00E-70	53	34		(U17857) hMLH1 gene product [Homo sapiens]
20767	ENU04561	ANI61C4238: 22-42	22-42	772-793	NAP	g3023682	998	332	9.00E-94	79	30		elongation factor 2 (EF-2) [Candida albicans]

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20768	ENU04562	ANI61S2955: 1..531			NAP		g4218005	140	43	0.002	25	25	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
20769	ENU04563	ANI61C1957: 22-41 422..1763		771-795	NAP		g461623	1173	92	2.00E-36	68	21	beta-galactosidase precursor (lactase) [Aspergillus niger]
20770	ENU04564	ANI61S3141: 182-209 612-631			NAP		g2062165	797	330	6.00E-90	87	38	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]
20771	ENU04565	ANI61C3056: 33-60 3300..1880		801-820	NAP		g3850089	772	183	6.00E-61	52	62	(AL033389) putative yeast cell division cycle CDC50 homolog [Schizosaccharomyces pombe]
20772	ENU04566	ANI61C8012: 22-45 5408..4491		810-829	NAP		g2842699	518	173	2.00E-42	54	43	putative ubiquitin carboxyl-terminal hydrolase C6G9.08 (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]
20773	ENU04567	ANI61S3854: 168-193 399-418 586..90			NAP		g3417425	202	53	5.00E-14	36	50	(AL031261) conserved hypothetical protein [Schizosaccharomyces pombe]
20774	ENU04568	ANI61C1100 33-53 598-622 0:8321..9087			NAP		g643443	769	225	1.00E-78	72	39	(U08104) PHOG [Penicillium chrysogenum]
20775	ENU04569	ANI61C1131 103-120 795-817 8:1..839			NAP		g1723773	335	144	7.00E-34	36	39	hypothetical 81.2 KD protein in MES1-FOL2 intergenic region [Saccharomyces cerevisiae]
20776	ENU04570	ANI61S2538: 220-247 585-605 671..1			NAP		g1723448	242	120	1.00E-26	43	31	hypothetical protein C56F8.17C in chromosome I [Schizosaccharomyces pombe]
20777	ENU04571	ANI61C5097: 97-118 482-503 525..1			NAP		g2370479	146	71	7.00E-12	29	21	(Z98849) putative centromere protein [Schizosaccharomyces pombe]
20778	ENU04572	ANI61C2309: 22-46 762-780 1195..1			NAP		g544368	215	75	4.00E-14	29	51	galactose-proton symport (galactose transporter) [Escherichia coli]
20779	ENU04573	ANI61C9634: 22-46 642..1942		810-829	NAP		g2661622	640	145	4.00E-46	48	65	(AL009197) hypothetical protein phosphatase [Schizosaccharomyces pombe]
20780	ENU04574	ANI61C9830: 33-52 1643..363		683-702	NAP		g1729868	1503	367	e-101	72	53	"probable T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta) [Schizosaccharomyces pombe]"
20781	ENU04575	ANI61S3302: 180-207 443-470 567..1			NAP		g1397290	139	44	4.00E-11	47	67	(U61949) Similar to cytidine deaminase. [Caenorhabditis elegans]

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20782	ENU04576	ANI61C3245: 22-42 2557..1	709-735	NAP		g2342601	1176	183	1.00E-45	35	5		(X89442) peptide synthetase [Metarhizium anisopliae]
20783	ENU04577	ANI61C7535: 984..162		NAP		g4481947	211	65	4.00E-21	36	99		(AL035637) hypothetical protein. [Schizosaccharomyces pombe]
20784	ENU04578	ANI61C1091 33-52 8:903..1	784-803	NAP		g4454039	482	169	2.00E-41	47	31		(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]
20785	ENU04579	ANI61C6944: 38-57 2235..523	781-803	NAP		g3777495	1275	284	7.00E-76	65	27		(U92083) calcium transporting ATPase [Pichia angusta]
20786	ENU04580	ANI61C7384: 23-46 3181..3930	704-729	NAP		g128397	962	334	3.00E-91	99	100		nuclear movement protein NUDC [Emicella nidulans]
20787	ENU04581	ANI61C7182: 2146..2514		NAP		g1870209	235	74	8.00E-13	46	30		(AC000133) ORF [Emicella nidulans]
20788	ENU04582	ANI61C1122 27-54 4:3002..4504	761-780	NAP		g4836423	138	34	1.4				(AF119670) integral membrane protein [Magnaporthe grisea]
20789	ENU04583	ANI61C7682: 78-105 843..1	749-776	NAP		g4164428	473	205	5.00E-52	49	19		(AL035247) putative pre-mrna splicing factor rna helicase
20790	ENU04584	ANI61C8016: 22-44 4149..2537	767-794	NAP		g3901117	970	135	2.00E-44	38	45		[Schizosaccharomyces pombe] (AJ012752) maltose permease
20791	ENU04585	ANI61C1556: 66-85 505..2127	772-791	NAP		g1723187	505	80	3.00E-14	41	24		[Saccharomyces cerevisiae] 112.3 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae]
20792	ENU04586	ANI61C5421: 118-137 663..1	528-546	NAP		g1805262	336	147	6.00E-35	35	10		"(U75347) fatty acid synthase, beta subunit [Emicella nidulans]"
20793	ENU04587	ANI61C6728: 85-111 1..690	630-649	NAP		g418345	129	72	4.00E-12	39	46		probable methionyl-TRNA formyltransferase precursor [Saccharomyces cerevisiae]
20794	ENU04588	ANI61C5679: 22-47 1..1011	723-742	NAP		g189036	121	71	1.00E-11	19	20		(M31013) nonmuscle myosin heavy chain (NMHC) [Homo sapiens]
20795	ENU04589	ANI61C2763: 55-74 1301..950	307-331	NAP		g3264834	279	118	2.00E-26	44	33		(AF072541) xyliol dehydrogenase; XDH [Galactocandida mastotermitis]
20796	ENU04590	ANI61C7721: 23-44 441..1325	803-829	NAP		g2673947	287	98	1.00E-22	31	20		(U62931) multidrug resistance protein 1 [Aspergillus flavus]
20797	ENU04591	ANI61C1672: 23-50 599..1	430-449	NAP		g3859681	485	128	2.00E-49	50	60		(AL033503) transcription regulatory protein [Candida albicans]
20798	ENU04592	ANI61C9504: 49-72 1510..986	480-504	NAP		g465847	336	83	4.00E-33				hypothetical 66.5 KD protein F02A9.5 in chromosome III []

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20799	ENU04593	ANI61C9338: 22-45 3025..1	22-45	711-737	NAP		g2276359	1861	273	1.00E-72	38	11	putative phosphatidylinositol 3-kinase [Schizosaccharomyces pombe]
20800	ENU04594	ANI61C6660: 45-64 903..577	45-64	453-477	NAP		g42931	138	131	3.00E-30	31	100	(X56175) ORF 2 (AA 1 - 109) [Escherichia coli]
20801	ENU04595	ANI61C9595: 106-128 1137..701	106-128	389-414	NAP		g1709760	271	87	1.00E-21	50	47	putative proteasome component PRE6 (macropain subunit) (multicatalytic endopeptidase complex subunit) [Schizosaccharomyces pombe]
20802	ENU04596	ANI61C6006: 22-43 911..1862	22-43	709-736	NAP		g1255430	348	125	4.00E-28	37	71	(U53155) No definition line found [Caenorhabditis elegans]
20803	ENU04597	ANI61C7769: 1865..985			NAP		g3873958	152	92	6.00E-18	26	79	(Z81458) similar to transposable element [Caenorhabditis elegans]
20804	ENU04598	ANI61C4415: 22-44 1515..3198	22-44	698-720	NAP		g4506221	665	60	2.00E-31	40	50	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 [Homo sapiens]"
20805	ENU04599	ANI61C5780: 23-47 1201..627	23-47	518-545	NAP		g2501434	521	125	3.00E-53	63	100	ubiquitin-conjugating enzyme E2-18 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) [Schizosaccharomyces pombe]
20806	ENU04600	ANI61C7849: 30-57 4095..4955	30-57	712-731	NAP		g3947746	527	220	1.00E-56	56	29	(AJ009960) DNA photolyase [Trichoderma harzianum]
20807	ENU04601	ANI61C7563: 31-50 1404..1023	31-50	334-360	NAP		g3309657	372	159	1.00E-38	60	15	(AF074944) RRM3/PIF1 helicase homolog [Schizosaccharomyces pombe]
20808	ENU04602	ANI61C1080: 25-44 7..858..1	25-44	774-794	NAP		g102827	63	72	4.00E-12			alpha-latrotoxin precursor - black widow spider [Latrodectus tenebrosus]
20809	ENU04603	ANI61C6782: 26-45 1..1076	26-45	778-805	NAP		g731421	377	98	2.00E-34	38	47	hypothetical 53.3 KD protein in HXT8-CAN1 intergenic region [Saccharomyces cerevisiae]
20810	ENU04604	ANI61C4065: 218-238 1..443	218-238	385-406	NAP		g1723643	217	78	4.00E-20	41	33	hypothetical 44.9 KD protein in SEC9-MSB2 intergenic region [Saccharomyces cerevisiae]
20811	ENU04605	ANI61C5853: 22-45 757..1772	22-45	807-826	NAP		g3738190	706	196	2.00E-49	43	82	(AL031854) putative ras related GTP-binding protein [Schizosaccharomyces pombe]

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20812	ENU04606	ANI61C1054 1:2939..1	39-56	724-746	NAP		g2956769	1614	169	9.00E-60	54	21	(AL022103) phosphatidylinositol phosphate phosphatase; synaptojanin-like [Schizosaccharomyces pombe] (Z99167) hypothetical conserved protein [Schizosaccharomyces pombe] hypothetical protein YOL124c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae] (Y16563) Bassoon [Rattus norvegicus]
20813	ENU04607	ANI61C7324; 50-69 4754..5464	50-69	670-690	NAP		g2408075	436	188	4.00E-47	41	98	
20814	ENU04608	ANI61C2440; 186-213 1..643	186-213	589-608	NAP		g2132014	175	92	3.00E-18	37	39	
20815	ENU04609	ANI61S1755; 1..588			NAP		g3413504	91	44	0.0007	22	4	
20816	ENU04610	ANI61C4426; 41-64 844..1	41-64	717-743	NAP		g2147805	319	161	5.00E-39	36	33	NarB protein - Oscillatoria chalybea [Oscillatoria chalybea]
20817	ENU04611	ANI61C3356; 27-48 976..1	27-48	723-749	NAP		g1708850	222	93	3.00E-18	38	34	probable leukotriene A-4 hydrolase (LTA-4 hydrolase) (leukotriene A(4) hydrolase) [Saccharomyces cerevisiae]
20818	ENU04612	ANI61C4165; 28-47 3186..2199	28-47	774-793	NAP		g417318	589	185	3.00E-46	44	59	MSS51 protein [Saccharomyces cerevisiae]
20819	ENU04613	ANI61C1138 1:971..1478	27-46	398-416	NAP		g1172568	198	80	6.00E-17	48	73	low molecular weight phosphotyrosine protein phosphatase (low molecular weight cytosolic acid phosphatase) (PTPASE) (small tyrosine phosphatase) [Schizosaccharomyces pombe]
20820	ENU04614	ANI61C5427; 209-228 1940..1520	209-228	366-385	NAP		g1549231	121	38	0.000003	31	18	(D50497) chloride channel (ClC-5) [Rattus rattus]
20821	ENU04615	ANI61C1005 7:2999..584	23-47	800-822	NAP		g2132992	242	86	3.00E-16	27	25	probable membrane protein YPL183c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae] (AC000133) ORF [Emeticella nidulans]
20822	ENU04616	ANI61C1355; 203-222 2053..2529	203-222	459-478	NAP		g1870229	817	300	3.00E-81	97	100	
20823	ENU04617	ANI61C5998; 22-42 7885..4728	22-42	802-821	NAP		g1166378	525	86	3.00E-16			"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
20824	ENU04618	ANI61C1102 6:1..629	107-127	506-527	NAP		g1805251	250	120	9.00E-27	35	37	(U58946) transposase [Aspergillus awamori]
20825	ENU04619	ANI61C7487; 22-43 243..1014	22-43	713-740	NAP		g2385369	466	146	9.00E-41	53	98	(AJ001421) Rer1 protein [Homo sapiens]
20826	ENU04620	ANI61C2085; 22-48 952..441	22-48	460-479	NAP		g665573	64	44	0.0006	31	98	(U20323) ankyrin-like protein [Saccharomyces cerevisiae]
20827	ENU04621	ANI61C3624; 35-54 5678..1	35-54	630-649	NAP		g481866	2935	223	8.00E-62	44	8	enniatin synthetase - fungus (Fusarium scirpi) [Fusarium scirpi]

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20828	ENU04622	ANI61C4110: 73-100 1..415	295-317	NAP			g2130022	117	66	1.00E-10	35	37	aldose reductase homolog - wild oat [Avena fatua]
20829	ENU04623	ANI61C3096: 23-43 1..1198	777-800	NAP			g2132857	116	41	0.014			probable membrane protein YOL158c - yeast (Saccharomyces cerevisiae)
20830	ENU04624	ANI61C5542: 22-49 165..578	429-454	NAP			g137024	321	116	1.00E-25			[Saccharomyces cerevisiae] uridylyate kinase (UK) (uridine monophosphate kinase) (UMP kinase)
20831	ENU04625	ANI61C3542: 42-61 3119..633	803-829	NAP			g2499558	386	120	1.00E-26			[Saccharomyces cerevisiae] hypothetical 84.2 KD protein SLR0473
20832	ENU04626	ANI61C2155: 27-46 1315..1	722-741	NAP			g1084969	1548	399	e-129	97	42	[Synchocystis sp.] sulfate adenylyltransferase (EC 2.7.7.4) - Emericella nidulans [Emericella nidulans]
20833	ENU04627	ANI61C5633: 102-129 1..685	586-612	NAP			g3929349	659	244	4.00E-64	54	47	C-14 sterol reductase (sterol C14-reductase) [Nectria haematococca]
20834	ENU04628	ANI61S4409: 29-56 1..316	272-295	NAP			g3549662	558	230	3.00E-60	96	23	(AL031394) hypothetical protein [Arabidopsis thaliana]
20835	ENU04629	ANI61C681:6 22-45 55..1	525-552	NAP			g2132903	385	174	6.00E-43	55	23	probable membrane protein YOR165w - yeast (Saccharomyces cerevisiae)
20836	ENU04630	ANI61C6221: 41-62 1..476	407-434	NAP			g115689	306	132	2.00E-30	60	38	[Saccharomyces cerevisiae] nuclear protein SNF4 (regulatory protein CAT3) [Saccharomyces cerevisiae]
20837	ENU04631	ANI61C4344: 22-46 3083..1150	790-809	NAP			g2104447	961	169	2.00E-41	39	47	(Z95396) heat shock protein 70 homolog [Schizosaccharomyces pombe]
20838	ENU04632	ANI61C9952: 219-245 858..1	614-639	NAP			g2507475	595	242	3.00E-63	46	16	paired amphipathic helix protein [Saccharomyces cerevisiae]
20839	ENU04633	ANI61C5160: 68-87 1874..488	784-803	NAP			g1353390	167	68	1.00E-10			(U34998) Rad9 [Coprinus cinereus]
20840	ENU04634	ANI61C4215: 22-45 1039..2126	807-829	NAP			g2498838	508	78	2.00E-42	47	72	meiotic recombination protein REC14 [Schizosaccharomyces pombe]
20841	ENU04635	ANI61C6750: 1549..860		NAP			g731690	152	87	9.00E-17	40	100	hypothetical 20.9 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
20842	ENU04636	ANI61C8558: 28-47 236..696	455-479	NAP			g2498866	84	58	0.000000	37	36	RAS suppressor protein 1 (RSU-1) (RSP-1 protein) (RSP-1) [Homo sapiens]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20843	ENU04637	ANI61C9152: 9484..10108	26-45	537-556	NAP		g4027860	858	194	6.00E-49	98	24	U47540) TamA [Emericella nidulans]
20844	ENU04638	ANI61C8418: 1549..1857			NAP		g122094	461	157	5.00E-38	92	83	histone H4.2 [Emericella nidulans]
20845	ENU04639	ANI61C1129: 71..1664	96-119	725-749	NAP		g1546072	707	148	5.00E-35	35	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
20846	ENU04640	ANI61C1103: 4:3908..5575	23-50	793-820	NAP		g3636	447	118	4.00E-26	28	53	(X55713) putative cytochrome P450 [Saccharomyces cerevisiae]
20847	ENU04641	ANI61C1269: 3063..1220	22-46	804-829	NAP		g2196560	165	32	4			(AB004690) Mis6 [Schizosaccharomyces pombe]
20848	ENU04642	ANI61C4393: 1..785	72-91	742-759	NAP		g120777	660	257	6.00E-68	50	53	succinate-semialdehyde dehydrogenase (NADP+) (SSDH) [Escherichia coli]
20849	ENU04643	ANI61C3785: 1270..1	24-51	724-749	NAP		g2226061	716	226	1.00E-58	46	51	(AF005040) folypolyglutamate synthetase; FPGS [Neurospora crassa]
20850	ENU04644	ANI61C8146: 469..1	102-124	454-479	NAP		g1749638	387	157	5.00E-38	62	53	"(D89215) similar to Saccharomyces cerevisiae transaldolase, SWISS-PROT Accession Number P15019 [Schizosaccharomyces pombe]"
20851	ENU04645	ANI61C3784: 637..1	47-66	509-533	NAP		g3236237	60	66	1.00E-17	26	63	(AC004684) putative ribitol dehydrogenase [Arabidopsis thaliana]
20852	ENU04646	ANI61C8433: 1..377	24-43	332-356	NAP		g1172766	328	146	8.00E-35			adenylosuccinate synthetase (IMP--aspartate ligase) [Saccharomyces cerevisiae]
20853	ENU04647	ANI61C8966: 5392..6501	44-63	711-730	NAP		g2132445	435	86	3.00E-16	40	27	probable membrane protein YDL148c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
20854	ENU04648	ANI61C9765: 1..1767	29-48	775-798	NAP		g1723249	2140	257	e-103	67	23	hypothetical 137.2 KD protein C27F1.09C in chromosome I [Schizosaccharomyces pombe]
20855	ENU04649	ANI61C5247: 3740..5201	40-59	667-686	NAP		g2499017	1022	173	7.00E-64	49	49	"alpha, alpha-trehalose-phosphate synthase (UDP-forming) 1 (trehalose-6-phosphate synthase) (UDP-glucose-glucosephosphate glucosyltransferase) [Aspergillus niger]"
20856	ENU04650	ANI61C1061: 8:121..892	22-48	725-751	NAP		g4154667	126	48	0.000000	29	71	(AE001454) fructose-BISphosphate aldolase [Helicobacter pylori 199]
20857	ENU04651	ANI61C388:9 35..1	22-44	672-691	NAP		g757832	187	69	2.00E-16	30	44	(Z37980) hypothetical 4-hydroxyphenylacetate permease [Escherichia coli]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20858	ENU04652	ANI61S3598: 1..644			NAP		g3913423	356	95	4.00E-19	48	59	S-adenosylmethionine decarboxylase PROenzyme (ADOMETDC) (SAMDC) [Nicotiana tabacum]
20859	ENU04653	ANI61C9728: 67-86	788-807		NAP		g135503	1230	438	e-122	93	58	tubulin gamma chain [Emmericella nidulans]
20860	ENU04654	ANI61C7518: 28-47 373..2142	729-748		NAP		g2492661	2917	579	e-165	96	12	putative sterigmatocystin biosynthesis polyketide synthase (PKS) [Emmericella nidulans]
20861	ENU04655	ANI61S1593: 1..606			NAP		g283032	141	34	0.002	29	55	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
20862	ENU04656	ANI61S51:1..556			NAP		g2501326	555	212	6.00E-55	72	29	pyruvate decarboxylase [Emmericella nidulans]
20863	ENU04657	ANI61C1227: 22-49 1831..968	806-827		NAP		g1730031	511	190	1.00E-47	50	98	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) [Bacillus subtilis]
20864	ENU04658	ANI61C5694: 102-129 1..808	667-692		NAP		g1169440	1343	531	e-150	97	6	"dynein heavy chain, cytosolic (DYHC) [Emmericella nidulans]"
20865	ENU04659	ANI61C5170: 51-71 1373..621	710-732		NAP		g3766378	225	52	6.00E-10	42	100	protein [Schizosaccharomyces pombe]
20866	ENU04660	ANI61C9574: 23-50 1187..1572	449-468		NAP		g2622925	91	66	2.00E-10	28	67	(AE000934) unknown [Methanobacterium thermoautotrophicum]
20867	ENU04661	ANI61C3829: 34-60 1..498	443-466		NAP		g4115913	129	82	1.00E-19	34	41	"(AF118222) contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana]"
20868	ENU04662	ANI61C1010 5:1221..1			NAP		g1870209	414	106	2.00E-22	33	50	(AC000133) ORF [Emmericella nidulans]
20869	ENU04663	ANI61S3791: 1..845			NAP		g2133632	118	48	0.00008	20	20	sperm tail-specific protein mst101(2)- fruit fly (Drosophila hydei) []
20870	ENU04664	ANI61C3055: 22-44 2351..2686	377-398		NAP		g2120651	244	100	1.00E-20	47	38	"hydroxyquinol 1,2-dioxygenase - Pseudomonas cepacia [Burkholderia cepacia]"
20871	ENU04665	ANI61C8620: 43-62 4660..6246	784-804		NAP		g2894281	872	257	5.00E-68	46	36	(AL021838) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20872	ENU04666	ANI61S1089: 1..536			NAP		g2117904	150	69	3.00E-11	34	48	ribose-phosphate pyrophosphokinase (EC 2.7.6.1) PRS1 - yeast (Candida albicans) []
20873	ENU04667	ANI61C7703: 22-47	797-821		NAP		g1063421	581	74	5.00E-18	33	43	(L48797) toxin pump [Cochliobolus carbonum]
20874	ENU04668	ANI61C1106 66-89	589-614		NAP		g729075	326	95	5.00E-19	52	99	cell division control protein 31 [Saccharomyces cerevisiae]
20875	ENU04669	ANI61C1313:1 116-137	435-457		NAP		g1083855	133	79	2.00E-14	33	1	cyclosporin synthetase - Tolypocladium inflatum [Tolypocladium inflatum]
20876	ENU04670	ANI61C6199: 618..1309			NAP		g2305218	501	129	3.00E-50	54	59	(AF010263) tartrate dehydrogenase [Agrobacterium vitis]
20877	ENU04671	ANI61C1123 22-49	700-727		NAP		g2673951	671	79	3.00E-16	31	18	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus]
20878	ENU04672	ANI61C4534: 102-121	621-640		NAP		g465516	260	105	1.00E-25	48	74	hypothetical 23.1 KD protein in SHP1-PTC3 intergenic region
20879	ENU04673	ANI61S2960: 1..547			NAP		g3329623	189	41	0.0003	24	53	[Saccharomyces cerevisiae] (AF078790) No definition line found
20880	ENU04674	ANI61C3402: 115-134	615-634		NAP		g2132933	722	191	3.00E-60	60	72	[Caenorhabditis elegans] probable membrane protein YOR271c - yeast (Saccharomyces cerevisiae)
20881	ENU04675	ANI61S4333: 29-48	436-455		NAP		g542225	448	136	7.00E-32	66	42	[Saccharomyces cerevisiae] ribosomal protein L4.e - fission yeast (Schizosaccharomyces pombe) []
20882	ENU04676	ANI61C1943: 102-124	360-381		NAP		g1705917	550	222	1.00E-57	57	11	probable clathrin heavy chain [Schizosaccharomyces pombe]
20883	ENU04677	ANI61C9505: 71-98	540-567		NAP		g4049509	232	106	1.00E-22	31	24	(AL034563) elongation factor g [Schizosaccharomyces pombe]
20884	ENU04678	ANI61C1094 41-60	626-643		NAP		g2132968	1222	135	4.00E-31	33	22	probable membrane protein YPL012w - yeast (Saccharomyces cerevisiae)
20885	ENU04679	ANI61C1049 112-131	805-829		NAP		g4107287	223	61	8.00E-15	32	45	[Saccharomyces cerevisiae] (AL035076) putative allantoinase permease [Schizosaccharomyces pombe]
20886	ENU04680	ANI61C9717: 27-46	785-812		NAP		g4098647	751	257	7.00E-68	51	56	"(U80668) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]"
20887	ENU04681	ANI61C9944: 23-47	629-648		NAP		g4106673	796	171	3.00E-85	66	59	(AL035064) queuine trna-ribosyltransferase [Schizosaccharomyces pombe]

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20888	ENU04682	ANI61C7199: 68-87 1012..633		306-325	NAP		g730917	307	78	1.00E-18			"T-complex protein 1, beta subunit (TCP-1-beta) (CCT-beta) [Saccharomyces cerevisiae]"
20889	ENU04683	ANI61C1075: 24-44 3:2090..509		803-829	NAP		g1723251	417	70	3.00E-15	29	59	hypothetical 50.9 KD protein C3F10.06C in chromosome I [Schizosaccharomyces pombe]
20890	ENU04684	ANI61C2651: 22-49 1783..670		785-805	NAP		g3123261	154	70	2.00E-11			meiotic recombination protein REC12 [Schizosaccharomyces pombe]
20891	ENU04685	ANI61C9331: 22-41 1110..1		732-749	NAP		g1063421	519	108	1.00E-28	44	40	[Schizosaccharomyces pombe] (L48797) toxin pump [Cochliobolus carbonum]
20892	ENU04686	ANI61S29:1.. 654			NAP		g2635181	553	213	7.00E-55	56	70	(Z99117) similar to protease [Bacillus subtilis]
20893	ENU04687	ANI61C9880: 22-41 1565..273		808-829	NAP		g2498765	469	107	1.00E-28			peroxisomal membrane protein PEX16 (peroxin-16) [Yarrowia lipolytica]
20894	ENU04688	ANI61C891:1 51-69 ..582		457-481	NAP		g1805251	124	73	1.00E-16	30	29	(U58946) transposase [Aspergillus awamori]
20895	ENU04689	ANI61C3704: 69-89 1..890		805-823	NAP		g4586103	199	67	1.00E-22	33	76	(AL049638) putative protein [Arabidopsis thaliana]
20896	ENU04690	ANI61C758:3 22-48 332..1		714-741	NAP		g2497080	1119	125	5.00E-30	32	16	hypothetical 171.1 KD protein in YL16A-DAK1 intergenic region [Saccharomyces cerevisiae]
20897	ENU04691	ANI61S2532: 1..514			NAP		g2119707	127	40	0.01	32	61	proline-rich protein precursor - rat []
20898	ENU04692	ANI61C883:8 22-45 86..1386		456-479	NAP		g1176053	156	90	1.00E-19	34	50	hypothetical 33.3 KD protein in ADE3-SER2 intergenic region [Saccharomyces cerevisiae]
20899	ENU04693	ANI61C2209: 22-42 1457..1		719-738	NAP		g1077575	182	62	0.000000	27	41	hypothetical protein YDR117c - yeast (Saccharomyces cerevisiae)
20900	ENU04694	ANI61C9811: 31-50 276..1330		767-786	NAP		g120777	947	310	1.00E-83	56	58	succinate-semialdehyde dehydrogenase (NADP+) (SSDH) [Escherichia coli]
20901	ENU04695	ANI61C8000: 41-60 959..1		727-749	NAP		g1703361	998	370	e-102			"ARG-6 protein precursor (contains: N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase), and acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-... [Neurospora crassa]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20902	ENU04696	ANI61C7533: 3582..4673	22-46	805-829	NAP		g3850084	370	87	2.00E-16	36	75	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
20903	ENU04697	ANI61C6751: 1..338	120-147	294-316	NAP		g3150262	196	80	5.00E-15	38	32	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
20904	ENU04698	ANI61C6031: 30-54	647-673		NAP		g113314	1311	482	e-135	96	7	delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emericella nidulans]
20905	ENU04699	ANI61C1084 6:2451..3573	51-70	714-733	NAP		g2132014	611	233	1.00E-60	45	61	hypothetical protein YOL124c - yeast (Saccharomyces cerevisiae)
20906	ENU04700	ANI61C201:1 624..1266	94-113	308-335	NAP		g2131347	264	68	2.00E-11	52	19	[Saccharomyces cerevisiae] hypothetical protein YDL153c - yeast (Saccharomyces cerevisiae)
20907	ENU04701	ANI61C4912: 3841..3182	49-72	600-627	NAP		g3122266	603	171	4.00E-60	65	56	[Saccharomyces cerevisiae] eukaryotic translation initiation factor 3 delta subunit (EIF-3 delta)
20908	ENU04702	ANI61C7350: 2513..1876	199-218	594-617	NAP		g2507129	395	112	3.00E-24	40	36	[Schizosaccharomyces pombe] transporter protein SMF1/ESP1
20909	ENU04703	ANI61C2646: 1..595			NAP		g4127832	306	140	8.00E-33	39	37	[Saccharomyces cerevisiae] (Y17243) cytochrome P450 [Gibberella fujikuroi]
20910	ENU04704	ANI61C1132 1:1594..2423	23-43	703-729	NAP		g464369	221	78	8.00E-23	32	35	phenol 2-monooxygenase (phenol hydroxylase) [Trichosporon cutaneum]
20911	ENU04705	ANI61C7309: 545..1	71-92	460-483	NAP		g2956774	62	48	0.00003	27	72	(AL022103) hypothetical protein. [Schizosaccharomyces pombe]
20912	ENU04706	ANI61C332:1 ..558	81-99	421-438	NAP		g585251	318	134	4.00E-31	43	36	polyketide synthase HETM [Anabaena sp.]
20913	ENU04707	ANI61C101:1 ..1001	22-46	801-828	NAP		g1870209	283	87	8.00E-24	32	50	(AC000133) ORF [Emericella nidulans]
20914	ENU04708	ANI61C3232: 1917..1	25-45	720-747	NAP		g2492658	3245	541	e-153	97	14	putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emericella nidulans]
20915	ENU04709	ANI61C1335: 1..389	48-70	349-368	NAP		g585668	413	152	1.00E-36	62	34	polygalacturonase precursor (PG) (pectinase) [Gibberella fujikuroi]
20916	ENU04710	ANI61C1053 0:722..1			NAP		g2133039	447	198	5.00E-50	48	15	probable membrane protein YPR184w - yeast (Saccharomyces cerevisiae)
20917	ENU04711	ANI61C4364: 1..1567	30-49	725-747	NAP		g2342601	814	123	2.00E-27	30	5	[Saccharomyces cerevisiae] (X89442) peptide synthetase [Metarhizium anisopliae]

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20918	ENU04712	ANI61S2752: 1..605			NAP		g4760549	77	53	0.000001			(AB019494) IDN3 [Homo sapiens]
20919	ENU04713	ANI61C7196: 22-49	777-804		NAP		g3859775	415	111	2.00E-31	52	53	(Z54328) putative aminopeptidase p [Schizosaccharomyces pombe]
20920	ENU04714	ANI61C9312: 22-46	802-829		NAP		g3915187	556	132	3.00E-30	33	14	probable N-end-recognizing protein (ubiquitin-protein ligase E3 component) (N-recognin) [regulatory protein alcR - Emericella nidulans [Emericella nidulans]]
20921	ENU04715	ANI61C9006: 42-61	697-716		NAP		g83716	3301	404	e-141	95	32	"erythronolide synthase, modules 1 and 2 (ORF 1) (6-deoxyerythronolide B synthase I) (DEBS 1) [hypothetical protein C22F3.14C in chromosome I [AL031824] putative transcriptional regulator [Schizosaccharomyces pombe]
20922	ENU04716	ANI61C1084 22-44	623-643		NAP		g416965	658	50	3.00E-21	37	7	dolichyl-phosphate-mannose--protein mannosyltransferase 4 [Saccharomyces cerevisiae]
20923	ENU04717	ANI61C6533: 22-48	727-749		NAP		g1175451	842	152	3.00E-36			6-hydroxy-D-nicotine oxidase (6-HDNO) [Arthrobacter oxidans]
20924	ENU04718	ANI61C5137: 88-110	741-760		NAP		g3702632	592	137	3.00E-63	43	41	sulfur metabolite repression control protein [Emericella nidulans]
20925	ENU04719	ANI61C419:1 23-46	412-431		NAP		g1172542	388	168	3.00E-41	47	22	hypothetical 98.4 KD protein C24H6.13 in chromosome I [Schizosaccharomyces pombe]
20926	ENU04720	ANI61C8353: 26-45	776-794		NAP		g122805	311	109	3.00E-23	30	53	[U07366] eIF-5A [Candida albicans]
20927	ENU04721	ANI61C3877: 1384..1			NAP		g3122851	2113	284	e-134	89	41	hypothetical protein VSP-3 - Chlamydomonas reinhardtii [Chlamydomonas reinhardtii]
20928	ENU04722	ANI61C8873: 8184..7035			NAP		g1175441	458	83	3.00E-15	27	31	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
20929	ENU04723	ANI61C1126 4:323..1	102-123	448-475	NAP		g4204352	396	166	1.00E-40	78	64	beta-glucosidase [Candida wickerhamii]
20930	ENU04724	ANI61C4166: 121-140	505-524		NAP		g1076211	227	45	0.0006	28	43	(U97079) U5-116kD [Mus musculus]
20931	ENU04725	ANI61C6980: 22-44	561-582		NAP		g2213560	369	164	4.00E-40	44	98	
20932	ENU04726	ANI61C9955: 22-49	760-783		NAP		g534844	501	184	7.00E-46	55	39	
20933	ENU04727	ANI61C1013 23-50	538-558		NAP		g2105430	316	145	4.00E-34	45	17	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20934	ENU04728	ANI61S4589: 1..553			NAP		g82698	177	47	0.00008	35	54	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]
20935	ENU04729	ANI61C1053 45-64	792-819		NAP		g416643	231	65	7.00E-10	32	58	aristolochene synthase (sesquiterpene cyclase) (AS) [Penicillium roqueforti] (AC004521) unknown protein [Arabidopsis thaliana]
20936	ENU04730	ANI61C9379: 23-50	467-490		NAP		g3128203	134	63	0.000000	36	75	hypothetical 17.5 KD protein in chromosome II [Schizosaccharomyces pombe]
20937	ENU04731	ANI61C4278: 22-42	652-671		NAP		g3915405	146	79	4.00E-14	37	96	transduction protein [Schizosaccharomyces pombe]
20938	ENU04732	ANI61C1110 105-125	643-665		NAP		g3925752	276	68	1.00E-22	41	58	(AL034352) putative signal transduction protein [Schizosaccharomyces pombe]
20939	ENU04733	ANI61S3754: 31-56	371-390		NAP		g2911045	695	187	2.00E-73	95	51	(AL021961) putative protein [Arabidopsis thaliana]
20940	ENU04734	ANI61C9298: 1..508			NAP		g1401057	158	104	1.00E-21	25	14	(U40375) Supt6h [Mus musculus]
20941	ENU04735	ANI61S3133: 46-65	427-450		NAP		g4105798	164	99	2.00E-20	36	43	(AF049930) PGP237-11 [Petunia x hybrida]
20942	ENU04736	ANI61C7989: 71-89	418-441		NAP		g3880413	160	66	1.00E-10	33	46	(Z81137) Similarity to Yeast YIP1 protein (SW:P53039); cDNA EST EMBL:T01608 comes from this gene; cDNA EST EMBL:C07393 comes from this gene; cDNA EST EMBL:C07550 comes from this gene; cDNA EST EMBL:C08746 comes from this gene; ... []
20943	ENU04737	ANI61C5949: 55-75	594-612		NAP		g2493011	323	151	5.00E-36	37	13	probable calcium-transporting ATPase 8 [Saccharomyces cerevisiae] (AF116827) unknown [Homo sapiens]
20944	ENU04738	ANI61C9477: 30-49	806-829		NAP		g4768831	418	38	0.12			(AL035536) putative DNA polymerase accessory protein [Schizosaccharomyces pombe]
20945	ENU04739	ANI61C1110 28-47	769-796		NAP		g4455787	886	195	4.00E-52	52	66	hypothetical 48.1 KD protein in TUB1-CPR3 intergenic region [Saccharomyces cerevisiae]
20946	ENU04740	ANI61C5813: 41-60	734-761		NAP		g1730621	585	223	1.00E-61	57	56	putative enoyl-CoA hydratase [Mycobacterium leprae]
20947	ENU04741	ANI61C6657: 33-52	422-445		NAP		g1706567	89	59	0.000000	25	40	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
20948	ENU04742	ANI61C5440: 1052..1	90-109	748-767	NAP		g728743	1212	322	e-103			"6-phosphogluconate dehydrogenase, decarboxylating 1 [Saccharomyces cerevisiae]"
20949	ENU04743	ANI61C3035: 105-130 910..447	416-443		NAP		g4056553	133	86	1.00E-16	39	20	(AL034583) putative exonuclease [Schizosaccharomyces pombe]
20950	ENU04744	ANI61C5064: 37-56 867..1	804-829		NAP		g231714	212	99	5.00E-20	36	24	CDC21 protein []
20951	ENU04745	ANI61C7394: 107-126 1616..1134	401-420		NAP		g125155	283	127	4.00E-29	41	71	Adenylate kinase 2 (ATP-AMP transphosphorylase) [Saccharomyces cerevisiae]
20952	ENU04746	ANI61C1243: 105-125 1..479	349-371		NAP		g114251	175	51	1.00E-12	41	40	L-asparaginase I (L-asparagine amidohydrolase I) [Escherichia coli]
20953	ENU04747	ANI61C5328: 24-45 1..1213	762-786		NAP		g3560207	361	89	3.00E-17	35	46	(AL031536) fnx1p. [Schizosaccharomyces pombe]
20954	ENU04748	ANI61C8350: 22-44 2767..4671	766-788		NAP		g2791647	470	89	4.00E-17	31	42	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]
20955	ENU04749	ANI61S1354: 1..713			NAP		g1079170	137	52	0.000006	31	61	larval glue protein Lgp-3 precursor - fruit fly (Drosophila virilis) [Drosophila virilis]
20956	ENU04750	ANI61C9637: 41-60 1067..103	791-812		NAP		g4154817	480	107	1.00E-47	42	87	(AE001466) putative [Helicobacter pylori J99]
20957	ENU04751	ANI61C7698: 22-49 1010..1	723-746		NAP		g4521247	1397	494	e-139	92	57	(AB007770) translation elongation factor 1 alpha [Aspergillus oryzae]
20958	ENU04752	ANI61C291:1 059..1			NAP		g113314	1686	492	e-141	93	7	delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emericella nidulans]
20959	ENU04753	ANI61C1116 7:300..1589	22-48	763-783	NAP		g2635715	530	111	1.00E-35	41	63	(Z99120) similar to Na+/nucleoside cotransporter [Bacillus subtilis]
20960	ENU04754	ANI61C7546: 31-51 2147..3310	807-828		NAP		g2497952	221	98	1.00E-19			hypothetical hydrolase/peptidase Y4TM [Rhizobium sp. NGR234]
20961	ENU04755	ANI61S4137: 1..755			NAP		g283032	161	32	0.013	35	59	hydroxyproline-rich glycoprotein - perennial teasinte [Zea diploperennis]
20962	ENU04756	ANI61C936:6 35..1	49-68	494-515	NAP		g3560228	423	157	6.00E-43	50	61	(AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]
20963	ENU04757	ANI61C1316: 47-73 848..1	725-747		NAP		g2804612	1030	238	2.00E-89	83	37	(U81165) MOD-E [Podospora anserina]

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20964	ENU04758	ANI61S4517: 24-47 1..440	24-47	373-393	NAP		g2330857	411	175	2.00E-43	60	10	(Z98533) phosphoribosylformylglycinamidine synthase [Schizosaccharomyces pombe]
20965	ENU04759	ANI61C3920: 22-46 2244..1	22-46	723-746	NAP		g3650404	1579	148	4.00E-35	42	28	(AL031739) eukaryotic translation initiation factor 3 subunit [Schizosaccharomyces pombe]
20966	ENU04760	ANI61C9383: 24-51 1..3966	24-51	807-826	NAP		g416765	1139	164	5.00E-40	27	13	general negative regulator of transcription subunit 1 [Saccharomyces cerevisiae]
20967	ENU04761	ANI61C8310: 106-125 378..1	106-125	459-479	NAP		g1703347	311	85	8.00E-26	51	67	adenine phosphoribosyltransferase 1 (APRT 1) [Saccharomyces cerevisiae]
20968	ENU04762	ANI61S2708: 1..750			NAP		g2493749	132	36	0.21	23	14	240 kD protein of rod photoreceptor CNG-channel [Bos taurus]
20969	ENU04763	ANI61C3037: 23-45 575..1	23-45	519-546	NAP		g1352954	224	96	2.00E-19	35	25	hypothetical 77.7 kD protein in CCT3-CCT8 intergenic region [Saccharomyces cerevisiae]
20970	ENU04764	ANI61C1117: 220-238 3..924..214	220-238	638-657	NAP		g136682	333	140	8.00E-33	39	99	ubiquitin carboxyl-terminal hydrolase isozyme L3 (UCH-L3) (ubiquitin thiolesterase L3) [Homo sapiens]
20971	ENU04765	ANI61C6434: 23-44 2648..1866	23-44	712-731	NAP		g1076802	75	46	0.0003			extensin-like protein - maize [Zea mays]
20972	ENU04766	ANI61C26:81 7..1	222-244	736-763	NAP		g1705828	1119	298	3.00E-85	95	23	chitin synthase 2 (chitin-UDP acetylglucosaminyl transferase 2) [Emicella nidulans]
20973	ENU04767	ANI61C8888: 25-52 282..1609	25-52	713-737	NAP		g730755	837	129	2.00E-50	54	45	transporter protein SMF2 [Saccharomyces cerevisiae]
20974	ENU04768	ANI61C4526: 22-45 1314..1	22-45	809-828	NAP		g3650406	754	199	1.00E-50	47	26	(AL031739) 26S proteasome regulatory subunit [Schizosaccharomyces pombe]
20975	ENU04769	ANI61C1120: 22-44 11172..12742	22-44	714-731	NAP		g125727	701	141	1.00E-39			killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase [Kluyveromyces lactis])
20976	ENU04770	ANI61C7885: 102-122 1238..835	102-122	334-353	NAP		g1711623	159	38	0.000000 41 02	41	11	"alanyl-TRNA synthetase, cytoplasmic (alanine--TRNA ligase) (ALARS) [Saccharomyces cerevisiae]"
20977	ENU04771	ANI61C6793: 59-78 1..648	59-78	571-591	NAP		g3135013	755	302	1.00E-81	68	24	(AJ005963) 100 kDa protein [Ajellomyces capsulatus]
20978	ENU04772	ANI61C7746: 95-114 4718..4215	95-114	451-478	NAP		g1351714	190	73	1.00E-12	25	33	putative transporter C11D3.18C [Schizosaccharomyces pombe]

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20979	ENU04773	ANI61C1049: 1..716	48-69	588-615	NAP		g3288709	996	277	e-109	89	15	(AB010442) PMR1 [Penicillium digitatum]
20980	ENU04774	ANI61C8780: 48-65	799-826		NAP		g130333	554	154	6.00E-37	47	68	pectin lyase D precursor (PLD) (pectin lyase I) (PLI) [Aspergillus niger]
20981	ENU04775	ANI61C1252: 1290..2143	114-133	435-462	NAP		g400069	841	261	5.00E-87			insertion element IS1 protein INSB [Escherichia coli]
20982	ENU04776	ANI61C1269: 496..1			NAP		g2145993	125	69	4.00E-11	28	97	yfcA protein - Mycobacterium leprae [Mycobacterium leprae]
20983	ENU04777	ANI61C9834: 291..1042	65-84	798-816	NAP		g3402279	702	156	1.00E-54	49	78	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]
20984	ENU04778	ANI61C3653: 6235..7555	121-140	342-361	NAP		g134920	101	47	0.00008	26	30	sulfated surface glycoprotein 185 (SSG 185) [Volvox carteri]
20985	ENU04779	ANI61C6617: 1..458	23-42	576-595	NAP		g1079456	471	192	2.00E-49	60	62	"actin-capping protein beta chain, splice form 2 - chicken [Gallus gallus]"
20986	ENU04780	ANI61S1139: 4827..5522			NAP		g1572721	133	38	0.044	31	13	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
20987	ENU04781	ANI61C8129: 1..586	22-46	621-640	NAP		g730240	249	142	3.00E-33	34	54	osmotic growth protein 1 [Saccharomyces cerevisiae]
20988	ENU04782	ANI61C1094: 223..1094	186-204	729-748	NAP		g3560228	476	98	7.00E-31	43	77	(AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]
20989	ENU04783	ANI61C7234: 1..831			NAP		g2499716	1440	303	e-109	83	55	"exopolysaccharuronase precursor (exoPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"
20990	ENU04784	ANI61C9604: 6879..6438			NAP		g729650	258	98	3.00E-20	44	30	"exoglucanase I precursor (exocellobiohydrolase I) (1,4-beta-cellobiohydrolase) [Penicillium janthinellum]"
20991	ENU04785	ANI61C6076: 2446..1907	22-45	496-515	NAP		g1197667	96	31	5.1	29	98	(U46857) vitellogenin [Anolis pulchellus]
20992	ENU04786	ANI61C5316: 1377..972	68-87	362-381	NAP		g1174622	227	84	5.00E-16	52	19	"T-complex protein 1, theta subunit (TCP-1-theta) (CCT-theta) [Saccharomyces cerevisiae]"
20993	ENU04787	ANI61C9088: 1167..592	111-130	532-555	NAP		g2826168	193	57	0.000000	36	42	(AB010714) salicylate hydroxylase [Pseudomonas putida]

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20994	ENU04788	ANI61C5537: 22-43	456-479	NAP			g729763	198	101	4.00E-21	38	80	30 KD heat shock protein [Emericella nidulans]
20995	ENU04789	ANI61C753:7 22-49	702-721	NAP			g1083855	150	92	4.00E-18	26	1	cyclosporin synthetase - Tolypocladium inflatum [Tolypocladium inflatum]
20996	ENU04790	ANI61C1830: 107-129	802-821	NAP			g2501686	919	349	3.00E-95	59	16	hypothetical 187.1 KD protein in OGG1-CNA2 intergenic region [Saccharomyces cerevisiae]
20997	ENU04791	ANI61C8954: 93-112	556-579	NAP			g3978466	462	108	1.00E-47	45	29	(AF086822) dihydroxyacetone synthase [Candida boidinii]
20998	ENU04792	ANI61C1899: 35-54	805-829	NAP			g2501202	1767	272	e-108	75	51	protein disulfide isomerase precursor (PDI) [Aspergillus niger]
20999	ENU04793	ANI61C3322: 164-183	454-479	NAP			g1722894	379	159	9.00E-39	52	42	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-l-arabinofuranosidase (arabinosidase) [Bacteroides ovatus]"
21000	ENU04794	ANI61C1684: 22-41	781-808	NAP			g2330829	557	170	1.00E-41	40	18	(Z98530) hypothetical protein [Schizosaccharomyces pombe]
21001	ENU04795	ANI61C1574: 120-137	492-511	NAP			g2293194	99	57	0.000000	28	41	(AF0082220) yteR [Bacillus subtilis]
21002	ENU04796	ANI61C1236: 22-45	766-792	NAP			g125462	1460	573	e-163			"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3')I) [Cloning vector pHIND2.2]"
21003	ENU04797	ANI61C5865: 108-127	724-750	NAP			g2492799	589	161	8.00E-58	44	72	putative sterigmatocystin biosynthesis dehydrogenase STCV [Emericella nidulans]
21004	ENU04798	ANI61C1994: 29-51	370-389	NAP			g4884104	110	57	0.000000			(AL050060) hypothetical protein [Homo sapiens]
21005	ENU04799	ANI61S1320: 842..422		NAP			g3874243	147	50	0.00002	20	50	(Z70204) similar to PHD-finger.; cDNA EST EMBL:T00556 comes from this gene; cDNA EST yk34447.5 comes from this gene [Caenorhabditis elegans]
21006	ENU04800	ANI61C1743: 24-44	733-755	NAP			g3261605	699	185	3.00E-61	45	14	(Z74697) ppsA [Mycobacterium tuberculosis]
21007	ENU04801	ANI61C7911: 22-48	776-797	NAP			g2894293	507	105	6.00E-28	35	47	(AL021837) hypothetical protein [Schizosaccharomyces pombe]

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21008	ENU04802	ANI61C8612: 102-125 1..363	102-125	294-314	NAP		g2239205	198	90	5.00E-18	37	48	(Z97209) hypothetical protein [Schizosaccharomyces pombe] transcription initiation protein SPT6 [Saccharomyces cerevisiae]
21009	ENU04803	ANI61C8663: 28-49 88..1251	28-49	806-828	NAP		g134854	269	92	4.00E-18	27	19	(U58946) transposase [Aspergillus awamori]
21010	ENU04804	ANI61C1850: 25-52 1003..1	25-52	720-747	NAP		g1805251	849	272	3.00E-72	54	50	(AC000133) f4p06 [Emericella nidulans]
21011	ENU04805	ANI61C5897: 33-52 3555..4214	33-52	590-617	NAP		g1870216	1136	416	e-116	100	100	(AL034583) putative exonuclease [Schizosaccharomyces pombe]
21012	ENU04806	ANI61C9479: 22-44 1214..1	22-44	792-818	NAP		g4056553	300	94	1.00E-18	39	34	mitochondrial respiratory chain complexes assembly protein RCA1 (TAT-binding homolog 12) [Saccharomyces cerevisiae]
21013	ENU04807	ANI61C1226: 101-120 537..1	101-120	424-444	NAP		g1710045	274	106	2.00E-22	38	21	(AL021748) major facilitator superfamily protein [Schizosaccharomyces pombe]
21014	ENU04808	ANI61C6000: 22-47 7848..5903	22-47	806-827	NAP		g2842516	484	88	7.00E-17			(AL023594) 40s ribosomal protein s4 type [Schizosaccharomyces pombe]
21015	ENU04809	ANI61C7282: 22-49 1394..1868	22-49	376-399	NAP		g3150141	504	128	2.00E-48	73	51	(S83229) beta-isopropylmalate dehydrogenase=isozyme [Aspergillus niger]
21016	ENU04810	ANI61C1158: 43-63 5639..4409	43-63	791-810	NAP		g1911743	1514	320	e-103	84	65	cell division control protein 48 [Saccharomyces cerevisiae]
21017	ENU04811	ANI61C7741: 22-42 2414..4556	22-42	697-724	NAP		g1705679	2474	226	5.00E-99	78	31	probable membrane protein YLR324w - yeast [Saccharomyces cerevisiae]
21018	ENU04812	ANI61C3249: 52-70 1..1397	52-70	774-793	NAP		g1078072	247	85	8.00E-16	32	41	[Saccharomyces cerevisiae] (AJ005258) amyR [Aspergillus oryzae]
21019	ENU04813	ANI61C7670: 50-69 2104..4211	50-69	772-791	NAP		g3043376	261	60	0.000000			(U82084) unknown [bacteriophage Sfx]
21020	ENU04814	ANI61C6680: 30-47 528..1	30-47	482-507	NAP		g4099032	892	176	8.00E-74	96	58	hypothetical 28.0 KD protein C13C5.04 in chromosome I [Schizosaccharomyces pombe]
21021	ENU04815	ANI61S2301: 71-90 485..79	71-90	363-386	NAP		g1175364	183	82	2.00E-15	39	46	probable membrane protein YOL162w - yeast [Saccharomyces cerevisiae]
21022	ENU04816	ANI61C9378: 23-45 472..1418	23-45	775-802	NAP		g2132860	280	45	0.000000	42	91	[Saccharomyces cerevisiae]

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21023	ENU04817	ANI61C9378: 22-48 1..456	22-48	407-434	NAP		g2132861	363	84	2.00E-29	51	75	probable membrane protein YOL163w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21024	ENU04818	ANI61C1114 32-51 4:516..1	32-51	398-415	NAP		g2222786	422	108	3.00E-23	63	69	(Z97185) hypothetical protein [Schizosaccharomyces pombe]
21025	ENU04819	ANI61C2562: 51-70 1533..2108	51-70	449-468	NAP		g131768	569	211	3.00E-54	60	35	quinate permease (quinate transporter) [Emicella nidulans]
21026	ENU04820	ANI61C1106 30-49 5:1224..1	30-49	670-691	NAP		g3183329	713	136	6.00E-53	57	52	hypothetical aminotransferase C6B12.04C [Schizosaccharomyces pombe]
21027	ENU04821	ANI61C1024 94-115 9:9831..9292	94-115	494-519	NAP		g1293655	113	70	1.00E-11	26	27	(U51327) versicolorin B synthase [Aspergillus parasiticus]
21028	ENU04822	ANI61S1471: 631..28			NAP		g418604	857	328	2.00E-93	89	64	hypothetical 35.6 KD protein in RPME-TDK intergenic region (ORFP) []
21029	ENU04823	ANI61C8903: 102-125 1..1199	102-125	803-829	NAP		g232152	1231	421	e-132	97	51	G2/mitotic-specific cyclin B [Emicella nidulans]
21030	ENU04824	ANI61C7756: 22-49 1187..1	22-49	618-643	NAP		g3451467	569	212	4.00E-54	45	45	(AL031349) putative cystathionine gamma-synthase [Schizosaccharomyces pombe]
21031	ENU04825	ANI61C4392: 22-43 822..1	22-43	697-715	NAP		g3947592	448	121	2.00E-46			"(AL034364) similar to homogenisate 1,2-dioxygenase (EC 1.13.11.5) (homogenisicase) (homogenisate oxygenase) (homogenisic acid oxidase); cDNA EST yk385c12.5 comes from this gene; cDNA EST EMBL:D73328 comes from this gene; cD... []"
21032	ENU04826	ANI61S1672: 1..695			NAP		g2119707	77	55	0.000000	27	80	proline-rich protein precursor - rat []
21033	ENU04827	ANI61C1097 71-90 5:812..1721	71-90	805-829	NAP		g2496731	881	336	1.00E-91	67	92	hypothetical 30.2 KD protein Y40V [Rhizobium sp. NGR234]
21034	ENU04828	ANI61C3908: 22-44 798..1409	22-44	485-511	NAP		g586485	242	145	3.00E-34	35	50	hypothetical 45.5 KD protein in FIG1-GIP1 intergenic region [Saccharomyces cerevisiae]
21035	ENU04829	ANI61S49:1..530			NAP		g416876	238	47	5.00E-11	38	60	dihydrodipicolinate synthase (DHDPS) (vegetative protein 81) (VEG81) [Bacillus subtilis]

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21036	ENU04830	ANI61C1518: 22-43 1291..1	217-236	715-740	NAP	g1168464	1254	212	2.00E-78	57	53		monoamine oxidase N (MAO-N) [Aspergillus niger]
21037	ENU04831	ANI61C1133: 217-236 4062..5481	217-236	715-740	NAP	g118381	1019	228	6.00E-59	56	58		ornithine decarboxylase (ODC) [Neurospora crassa]
21038	ENU04832	ANI61C4437: 22-43 1625..2136	22-43	440-462	NAP	g4583351	1113	64	5.00E-10	27	30		(AF114167) lysosomal pepstatin insensitive protease [Canis familiaris]
21039	ENU04833	ANI61C2465: 57-76 776..3711	57-76	795-815	NAP	g1546072	1287	147	1.00E-34	40	9		(U68040) polyketide synthase [Cochliobolus heterostrophus]
21040	ENU04834	ANI61C9269: 26-53 1761..2743	26-53	808-829	NAP	g1805251	718	249	3.00E-65	44	51		(U58946) transposase [Aspergillus awamori]
21041	ENU04835	ANI61C9769: 102-127 1..572	102-127	526-551	NAP	g1870212	903	278	2.00E-74	94	97		(AC000133) ORF [Emericella nidulans]
21042	ENU04836	ANI61C6563: 121-144 1..495	121-144	378-405	NAP	g1351598	398	167	5.00E-41	47	31		hypothetical 59.6 KD protein C4G8.07C in chromosome I [Schizosaccharomyces pombe]
21043	ENU04837	ANI61C6365: 39-57 1..5956	39-57	728-749	NAP	g2342601	2803	145	3.00E-34	37	5		(X89442) peptide synthetase [Metarhizium anisopliae]
21044	ENU04838	ANI61C2860: 161-187 790..1	161-187	714-740	NAP	g1346361	269	142	1.00E-35	41	32		serine/threonine-protein kinase SHK2 [Schizosaccharomyces pombe]
21045	ENU04839	ANI61C9769: 22-47 596..1239	22-47	591-610	NAP	g1870213	1021	254	e-108	97	99		(AC000133) ORF [Emericella nidulans]
21046	ENU04840	ANI61C1028 60-79 7:1675..2204	60-79	443-461	NAP	g609350	549	228	3.00E-59	63	22		(U15099) methionine synthase [Saccharomyces cerevisiae]
21047	ENU04841	ANI61C1045 105-132 1:1..475	105-132	426-447	NAP	g1709181	288	117	2.00E-27	39	27		high affinity methionine permease [Saccharomyces cerevisiae]
21048	ENU04842	ANI61C2802: 43-62 2437..717	43-62	775-794	NAP	g4056555	849	86	3.00E-16				(AL034583) putative mitochondrial atp-dependent rna helicase precursor [Schizosaccharomyces pombe]
21049	ENU04843	ANI61S4378: 1..806			NAP	g1079170	144	31	0.04	31	69		larval glue protein Lgp-3 precursor - fruit fly (Drosophila virilis) [Drosophila virilis]
21050	ENU04844	ANI61C2758: 105-131 1..609	105-131	523-546	NAP	g2133266	875	319	1.00E-86	96	16		chromosome scaffold protein sudA - Emericella nidulans [Emericella nidulans]
21051	ENU04845	ANI61C5221: 22-45 6482..4482	22-45	806-828	NAP	g3282216	540	56	0.000000	3			(U68716) polyketide synthase homolog [Botryotinia fuckeliana]
21052	ENU04846	ANI61C1008 35-54 8:1..578	35-54	497-519	NAP	g135649	263	75	2.00E-13	41	31		"2,4-dichlorophenol 6-monoxygenase (2,4-dichlorophenol hydroxylase) (2,4-DCP hydroxylase) [Plasmid pJP4]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21053	ENU04847	ANI61C9706: 22-48 1522..6699	725-747	NAP			g1805262	3278	103	2.00E-45	39	13	"(U75347) fatty acid synthase, beta subunit [Emericella nidulans]"
21054	ENU04848	ANI61C3226: 58-77 813..1	676-695	NAP			g1723578	359	96	3.00E-29	50	60	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
21055	ENU04849	ANI61C1235: 22-49 924..72	783-810	NAP			g4557168	1419	530	e-150	97	99	(AF104442) inhibitor resistant beta lactamase TEM-54 [Escherichia coli]
21056	ENU04850	ANI61S1182: 1..976		NAP			g3153821	177	34	0.99	26	29	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
21057	ENU04851	ANI61C7768: 24-51 1983..2496	468-492	NAP			g3005097	502	109	2.00E-48	67	99	"(AF046872) Cu,Zn-superoxide dismutase [Candida albicans]"
21058	ENU04852	ANI61C4396: 55-76 1322..413	768-787	NAP			g1293655	416	155	4.00E-37	41	37	(U51327) versicolorin B synthase [Aspergillus parasiticus]
21059	ENU04853	ANI61C1049 22-46 0:4829..8034	775-802	NAP			g1834340	4837	489	e-138	95	18	(Z68904) ATP-binding cassette multidrug transporter [Emericella nidulans]
21060	ENU04854	ANI61C6622: 81-100 552..1	479-500	NAP			g131768	555	226	9.00E-59	60	34	quinase permease (quinase transporter) [Emericella nidulans]
21061	ENU04855	ANI61S1397: 1..369		NAP			g140011	497	182	1.00E-45	85	30	mitochondrial ribosomal protein S5 [Emericella nidulans]
21062	ENU04856	ANI61C1122 122-144 4:1..504	458-482	NAP			g2493391	359	155	1.00E-37	49	38	probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) [Emericella nidulans]
21063	ENU04857	ANI61C9762: 78-97 7481..7130	305-331	NAP			g731700	228	104	2.00E-22	41	31	hypothetical 42.4 KD protein in CDC12-ORC6 intergenic region [Saccharomyces cerevisiae]
21064	ENU04858	ANI61C957:1 102-125 ..653	516-543	NAP			g1703456	520	219	2.00E-56	52	18	cation-transporting ATPase PAT1 [Dictyostelium discoideum]
21065	ENU04859	ANI61C3989: 55-74 874..1	724-743	NAP			g1293655	332	78	8.00E-31	36	38	(U51327) versicolorin B synthase [Aspergillus parasiticus]
21066	ENU04860	ANI61C5606: 66-85 1..829	760-786	NAP			g4106374	910	178	1.00E-89	73	46	(AF069777) mitogen-activated protein kinase kinase CPK1 [Cryphonectria parasitica]
21067	ENU04861	ANI61S4332: 397..1		NAP			g3170523	637	258	1.00E-68	99	10	(AF053883) coatomer alpha subunit [Emericella nidulans]
21068	ENU04862	ANI61C9112: 22-48 4843..4071	725-752	NAP			g464738	138	58	0.000000			translocation protein SEC66 (HSS1 protein) [Saccharomyces cerevisiae]

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21069	ENU04863	ANI61C320:1 744..2877			NAP		g940860	461	147	8.00E-35	51	29	(X90565) MYO2 [Saccharomyces cerevisiae]
21070	ENU04864	ANI61C6479: 97-116 4155..5273		651-672	NAP		g1749498	176	95	5.00E-19	28	77	(D89145) similar to Saccharomyces cerevisiae ORF YGL092W
21071	ENU04865	ANI61C7648: 27-50 1..428		373-400	NAP		g1170421	180	60	3.00E-13	40	21	[Schizosaccharomyces pombe] HUS2 protein [Saccharomyces cerevisiae]
21072	ENU04866	ANI61C7910: 2260..1			NAP		g113314	3671	454	e-136	89	7	delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emmericella nidulans]
21073	ENU04867	ANI61C1224: 64-91 1..844		638-663	NAP		g462071	797	290	7.00E-85			"fatty acid synthase, subunit beta [Yarrowia lipolytica]"
21074	ENU04868	ANI61C9303: 27-54 4520..2714		805-829	NAP		g4755188	521	73	8.00E-24			(AC007018) unknown protein [Arabidopsis thaliana]
21075	ENU04869	ANI61C2783: 22-44 1067..2183		677-695	NAP		g2414579	545	216	1.00E-55	49	44	(Z99292) flavoprotein [Schizosaccharomyces pombe]
21076	ENU04870	ANI61C1014 50-69 6:1022..265		635-657	NAP		g1730743	387	183	9.00E-46	46	77	hypothetical 34.9 KD protein in MSK1-PDA2 intergenic region
21077	ENU04871	ANI61C3868: 22-49 3311..3872		436-461	NAP		g2494018	214	89	3.00E-17	35	79	[Saccharomyces cerevisiae] maltose O-acetyltransferase (maltose transacetylase) [Escherichia coli]
21078	ENU04872	ANI61C1035 22-49 4:592..1		515-534	NAP		g2315274	419	76	1.00E-32	49	51	(Y11113) endoglucanase IV [Hypocrea jecorina]
21079	ENU04873	ANI61C8581: 22-42 3239..4082		799-819	NAP		g3980401	213	127	7.00E-29	33	97	(AC004561) putative tropinone reductase [Arabidopsis thaliana]
21080	ENU04874	ANI61C27:1.. 24-51 2171		715-742	NAP		g586352	1238	134	1.00E-30	34	22	hypothetical 124.0 KD protein in PCS60-ABD1 intergenic region
21081	ENU04875	ANI61C1053 185-204 5:4916..3815		810-829	NAP		g2851424	181	100	1.00E-20	25	75	[Saccharomyces cerevisiae] hypothetical 37.5 KD protein in DEGA-NPRB intergenic region
21082	ENU04876	ANI61C7988: 40-59 770..1		665-691	NAP		g1175361	150	55	0.000000	29	51	[Bacillus subtilis] hypothetical 48.5 KD protein C13C5.02 in chromosome I
21083	ENU04877	ANI61C1202: 22-41 1..1694		786-808	NAP		g2342601	790	166	2.00E-40	37	5	[Schizosaccharomyces pombe] (X89442) peptide synthetase
21084	ENU04878	ANI61C5153: 40-59 216..1177		768-787	NAP		g1706176	977	316	2.00E-85	71	25	[Metarhizium anisopliae] cutinase transcription factor 1 alpha [Fusarium solani f. sp. pisii]

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21085	ENU04879	ANI61C6712: 2698..1	22-49	722-749	NAP		g1709997	726	48	0.0001			DNA repair protein RAD18 [Schizosaccharomyces pombe]
21086	ENU04880	ANI61C499:7 63-82	63-82	806-829	NAP		g2909648	548	157	5.00E-47	53	95	(AL021943) echA5 [Mycobacterium tuberculosis]
21087	ENU04881	140..6262	64-90	485-504	NAP		g1078626	954	346	5.00E-95	99	12	bimD protein - Emericella nidulans [Emericella nidulans]
21088	ENU04882	ANI61C4145: 1..559	102-123	291-310	NAP		g464435	303	126	6.00E-29	53	26	acid phosphatase precursor [Aspergillus niger]
21089	ENU04883	ANI61C6082: 1..333	68-87	804-826	NAP		g1805261	645	166	1.00E-44	40	13	"(U75347) fatty acid synthase, alpha subunit [Emericella nidulans]"
21090	ENU04884	1063..2399	42-61	257-276	NAP		g2392764	335	141	4.00E-34	78	17	(AC002534) hypothetical protein [Arabidopsis thaliana]
21091	ENU04885	ANI61C3838: 378	23-46	807-826	NAP		g3806120	2179	466	e-130	96	23	(AF097728) pyruvate carboxylase [Aspergillus terreus]
21092	ENU04886	45..1417	60-79	791-810	NAP		g3335173	373	71	1.00E-17			(AF071202) ABC transporter MOAT-B [Homo sapiens]
21093	ENU04887	ANI61C1035 0:3541..1	31-50	807-829	NAP		g1870208	2438	114	7.00E-25	99	58	(AC000133) ORF [Emericella nidulans]
21094	ENU04888	891..2338	22-43	810-829	NAP		g2495217	1971	436	e-121	78	57	glucokinase (glucose kinase) (GLK) [Aspergillus niger]
21095	ENU04889	ANI61C1042 0:5573..4046	23-50	801-827	NAP		g1077569	1088	208	3.00E-75	53	37	probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae)
21096	ENU04890	ANI61C5224: 1490..1	22-48	790-810	NAP		g2131132	213	90	1.00E-17	24	19	[Saccharomyces cerevisiae] UDPglucose--glycoprotein glucosyltransferase (EC 2.7.8.19) - fission yeast (Schizosaccharomyces pombe)
21097	ENU04891	ANI61C3404: 1..1086	35-54	780-805	NAP		g4160575	539	122	2.00E-49	53	42	[Schizosaccharomyces pombe] (AL035226) putative structure specific recognition protein, possible chromatin-associated HMG protein
21098	ENU04892	ANI61C2738: 962..1	151-170	702-721	NAP		g1730665	121	67	2.00E-10	29	91	[Schizosaccharomyces pombe] hypothetical 25.3 KD protein in TIM23-ARE2 intergenic region
21099	ENU04893	ANI61C3813 0:3069..3813	30-54	795-820	NAP		g4507295	250	85	4.00E-16	28	99	[Saccharomyces cerevisiae] syntaxin 7 [Homo sapiens]

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21100	ENU04894	ANI61C1038 22-46 4:670..1	22-46	535-562	NAP		g3790261	371	160	1.00E-38	43	65	(AL031966) putative quinone oxidoreductase [Schizosaccharomyces pombe]
21101	ENU04895	ANI61S1377: 70-89 455..1	70-89	378-397	NAP		g2494062	740	292	8.00E-79	98	51	hypothetical 30.8 KD protein in GIP-FDRA intergenic region [Escherichia coli]
21102	ENU04896	ANI61C1013 22-49 2:1461..48	22-49	766-789	NAP		g3873546	1129	190	6.00E-75	57	66	(AL033534) acetyl-coa acetyltransferase [Schizosaccharomyces pombe]
21103	ENU04897	ANI61C1117 105-128 2:1..565	105-128	377-401	NAP		g129302	329	132	2.00E-30	43	47	D-amino acid oxidase (DAMOX) (DAO) (DAAO) [Nectria haematococca]
21104	ENU04898	ANI61C4968: 22-48 1341..2630	22-48	769-788	NAP		g135139	1151	348	3.00E-95	57	47	"lysyl-TRNA synthetase, cytoplasmic (lysine--TRNA ligase) (LYSRS) [Saccharomyces cerevisiae]"
21105	ENU04899	ANI61C6717: 27-46 464..1907	27-46	806-829	NAP		g3660282	574	88	9.00E-30	39	54	"Chain A, Aspartate Aminotransferase From Saccharomyces Cerevisiae Cytoplasm []"
21106	ENU04900	ANI61C6446: 22-48 987..1	22-48	706-730	NAP		g1077167	152	73	3.00E-12	23	53	hypothetical protein YGL244w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21107	ENU04901	ANI61C989:1 63-86 ..2472	63-86	774-801	NAP		g1546072	903	55	0.000000	21	9	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21108	ENU04902	ANI61C4177: 22-44 625..1138	22-44	428-447	NAP		g141305	472	172	6.00E-47			YPT1-related protein 2 [Schizosaccharomyces pombe]
21109	ENU04903	ANI61C7502: 27-50 1..4479	27-50	795-822	NAP		g1351721	1692	296	2.00E-85	56	10	putative translational activator C18G6.05C (GCN1 homolog) [Schizosaccharomyces pombe]
21110	ENU04904	ANI61C7090: 23-43 2341..873	23-43	794-813	NAP		g3170246	1708	398	e-128	98	49	(AF043230) trehalose-6-phosphate synthase subunit 1 [Emericella nidulans]
21111	ENU04905	ANI61C4732: 96-115 906..562	96-115	302-321	NAP		g3287841	94	54	0.000000	30	19	glucose oxidase precursor (glucose oxyhydrase) (GOD) (beta-D-glucose:oxygen 1-oxido-reductase) [Talaromyces flavus]
21112	ENU04906	ANI61C5835: 1256..1			NAP		g3283373	230	82	4.00E-15	30	28	(AF067650) sarcosine dehydrogenase [Rattus norvegicus]

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21113	ENU04907	ANI61C6337: 71-90 25..904		800-819	NAP		g3451309	427	140	6.00E-45	40	95	(AL031324) transcription initiation factor IIE beta subunit (TFIIE-beta) [Schizosaccharomyces pombe]
21114	ENU04908	ANI61C6864: 22-48 2562..4261		804-824	NAP		g4063002	937	228	4.00E-59	42	35	(AB021703) fr [Neurospora crassa]
21115	ENU04909	ANI61S4630: 561..258			NAP		g2213547	201	95	1.00E-19	46	33	(Z97052) putative ubiquinone biosynthesis methyltransferase [Schizosaccharomyces pombe]
21116	ENU04910	ANI61C4391: 33-52 5103..4750		411-430	NAP		g1723516	327	144	4.00E-34	59	53	hypothetical 24.4 KD protein C22E12.02 in chromosome I [Schizosaccharomyces pombe]
21117	ENU04911	ANI61C1164: 31-53 2089..1757		247-266	NAP		g101797	469	195	8.00E-50	85	33	quinate 5-dehydrogenase (EC 1.1.1.24) - Emericella nidulans [] [Schizosaccharomyces pombe]
21118	ENU04912	ANI61C8818: 122-142 4250..3805		397-416	NAP		g3170523	546	191	2.00E-48	94	10	(AF053883) coatomer alpha subunit [Emericella nidulans]
21119	ENU04913	ANI61C2376: 30-49 159..1272		786-805	NAP		g2497129	446	111	6.00E-24	38	72	hypothetical 38.2 KD protein in SUB1-ARGR1 intergenic region [Saccharomyces cerevisiae]
21120	ENU04914	ANI61C3368: 22-41 3477..1762		800-827	NAP		g1351682	425	82	3.00E-16	28	48	hypothetical 53.5 KD protein C1F5.07C in chromosome I [Schizosaccharomyces pombe]
21121	ENU04915	ANI61C9569: 24-43 2051..741		804-829	NAP		g1154950	129	47	2.00E-11	27	35	(X94769) choline dehydrogenase [Rattus rattus]
21122	ENU04916	ANI61C8170: 28-47 1..2682		775-794	NAP		g2147662	1979	238	4.00E-62	46	12	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium [Colletotrichum lagenarium]
21123	ENU04917	ANI61C6409: 95-114 678..1		551-577	NAP		g730338	774	289	1.00E-77	67	36	lysophospholipase precursor (phospholipase B) [Penicillium chrysogenum]
21124	ENU04918	ANI61C9456: 46-65 1444..667		734-757	NAP		g1173091	497	171	4.00E-42	49	63	ran GTPASE activating protein 1 (RNA1 protein) [Schizosaccharomyces pombe]
21125	ENU04919	ANI61C9369: 84-106 1..548		500-527	NAP		g1703371	253	93	8.00E-24	43	22	sterol O-acyltransferase 2 (sterol-ester synthase 2) [Saccharomyces cerevisiae]

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21126	ENU04920	ANI61C7770: 828..1	72-91	689-710	NAP		g1352918	517	179	6.00E-45	44	55	CAAX prenyl protease 1 (prenyl protein-specific endoprotease 1) (PPSEP 1) (A-factor converting enzyme) [Saccharomyces cerevisiae]
21127	ENU04921	ANI61C8438: 37-56 1194..1	37-56	745-764	NAP		g4499843	609	91	2.00E-19	38	53	(AJ011965) oxidoreductase [Claviceps purpurea]
21128	ENU04922	ANI61S3872: 181-202 500..1	181-202	432-459	NAP		g992919	185	91	4.00E-18	32	26	alpha-glucoside permease [Saccharomyces cerevisiae]
21129	ENU04923	ANI61C2942: 22-43 602..1304	22-43	643-660	NAP		g984373	687	198	2.00E-69	66	58	(U32375) tartrate dehydrogenase [Agrobacterium vitis]
21130	ENU04924	ANI61C1073: 117-136 8..1.462	117-136	418-439	NAP		g3130036	372	128	2.00E-37	60	35	(AL023534) putative methionine aminopeptidase 1
21131	ENU04925	ANI61C7314: 44-63 1552..1021	44-63	480-507	NAP		g3395587	183	53	1.00E-14	45	52	[Schizosaccharomyces pombe] (AL031179) atp synthase delta chain family; oligomycin sensitivity conferring protein
21132	ENU04926	ANI61C2478: 22-48 5432..5833	22-48	454-478	NAP		g118292	258	109	1.00E-23	38	100	[Schizosaccharomyces pombe] 4-carboxymuconolactone decarboxylase (CMD) [Acinetobacter calcoaceticus]
21133	ENU04927	ANI61C4431: 27-46 165..1091	27-46	807-828	NAP		g2132120	139	175	5.00E-43	27	19	hypothetical protein YOR296w - yeast (Saccharomyces cerevisiae)
21134	ENU04928	ANI61C6376: 22-47 3864..2374	22-47	805-828	NAP		g3548818	348	134	1.00E-30	37	64	[Saccharomyces cerevisiae] (AC005313) unknown protein [Arabidopsis thaliana]
21135	ENU04929	ANI61C8026: 26-45 1..1798	26-45	613-632	NAP		g2130442	1140	129	5.00E-34	33	29	hypothetical protein SPAC8A4.01c - fission yeast (Schizosaccharomyces pombe) (fragment)
21136	ENU04930	ANI61C5280: 40-59 1840..2502	40-59	605-624	NAP		g2120955	387	175	2.00E-43	46	67	[Schizosaccharomyces pombe] ORF5 - Alcaligenes eutrophus [Ralstonia eutropha]
21137	ENU04931	ANI61C7663: 24-43 1639..1	24-43	704-731	NAP		g2493479	860	196	2.00E-49	47	21	"dynactin, 150 KD isoform (150 KD dynein-associated polypeptide) (DP-150) (DAP-150) (P150-glued) [Neurospora crassa]"
21138	ENU04932	ANI61S996:1. 28-48 .300	28-48	249-273	NAP		g2494589	129	58	0.000000	37	22	putative folypolyglutamate synthase (folypoly-gamma-glutamate synthetase) (FPGS) [Saccharomyces cerevisiae]

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21139	ENU04933	ANI61C1866: 1576..1092	42-61	436-463	NAP		g2997731	650	222	1.00E-57	68	48	(AF054512) endoglucanase V [Aspergillus aculeatus]
21140	ENU04934	ANI61C7308: 1..637	113-132	524-543	NAP		g2117031	538	190	7.00E-51	62	37	(X94220) rhamnogalacturonase [Aspergillus niger]
21141	ENU04935	ANI61C6373: 22-49	680-702		NAP		g1546072	828	75	7.00E-13			(U68040) polyketide synthase [Cochliobolus heterostrophus]
21142	ENU04936	ANI61C1004: 22-47	809-829		NAP		g2465160	1351	92	5.00E-38	41	24	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
21143	ENU04937	ANI61C6032: 152-171	533-558		NAP		g1723241	167	72	4.00E-12	29	29	hypothetical 60.7 KD protein C26A3.15C in chromosome I [Schizosaccharomyces pombe]
21144	ENU04938	ANI61C3309: 27-46	768-787		NAP		g2440206	1169	155	7.00E-59	56	33	(Z99532) putative integral membrane protein [Schizosaccharomyces pombe]
21145	ENU04939	ANI61C9915: 58-81	805-825		NAP		g1169440	1451	321	e-150	97	6	"dynein heavy chain, cytosolic (DYHC) [Emicella nidulans]"
21146	ENU04940	ANI61C4247: 23-45	752-778		NAP		g2342601	1009	261	6.00E-69	47	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21147	ENU04941	ANI61C3772: 72-91	253-272		NAP		g549657	284	98	2.00E-20	54	24	hypothetical 49.0 KD protein UFD4-CAP1 intergenic region [Saccharomyces cerevisiae]
21148	ENU04942	ANI61C7930: 44-63	611-632		NAP		g3334134	203	48	0.00006	30	36	chromatin assembly factor 1 P90 subunit (CAF-1 90 KD subunit) (RAP1 localization factor 2) [Saccharomyces cerevisiae]
21149	ENU04943	ANI61C9002: 57-76	447-466		NAP		g3687473	191	52	2.00E-10	44	99	(AL031798) WD repeat protein [Schizosaccharomyces pombe]
21150	ENU04944	ANI61S3829: 1069..579			NAP		g758803	90	46	0.0001	24	33	(U23828) penitrophin-95 precursor [Lucilia cuprina]
21151	ENU04945	ANI61C4391: 22-40	712-731		NAP		g3114719	949	72	4.00E-12	38	13	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
21152	ENU04946	ANI61C1720: 116-138	721-748		NAP		g2791647	409	82	9.00E-23	29	48	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]
21153	ENU04947	ANI61C1069: 22-48	383-402		NAP		g2132249	348	123	6.00E-28	56	72	hypothetical protein YPL252c - yeast (Saccharomyces cerevisiae)
21154	ENU04948	ANI61S3700: 113-132	408-428		NAP		g2462832	700	184	6.00E-69	92	26	[Saccharomyces cerevisiae] (AF000657) similar to Bacillus CotA [Arabidopsis thaliana]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21155	ENU04949	ANI61C8568: 22-45 576..1	22-45	453-475	NAP		g4176522	291	136	2.00E-31	30	47	(AL035263) hypothetical protein [Schizosaccharomyces pombe]
21156	ENU04950	ANI61C8225: 39-62 1446..182	39-62	806-829	NAP		g3264834	810	109	1.00E-45	46	77	(AF072541) xyloitol dehydrogenase; XDH [Galactocandida mastotermitis]
21157	ENU04951	ANI61C4401: 22-43 2831..3759	22-43	663-690	NAP		g1351102	282	124	2.00E-34	44	53	putative agmatinase precursor (agmatine ureohydrolase) (AUH) [Schizosaccharomyces pombe]
21158	ENU04952	ANI61S4151: 31-51 6..468	31-51	245-271	NAP		g4514357	215	82	1.00E-17	35	100	(AB013376) unknown [Bacillus halodurans]
21159	ENU04953	ANI61C1075 9:730..1	197-216	568-587	NAP		g730745	327	132	2.00E-30	38	17	osmolarity two-component system protein SLN1 [Saccharomyces cerevisiae]
21160	ENU04954	ANI61C279:1 ..547	111-129	501-526	NAP		g3319315	271	104	5.00E-22	49	15	(AF074951) cellobiose dehydrogenase [Thielavia heterothallica]
21161	ENU04955	ANI61C1025: 23-48 556..1	23-48	428-447	NAP		g1723260	396	173	8.00E-43	52	27	hypothetical GTP-binding protein C3F10.16C in chromosome I [Schizosaccharomyces pombe]
21162	ENU04956	ANI61C9690: 27-54 2664..4755	27-54	688-715	NAP		g1166378	569	111	8.00E-24	32	25	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]" (AF095741) unknown [Rattus norvegicus]
21163	ENU04957	ANI61C1050 9:1129..493	32-51	472-491	NAP		g3747107	96	67	1.00E-10	35	38	alpha-glucuronidase precursor (alpha-glucosiduronase) [Aspergillus tubingensis]
21164	ENU04958	ANI61C7276: 6137..5602			NAP		g3912991	237	110	8.00E-24	39	19	coat assembly complex beta adaptin subunit [Rattus norvegicus]
21165	ENU04959	ANI61C5836: 56-77 725..1	56-77	597-624	NAP		g4557469	620	185	4.00E-66			hypothetical 62.3 KD protein in PTP3-IL V1 intergenic region [Saccharomyces cerevisiae]
21166	ENU04960	ANI61C5110: 22-43 1121..1	22-43	712-731	NAP		g731485	811	159	5.00E-73	51	48	(D64006) Ap-4-A phosphorylase II [Synechocystis sp.]
21167	ENU04961	ANI61C5433: 687..1068			NAP		g1001338	87	65	2.00E-12	27	50	hypothetical 36.4 KD protein in POP2-HOL1 intergenic region [Saccharomyces cerevisiae]
21168	ENU04962	ANI61C3958: 79-98 501..1	79-98	370-389	NAP		g1730686	96	39	0.014	25	45	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21169	ENU04963	ANI61C84:10 39..1	22-41	712-731	NAP		g2132651	712	249	3.00E-65	42	48	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus]
21170	ENU04964	ANI61S1096: 38-57 1..683	38-57	445-464	NAP		g2673951	655	210	3.00E-58	66	16	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21171	ENU04965	ANI61C5094: 107-126 1..394	107-126	353-372	NAP		g584806	431	180	4.00E-45	62	23	"ATP synthase alpha chain, mitochondrial precursor [Neurospora crassa]"
21172	ENU04966	ANI61C3659: 48-68 1..416	48-68	291-310	NAP		g849206	519	213	4.00E-55	74	26	(U28373) Etf1p: Elongation factor 2 (Swiss Prot. accession number P32324). Note that the entire gene is not included in this cosmid.
21173	ENU04967	ANI61C2382: 49-76 1..954	49-76	614-641	NAP		g1351604	150	52	2.00E-10	26	66	[Saccharomyces cerevisiae] hypothetical 40.0 KD protein C4G8.14C in chromosome I []
21174	ENU04968	ANI61C1180: 22-47 845..2067	22-47	684-709	NAP		g2408064	161	94	9.00E-19	29	23	(Z99165) hypothetical protein [Schizosaccharomyces pombe]
21175	ENU04969	ANI61C2243: 22-41 1424..1	22-41	728-749	NAP		g2408021	352	120	1.00E-26	37	41	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
21176	ENU04970	ANI61C2141: 22-43 438..1496	22-43	658-677	NAP		g4249560	1044	268	1.00E-90	72	51	[Schizosaccharomyces pombe] (AB003109) beta-glucosidase [Humicola grisea var. thermoidaea]
21177	ENU04971	ANI61C9921: 24-51 1..600	24-51	539-565	NAP		g549643	191	79	3.00E-14	33	18	hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region [Saccharomyces cerevisiae]
21178	ENU04972	ANI61C2170: 23-42 195..1309	23-42	714-740	NAP		g1709064	782	314	5.00E-85	57	75	MNN9 protein [Candida albicans]
21179	ENU04973	ANI61C7073: 68-88 5985..5584	68-88	360-381	NAP		g454438	317	111	2.00E-30	60	10	(L28110) LON gene of S. cerevisiae is downstream of the HAP 3 gene; Putative ATP-binding motif bp 1960 to bp 1986.; Putative catalytic site serine of serine proteases from bp 3109 to bp 3111 [Saccharomyces cerevisiae]
21180	ENU04974	ANI61C1121: 52-71 7..652..1	52-71	601-628	NAP		g731024	387	138	3.00E-32	40	49	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) [Saccharomyces cerevisiae]"
21181	ENU04975	ANI61C2031: 69-96 502..1	69-96	356-383	NAP		g2687850	120	77	9.00E-14	24	25	(Y15839) fatty acid transporter protein [Cochliobolus heterostrophus]
21182	ENU04976	ANI61S4631: 1..517			NAP		g4589850	142	62	0.000000	32	26	(AB025967) choriogenin Hminor [Oryzias latipes]
21183	ENU04977	ANI61C7290: 916..186			NAP		g2072023	420	138	3.00E-32	53	100	(U93506) symbiosis-related protein [Laccaria bicolor]
21184	ENU04978	ANI61C6657: 103-123 414..1	103-123	421-440	NAP		g1073534	185	89	2.00E-17	39	43	iucB protein - Escherichia coli [Escherichia coli]

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21185	ENU04979	ANI61C1051 2:5237..3644	28-55	807-829	NAP		g1085432	147	38	0.07			mucin (clone PGM-2A) - pig [Sus scrofa]
21186	ENU04980	ANI61C7282: 31-58 554..1	31-58	465-489	NAP		g4262216	336	138	2.00E-32	35	64	(AC006161) putative DNA binding protein [Arabidopsis thaliana]
21187	ENU04981	ANI61S1306: 1..655			NAP		g4218005	179	49	0.00003	21	31	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
21188	ENU04982	ANI61C1082 116-135 6:1..707	116-135	662-686	NAP		g4538673	116	70	1.00E-11	26	57	"(AL049474) putative lipid metabolism protein, sphingomyelinase family similarity [Schizosaccharomyces pombe]"
21189	ENU04983	ANI61C1252: 36-55 729..1091	36-55	418-436	NAP		g773414	434	183	8.00E-46	92	66	(U23751) beta galactosidase [Cloning vector pBBR1MCS-5]
21190	ENU04984	ANI61C439:9 319..9705			NAP		g2330831	228	108	3.00E-23	26	53	(Z98530) myo-inositol transporter [Schizosaccharomyces pombe]
21191	ENU04985	ANI61C8782: 29-50 942..1	29-50	720-739	NAP		g1351343	1615	547	e-155	98	26	positive regulator of purine utilisation [Emicella nidulans]
21192	ENU04986	ANI61C295:6 157-184 925..7990	157-184	797-824	NAP		g2648302	278	103	2.00E-32	44	86	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus]"
21193	ENU04987	ANI61C6797: 62-81 1073..1	62-81	715-735	NAP		g2146821	548	91	1.00E-17	36	39	alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae) []
21194	ENU04988	ANI61C346:8 139-166 06..369	139-166	433-452	NAP		g3136049	132	63	0.000000	36	38	(AL023592) putative phosphatidylinositol- glycan-class c protein [Schizosaccharomyces pombe]
21195	ENU04989	ANI61C7116: 2155..1			NAP		g2599548	1110	223	1.00E-57	40	34	(AF029346) chloride channel protein 3 [Oryctolagus cuniculus]
21196	ENU04990	ANI61C4598: 22-42 441..1	22-42	437-461	NAP		g1651554	745	294	2.00E-79	98	65	(D90748) Spermidine/putrescine transport system permease protein PotB. [Escherichia coli]
21197	ENU04991	ANI61C5425: 96-115 724..1	96-115	597-616	NAP		g2492660	334	129	2.00E-29	36	11	aflatoxin biosynthesis polyketide synthase (PKS) [Aspergillus parasiticus]
21198	ENU04992	ANI61C8486: 22-42 2325..3743	22-42	807-829	NAP		g1176339	671	209	2.00E-53	43	60	hypothetical 50.8 KD protein in MIR1-STE18 intergenic region [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21199	ENU04993	ANI61C948:1 ..580			NAP		g2190551	170	108	4.00E-23	28	38	"(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb Z71181). ESTs gb H36844.gb AA394956 come from this gene. [Arabidopsis thaliana]" (Z98598) hypothetical protein [Schizosaccharomyces pombe]" "glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) [Saccharomyces cerevisiae var. diastaticus]" (AB003109) beta-glucosidase [Humicola grisea var. thermoidea] (Z98981) hypothetical protein [Schizosaccharomyces pombe]" synapsin I splice form a - human []
21200	ENU04994	ANI61C4231: 22-41 1926..2480		414-435	NAP		g3859773	141	73	1.00E-12	32	20	"ankyrin 1, erythrocyte form 3 - human []"
21201	ENU04995	ANI61C6504: 65-84 1220..1		729-747	NAP		g728850	110	35	0.61			(Z98977) hypothetical protein [Schizosaccharomyces pombe]" (Z93388) predicted using GeneFinder; cDNA EST EMBL:D70912 comes from this gene; cDNA EST EMBL:D73452 comes from this gene; cDNA EST EMBL:D71574 comes from this gene; cDNA EST EMBL:D74229 comes from this gene; cDNA EST EMBL:D727... [] hypothetical 68.3 KD protein in PDX1-SNG1 intergenic region [Saccharomyces cerevisiae] (AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea] putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emericella nidulans]
21202	ENU04996	ANI61C1933: 1..571			NAP		g4249560	560	225	2.00E-58	66	34	
21203	ENU04997	ANI61C6870: 22-49 1120..1		806-829	NAP		g2388995	360	148	4.00E-35	36	56	
21204	ENU04998	ANI61S913:1. .754			NAP		g107749	124	71	1.00E-11	27	34	
21205	ENU04999	ANI61C2450: 74-93 1269..1		712-731	NAP		g1360744	340	84	3.00E-25	34	14	
21206	ENU05000	ANI61S719:4 23-41 91..1		451-470	NAP		g2656001	211	92	2.00E-18	39	20	
21207	ENU05001	ANI61C1120 22-49 5:9128..8237		802-829	NAP		g3879734	269	79	2.00E-18	38	93	
21208	ENU05002	ANI61C7395: 22-47 906..2125		744-764	NAP		g1723736	720	187	7.00E-47	43	43	
21209	ENU05003	ANI61C3250: 60-79 1100..1		726-743	NAP		g2625138	574	233	1.00E-60	39	17	
21210	ENU05004	ANI61C5872: 22-42 1..969		804-829	NAP		g2492658	1336	314	7.00E-85	99	12	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21211	ENU05005	ANI61C9398: 666..1	102-124	523-547	NAP		g2851654	282	71	4.00E-22	43	31	2-dehydro-3-deoxyphosphogalactonate aldolase (6-phospho-2-dehydro-3-deoxygalactonate aldolase) (2-oxo-3-deoxygalactonate 6-phosphate aldolase) / galactonate dehydratase [Escherichia coli]
21212	ENU05006	ANI61C1139 22-47 3:2741..4047	795-814		NAP		g2498757	378	96	3.00E-19	31	52	peroxisomal membrane protein PAS2 (peroxin-3) [Pichia pastoris]
21213	ENU05007	ANI61C5990: 1689..1400	102-124	250-267	NAP		g2499716	206	94	3.00E-19	45	22	"exopolysaccharonase precursor (exoPG) (galacturan 1,4-alpha-galacturonidase) (poly(1,4-alpha-D-galacturonide)galacturonohydrolase) [Aspergillus tubingensis]"
21214	ENU05008	ANI61C5102: 1..502	139-163	426-445	NAP		g3116147	179	67	2.00E-14	34	27	(AL023290) amino acid permease [Schizosaccharomyces pombe]
21215	ENU05009	ANI61C1061 26-46 3:945..1	722-749		NAP		g730745	63	48	0.00006	27	16	osmolality two-component system protein SLN1 [Saccharomyces cerevisiae]
21216	ENU05010	ANI61C5586: 1296..2033			NAP		g101797	1141	455	e-127	91	74	quinase 5-dehydrogenase (EC 1.1.1.24) - Emericella nidulans []
21217	ENU05011	ANI61C1129 2:2645..2267	164-183	336-358	NAP		g417321	189	83	8.00E-16	46	33	methylentetrahydrofolate dehydrogenase (NAD+)
21218	ENU05012	ANI61C1543: 928..625			NAP		g1870219	78	45	0.0002	30	99	[Saccharomyces cerevisiae] (AC000133) ORF [Emericella nidulans]
21219	ENU05013	ANI61C8821: 24-50 1284..376	791-818		NAP		g2498849	263	123	1.00E-27	33	86	replication factor-A protein 2 (single-stranded DNA-binding protein P30 subunit) [Schizosaccharomyces pombe]
21220	ENU05014	ANI61C7941: 118-137 928..1	719-736		NAP		g2257514	387	157	6.00E-40	38	51	(AB004535) ATP-dependent RNA helicase MSS116 precursor [Schizosaccharomyces pombe]
21221	ENU05015	ANI61C5148: 110-129 1..550	454-473		NAP		g2493491	44	46	0.0002	25	92	hypothetical protein MJ0304 [Methanococcus jannaschii]
21222	ENU05016	ANI61C7063: 3083..1			NAP		g2342601	1262	77	1.00E-13	27	4	(X89442) peptide synthetase [Metarhizium anisopliae]

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21223	ENU05017	ANI61C2576: 3088..4293	24-44	786-805	NAP		g1711573	610	156	6.00E-46	48	76	"probable succinyl-CoA ligase (GDP-forming), alpha-chain precursor (succinyl-CoA synthetase, alpha chain) (SCS-alpha) []"
21224	ENU05018	ANI61S335:5 39..1	63-90	486-509	NAP		g3860271	877	353	7.00E-97	97	20	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
21225	ENU05019	ANI61C1118 22-45 5:657..1	22-45	525-548	NAP		g585169	422	129	4.00E-45	49	27	UDP-glucose 4-epimerase (galactowaldenase) / aldose 1-epimerase (mutarotase) [Saccharomyces cerevisiae]
21226	ENU05020	ANI61C9007: 1.605	102-125	558-584	NAP		g730017	282	83	5.00E-20	50	26	cystathionine gamma-synthase (O-succinylhomoserine (thiol)-lyase) []
21227	ENU05021	ANI61C1183: 68-87 2222..1	68-87	717-736	NAP		g1723281	1051	122	3.00E-27	33	29	probable ATP-dependent DNA helicase C4H3.05 [Schizosaccharomyces pombe]
21228	ENU05022	ANI61C8411: 30-57 754..2343	30-57	779-799	NAP		g1175914	811	248	4.00E-65	42	34	hypothetical 95.4 KD protein in SEC4-MSH4 intergenic region [Saccharomyces cerevisiae]
21229	ENU05023	ANI61C1834: 1947..2749	104-131	756-782	NAP		g2353165	186	46	0.0002	34	97	(AF015561) RO10 [Neurospora crassa]
21230	ENU05024	ANI61S578:6 24..1			NAP		g1705828	157	69	9.00E-12	33	18	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emericella nidulans]
21231	ENU05025	ANI61C1040 41-60 4:1486..565	41-60	795-822	NAP		g2791526	118	41	0.000000	32	63	(AL021246) echA14 [Mycobacterium tuberculosis]
21232	ENU05026	ANI61C1120 22-48 1:1734..2597	22-48	781-802	NAP		g4033481	233	69	2.00E-20	29	53	putative tartrate transporter [Agrobacterium vitis]
21233	ENU05027	ANI61C3812: 22-49 545..1	22-49	503-524	NAP		g3522935	63	57	0.000000	25	59	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]
21234	ENU05028	ANI61C2852: 84-103 1883..1	84-103	714-736	NAP		g2833193	594	85	6.00E-16	28	34	HOS3 protein [Saccharomyces cerevisiae]
21235	ENU05029	ANI61C5843: 61-81 1.941	61-81	806-829	NAP		g2267601	306	120	1.00E-26	33	47	(AF009417) cytochrome P450 [Myrothecium roridum]
21236	ENU05030	ANI61C626:1 233..1	80-99	718-735	NAP		g4127832	601	144	6.00E-47	41	51	(Y17243) cytochrome P450 [Gibberella fujikuroi]
21237	ENU05031	ANI61C8459: 33-53 9479..5897	33-53	805-828	NAP		g1351618	585	67	1.00E-10			hypothetical 118.6 KD protein C29E6.03C in chromosome I [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21238	ENU05032	ANI61C1121: 22-42 4754..3724	22-42	802-829	NAP		g124871	489	151	6.00E-46	40	87	Inorganic pyrophosphatase (pyrophosphate phospho-hydrolase) (PPASE) [Kluyveromyces lactis] (AL031261) sulfate permease [Schizosaccharomyces pombe] (AC000133) ORF [Emeticella nidulans] (AL034583) putative nucleotide binding protein [Schizosaccharomyces pombe]
21239	ENU05033	ANI61C4611: 28-47 1755..1	28-47	728-747	NAP		g3417410	1275	252	2.00E-66	50	31	
21240	ENU05034	ANI61C1027 22-48 8:2501..4162	22-48	782-808	NAP		g1870209	2360	476	e-134	85	51	
21241	ENU05035	ANI61C1047 33-52 1:862..1278	33-52	413-432	NAP		g4056552	379	114	2.00E-36	59	43	
21242	ENU05036	ANI61C8687: 43-62 2011..1	43-62	626-645	NAP		g3912991	2086	419	e-116	67	33	alpha-glucuronidase precursor (alpha-glucosiduronase) [Aspergillus tubingensis] (AL022172) protein kinase [Schizosaccharomyces pombe] (S59774) RNA polymerase subunit [Saccharomyces cerevisiae] (ATP-dependent protease LA 2 [Myxococcus xanthus] hypothetical 27.5 KD protein in SPO1-SIS1 intergenic region [Saccharomyces cerevisiae] (Z79700) hypothetical protein Rv0976c [Mycobacterium tuberculosis] (AL022600) putative mannose-1-phosphate gaunyl transferase [Schizosaccharomyces pombe] peroxisomal assembly protein 5 - yeast (Pichia pastoris) [] extensin-like protein - maize [Zea mays] hypothetical 87.5 KD protein in ACS1-GCV3 intergenic region [Saccharomyces cerevisiae] "(U95181) 2,5 dihydroxyphenylacetate oxidase [Caenorhabditis elegans]" hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []
21243	ENU05037	ANI61C7437: 102-126 1159..637	102-126	454-473	NAP		g2980827	114	80	8.00E-15	41	32	
21244	ENU05038	ANI61C6321: 62-80 3230..2423	62-80	747-766	NAP		g1680605	442	100	1.00E-42	52	99	
21245	ENU05039	ANI61C2198: 141-162 983..1	141-162	718-745	NAP		g547861	611	246	2.00E-64	48	32	
21246	ENU05040	ANI61C4414: 22-46 259..1253	22-46	801-828	NAP		g1730705	400	90	6.00E-38	42	92	
21247	ENU05041	ANI61C6703: 51-73 3118..4359	51-73	805-829	NAP		g3261634	474	171	7.00E-42	42	40	
21248	ENU05042	ANI61C1053 22-42 3:1539..2879	22-42	616-634	NAP		g3080527	872	206	2.00E-52	43	65	
21249	ENU05043	ANI61S1767: 39-58 1..595	39-58	457-478	NAP		g539079	698	285	2.00E-76	70	16	
21250	ENU05044	ANI61S3339: 1..831 7:1..972			NAP		g1076802	116	37	0.000002	30	21	
21251	ENU05045	ANI61C1089 66-85	66-85	711-731	NAP		g731288	185	64	0.000000	25	35	
21252	ENU05046	ANI61C9718: 25-48 665..328	25-48	292-316	NAP		g4100190	153	87	5.00E-17	40	26	
21253	ENU05047	ANI61S371:1..490			NAP		g539218	96	43	0.002	16	30	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21254	ENU05048	ANI61C8803: 1..1327	31-50	806-829	NAP		g4502091	410	160	1.00E-38	33	7	"ankyrin 2, neuronal [Homo sapiens]"
21255	ENU05049	ANI61C8498: 22-47		808-829	NAP		g4176530	2328	277	3.00E-86	57	22	(AL035263) putative condensin subunit [Schizosaccharomyces pombe]
21256	ENU05050	5241..1481 ANI61C1137: 431..1282			NAP		g4468948	1258	490	e-138	92	49	(X00790) cytochrome oxidase 1 [Emicella nidulans]
21257	ENU05051	ANI61C4514: 643..349			NAP		g729967	150	75	1.00E-13	36	39	homocitrate dehydratase [Saccharomyces cerevisiae]
21258	ENU05052	ANI61C5723: 23-50		665-692	NAP		g3318897	453	221	4.00E-57	41	42	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ["
21259	ENU05053	ANI61C7280: 22-46		802-821	NAP		g3914344	344	128	6.00E-29			3-phytase precursor [Bacillus sp.]
21260	ENU05054	ANI61C1544: 112-132		711-733	NAP		g2828341	165	98	1.00E-19	30	18	(AB004305) mBLVR [Mus musculus]
21261	ENU05055	ANI61C8211: 69-87		747-766	NAP		g1077413	809	260	2.00E-87	66	99	hypothetical protein YLR186w - yeast (Saccharomyces cerevisiae)
21262	ENU05056	ANI61S9:1..5			NAP		g2465558	162	79	2.00E-14	37	74	[Saccharomyces cerevisiae] (AF011545) YedB [Bacillus subtilis]
21263	ENU05057	ANI61C9836: 22-45		804-828	NAP		g1351714	749	154	8.00E-37	34	55	putative transporter C11D3.18C [Schizosaccharomyces pombe]
21264	ENU05058	3361..1728 ANI61C8454: 48-68		766-785	NAP		g2132208	739	210	1.00E-53	41	31	hypothetical protein YPL150w - yeast (Saccharomyces cerevisiae)
21265	ENU05059	ANI61S13:69		157-174	NAP		g2804470	120	81	7.00E-15	28	16	[Saccharomyces cerevisiae] (AF043701) contains similarity to ankyrin repeats and protein kinases [Caenorhabditis elegans]
21266	ENU05060	ANI61C5161: 34-53		627-647	NAP		g3668157	513	82	5.00E-15			(AL031764) putative exocyst complex component [Schizosaccharomyces pombe]
21267	ENU05061	ANI61C229:1		33-59	NAP		g419963	226	73	3.00E-12	44	83	snRNP protein B - fruit fly (Drosophila melanogaster) [Drosophila melanogaster]
21268	ENU05062	ANI61C728:2			NAP		g3025214	231	80	1.00E-17	36	36	hypothetical 65.9 KD protein in SSP120-HAP1 intergenic region [Saccharomyces cerevisiae]
21269	ENU05063	ANI61C9372: 115-134		388-407	NAP		g2146853	325	90	1.00E-17	45	32	alpha-galactosidase (EC 3.2.1.22) III precursor - fungus (Trichoderma reesei) [Hypocrea jecorina]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21270	ENU05064	ANI61C6066: 299..757	192-211	455-479	NAP		g83697	633	254	4.00E-67	83	100	catabolic 3-dehydrogenase - Emericella nidulans [Emericella nidulans]
21271	ENU05065	ANI61C1113 8:1..1119	64-82	786-804	NAP		g2507475	365	93	2.00E-18	36	9	Paired amphipathic helix protein [Saccharomyces cerevisiae]
21272	ENU05066	ANI61C3518: 621..1	210-237	571-598	NAP		g538067	157	44	0.0008	29	14	(M77661) putative polypeptide [Magnaporthe grisea]
21273	ENU05067	ANI61C9741: 3618..2602	55-74	794-813	NAP		g2970627	725	289	2.00E-77	50	86	(AF051914) C-4 methyl sterol oxidase [Candida albicans]
21274	ENU05068	ANI61C9993: 1..720	107-130	673-699	NAP		g1723552	325	130	1.00E-29	44	62	putative mitochondrial carrier protein C12B10.09 [Schizosaccharomyces pombe]
21275	ENU05069	ANI61C4742: 73-92	621-638		NAP		g3183171	784	318	2.00E-86	61	25	"probable alanyl-tRNA synthetase, cytoplasmic (alanine--tRNA ligase) (ALARS) [Schizosaccharomyces pombe]"
21276	ENU05070	ANI61S4634: 227..538			NAP		g731584	114	31	6	35	60	hypothetical 17.1 KD protein in PUR5 3'region [Saccharomyces cerevisiae]
21277	ENU05071	ANI61C6461: 1..799	101-120	679-696	NAP		g2626826	170	137	2.00E-32	31	17	(D83967) YfK [Bacillus subtilis]
21278	ENU05072	ANI61C720:1 593..700	47-66	800-824	NAP		g4505823	640	267	8.00E-71	48	94	pirin [Homo sapiens]
21279	ENU05073	ANI61C276:1 870..3049	42-67	765-788	NAP		g2224775	595	226	2.00E-58	43	71	(Z97025) pyruvate carboxylase [Bacillus subtilis]
21280	ENU05074	ANI61C9649: 1..1530	26-45	650-677	NAP		g1546072	555	167	8.00E-41	37	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21281	ENU05075	ANI61S1135: 626..1			NAP		g4008576	172	53	0.000002	34	37	"(AL034491) similar to yeast transcription initiation factor iif, alpha subunit [Schizosaccharomyces pombe]"
21282	ENU05076	ANI61S1439: 58..757			NAP		g3329623	156	45	0.0007	17	69	(AF078790) No definition line found [Caenorhabditis elegans]
21283	ENU05077	ANI61C1060 8:1239..1	94-116	798-817	NAP		g1351343	1530	493	e-149	96	26	positive regulator of purine utilisation [Emericella nidulans]
21284	ENU05078	ANI61C8743: 3864..4464			NAP		g3646453	331	138	3.00E-32	38	100	(AL031603) putative succinate dehydrogenase cytochrome b subunit precursor [Schizosaccharomyces pombe]
21285	ENU05079	ANI61C7969: 486..170			NAP		g208131	126	64	5.00E-10	42	98	(M77169) beta-galactosidase alpha-peptide [Shuttle vector pJIR1457]

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21286	ENU05080	ANI61C9657: 3857..2196	44-63	800-820	NAP		g400269	1494	377	e-104	64	52	Methylmalonate-semialdehyde dehydrogenase precursor (acylating) (MMSDH) [Rattus norvegicus]
21287	ENU05081	ANI61C6968: 28-48	808-829		NAP		g1399263	1443	469	e-131	96	60	(U28383) cystathionine beta-lyase [Emicella nidulans]
21288	ENU05082	ANI61C1441: 121-141	664-683		NAP		g462168	617	248	3.00E-65	46	9	translational activator GCN1 [Saccharomyces cerevisiae]
21289	ENU05083	ANI61C249:5 801..1	93-112	317-344	NAP		g4757128	78	55	0.000000			(AJ238717) ZRP protein [Rattus norvegicus]
21290	ENU05084	ANI61S3273: 23..158			NAP		g283032	92	49	0.00003	27	57	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
21291	ENU05085	ANI61C6213: 22-41	805-829		NAP		g3283220	1109	200	1.00E-71	56	51	(AF061241) splicing factor hPRP17 [Homo sapiens]
21292	ENU05086	ANI61C3458: 102-121	666-685		NAP		g2673947	594	226	2.00E-58	52	18	(U62931) multidrug resistance protein 1 [Aspergillus flavus]
21293	ENU05087	ANI61S1524: 803..1			NAP		g168082	69	48	0.00004	35	17	(M59935) negative-acting regulatory protein [Emicella nidulans]
21294	ENU05088	ANI61C5043: 38-57	750-769		NAP		g3006156	905	175	6.00E-70	52	52	(AL022299) putative serine palmitoyltransferase [Schizosaccharomyces pombe]
21295	ENU05089	ANI61C1208: 8761..10108			NAP		g4867801	1922	49	0.00004			(AJ132442) phenylacetate 2-hydroxylase [Emicella nidulans]
21296	ENU05090	ANI61C2406: 118-137	638-658		NAP		g584839	599	239	1.00E-62			beta-glucuronidase (GUS) (beta-D-glucuronoside glucuronosohydrolase) [Escherichia coli]
21297	ENU05091	ANI61C1087 6:481..1			NAP		g2224699	97	67	9.00E-11	27	18	(AB002377) KIAA0379 [Homo sapiens]
21298	ENU05092	ANI61C721:5 65-87	468-492		NAP		g548669	313	151	3.00E-36	44	17	DNA repair protein RAD8 [Schizosaccharomyces pombe]
21299	ENU05093	ANI61C1097 93..1	719-746		NAP		g4481954	1614	363	e-100	74	31	(AL035637) putative protease subunit; chaperonin [Schizosaccharomyces pombe]
21300	ENU05094	ANI61C5311: 22-45	463-482		NAP		g543325	188	92	3.00E-20	33	56	small nuclear ribonucleoprotein U1A - mouse [Mus musculus]
21301	ENU05095	ANI61S3796: 3161..3692			NAP		g4490609	361	109	6.00E-28	53	22	(AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]
21302	ENU05096	ANI61S2956: 35-53	287-306		NAP		g2956768	109	45	0.00001	29	33	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21303	ENU05097	ANI61C9512: 1490..2267	23-50	736-757	NAP		g3183392	386	92	2.00E-36	45	99	hypothetical 24.1 KD protein C17A5.08 in chromosome I precursor [Schizosaccharomyces pombe]
21304	ENU05098	ANI61C6112: 26-45	722-749		NAP		g2633022	585	225	4.00E-58	43	31	(Z99107) yetA [Bacillus subtilis]
21305	ENU05099	ANI61C3343: 22-49	420-439		NAP		g1076211	101	33	1.6			hypothetical protein VSP-3 - Chlamydomonas reinhardtii [Chlamydomonas reinhardtii]
21306	ENU05100	ANI61C1093 22-44	808-829		NAP		g2982194	494	163	1.00E-39	38	5	(AF007865) bacitracin synthetase 1; BacA [Bacillus licheniformis]
21307	ENU05101	ANI61C9439: 102-123	414-438		NAP		g2967835	312	70	1.00E-27	55	34	(AF052061) polygalacturonase [Ophiostoma novo-ulmi]
21308	ENU05102	ANI61C1118 104-130	396-422		NAP		g558311	294	132	9.00E-31	52	34	(L35487) mannanase [Aspergillus aculeatus]
21309	ENU05103	ANI61C7701: 59-76	773-792		NAP		g2492756	1193	372	e-102	95	92	putative sterigmatocystin biosynthesis ketoreductase STCE [Emericella nidulans]
21310	ENU05104	ANI61C2235: 45-64	799-826		NAP		g3075511	823	58	0.000000	27	49	(AF059534) severin kinase [Dictyostelium discoideum]
21311	ENU05105	ANI61C5581: 1..502			NAP		g91209	123	57	0.000000	29	67	proline-rich protein MP2 - mouse (fragment) []
21312	ENU05106	ANI61C9514: 118-138	525-552		NAP		g1076211	60	43	0.001	27	34	hypothetical protein VSP-3 - Chlamydomonas reinhardtii [Chlamydomonas reinhardtii]
21313	ENU05107	ANI61C4192: 42-61	722-749		NAP		g2398720	1362	271	4.00E-72	51	27	(Y07919) beta-prime-adaptin protein [Mus musculus]
21314	ENU05108	ANI61C2192: 40-58	431-450		NAP		g1351227	385	148	2.00E-35	43	57	transcription elongation factor S-II (TFIIS) [Schizosaccharomyces pombe]
21315	ENU05109	ANI61C1130 48-71	782-806		NAP		g2440180	473	32	6.9			(Z99531) ubiquitin system protein [Schizosaccharomyces pombe]
21316	ENU05110	ANI61C7737: 60-80	484-507		NAP		g3121766	329	128	8.00E-30	72	68	ARP2/3 complex 20 KD subunit (P20-ARC) [Homo sapiens]
21317	ENU05111	ANI61S2227: 1..755			NAP		g4063042	154	39	0.033	30	11	(AF068065) GP900; mucin-like glycoprotein [Cryptosporidium parvum]
21318	ENU05112	ANI61C123:9 24-43	794-813		NAP		g1351703	856	284	7.00E-76	56	58	hypothetical 49.1 KD protein C11D3.06 in chromosome I [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21319	ENU05113	ANI61C5332: 27-46 1091..2649	27-46	802-829	NAP		g4033486	299	75	7.00E-13	91	37	putative tartrate transporter [Agrobacterium vitis]
21320	ENU05114	ANI61C4918: 22-44 1107..1	22-44	724-749	NAP		g1352677	1333	369	e-101	91	37	serine/threonine protein phosphatase 2B catalytic subunit (calmodulin- dependent calcineurin A subunit) [Emicella nidulans]
21321	ENU05115	ANI61C3944: 23-50 3311..1	23-50	797-817	NAP		g3764029	825	168	6.00E-53	43	9	(AB001995) Tellp [Schizosaccharomyces pombe]
21322	ENU05116	ANI61C8015: 69-88 35..834	69-88	756-775	NAP		g1362793	263	69	5.00E-11	33	99	emopamil-binding protein - human [Homo sapiens]
21323	ENU05117	ANI61C5643: 27-45 1526..2246	27-45	671-694	NAP		g1483603	128	105	3.00E-22	36	8	(X98690) Pristinamycin I synthase 2 [Streptomyces pristinaespiralis]
21324	ENU05118	ANI61C3986: 41-60 925..1	41-60	776-796	NAP		g2342601	437	188	5.00E-47	34	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21325	ENU05119	ANI61C8013: 45-71 1411..3361	45-71	805-829	NAP		g2388946	958	85	2.00E-33	36	48	"(Z98978) SPAC27E2.06c, putative methionyl-trna synthetase, le n:539aa, similar eg. to YGR171C, SYMM_ YEAST, P22438, methi onyl- trna synthetase; mitochondrial, (575aa), fasta scores, opt:396, E():0, (39.9% identity in 546 aa o... []"
21326	ENU05120	ANI61C2723: 34-53 1..998	34-53	735-754	NAP		g2492661	1471	440	e-123	97	11	putative sterigmatocystin biosynthesis polyketide synthase (PKS) [Emicella nidulans]
21327	ENU05121	ANI61S2128: 107-125 94..537	107-125	390-407	NAP		g1184121	130	66	1.00E-10	31	46	(U20808) auxin-induced protein [Vigna radiata]
21328	ENU05122	ANI61C1070 23-47 6:2792..1	23-47	656-683	NAP		g2507346	1768	335	2.00E-91	54	16	DNA-directed RNA polymerase I 190 KD polypeptide (A190) [Saccharomyces cerevisiae]
21329	ENU05123	ANI61C4506: 102-128 496..1	102-128	453-472	NAP		g1790870	214	75	4.00E-13	44	50	(U32622) toluenesulfonate zinc- independent alcohol dehydrogenase [Comamonas testosteroni]
21330	ENU05124	ANI61C4658: 23-43 1919..3382	23-43	799-823	NAP		g3261497	676	232	3.00E-60	43	18	(AL021070) ppsB [Mycobacterium tuberculosis]
21331	ENU05125	ANI61C4699: 489..1			NAP		g2462752	404	167	5.00E-41	51	20	(AC002292) Phosphatidylinositol 3- kinase [Arabidopsis thaliana]
21332	ENU05126	ANI61C4285: 42-61 2701..4130	42-61	765-784	NAP		g2497216	610	244	5.00E-64	49	35	hypothetical 83.4 KD protein in DSK2- CAT8 intergenic region [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21333	ENU05127	ANI61C7878: 1..585	22-42	528-547	NAP	ANI61C7878: 22-42	g1945326	184	91	5.00E-18	27	13	(Z72902) ORF YGR116w [Saccharomyces cerevisiae]
21334	ENU05128	ANI61S1312: 1..671			NAP	ANI61S1312: 1..671	g1572721	137	41	0.008	28	15	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
21335	ENU05129	ANI61C4899: 34-53	781-800		NAP	ANI61C4899: 34-53	g57554	201	101	5.00E-21	32	47	(X65296) carboxylesterase [Rattus rattus]
21336	ENU05130	ANI61C3565: 74-93	711-730		NAP	ANI61C3565: 74-93	g3913798	1464	439	e-122	72	52	"exoglucanase I precursor (exocellobiohydrolase I) (1,4-beta-cellobiohydrolase I) (beta-glucanocellobiohydrolase I) [Aspergillus aculeatus]"
21337	ENU05131	ANI61C9214: 218-244	802-829		NAP	ANI61C9214: 218-244	g1729921	198	57	0.000000	39	55	Lipase 2 (triacylglycerol lipase) [Saccharomyces cerevisiae]
21338	ENU05132	ANI61S831: 1..724			NAP	ANI61S831: 1..724	g1176993	383	168	3.00E-41	44	88	hypothetical 26.6 KD sensory transduction protein in IDH 3' region [Bacillus subtilis]
21339	ENU05133	ANI61C4796: 22-47	528-547		NAP	ANI61C4796: 22-47	g3915105	474	160	8.00E-39	61	33	threonine dehydratase precursor (threonine deaminase) [Arxula adeninivorans]
21340	ENU05134	ANI61C2653: 92-111	540-559		NAP	ANI61C2653: 92-111	g1130507	141	83	2.00E-15	31	46	(L41670) fumarylacetoacetate hydrolase [Emmericella nidulans]
21341	ENU05135	ANI61S957: 5	188-215	486-513	NAP	ANI61S957: 5	g1652748	345	150	5.00E-36	48	65	(D90908) hypothetical protein [Synecocystis sp.]
21342	ENU05136	ANI61C953: 7	22-43	653-679	NAP	ANI61C953: 7	g417321	527	205	2.00E-52	59	64	methylentetrahydrofolate dehydrogenase (NAD+)
21343	ENU05137	ANI61C1080	114-133	550-570	NAP	ANI61C1080	g82852	614	231	3.00E-63	61	45	[Saccharomyces cerevisiae] hypothetical protein (LAC12 3' region) - yeast (Kluyveromyces marxianus var. lactis) [Kluyveromyces lactis]
21344	ENU05138	ANI61C4415: 51-70	537-555		NAP	ANI61C4415: 51-70	g549009	201	67	4.00E-21	33	34	probable uroporphyrin-III C-methyltransferase (urogen III methylase) (SUMT) (uroporphyrinogen III methylase) (UROM)
21345	ENU05139	ANI61C55: 39	113-132	458-476	NAP	ANI61C55: 39	g3378433	233	80	6.00E-19	38	34	[Saccharomyces cerevisiae] (AF079317) flavoprotein subunit p-cresol methylhydroxylase
21346	ENU05140	ANI61C489: 5	118-135	507-528	NAP	ANI61C489: 5	g4185903	717	291	2.00E-78	80	32	[Sphingomonas aromaticivorans] (AJ132432) fimbria [Gibberella pulicaris]

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21347	ENU05141	ANI61C3097: 1..723	113-132	625-647	NAP	ANI61C3097: 113-132	g417038	640	193	2.00E-64	65	45	transcriptional activator GCN5 [Saccharomyces cerevisiae]
21348	ENU05142	ANI61C1204: 205-228 2320..1588	685-712		NAP	ANI61C1204: 205-228 2320..1588	g4539186	192	111	7.00E-24	31	58	(AL049485) probable zinc-binding alcohol dehydrogenase [Streptomyces coelicolor]
21349	ENU05143	ANI61C1041 27-47 5:1659..2650	662-689		NAP	ANI61C1041 27-47 5:1659..2650	g731836	448	155	4.00E-50	51	37	probable mannosyltransferase KTR7 [Saccharomyces cerevisiae]
21350	ENU05144	ANI61C4688: 22-40 1090..1	730-752		NAP	ANI61C4688: 22-40 1090..1	g549443	1580	257	e-126	96	12	confidial green pigment synthase [Emmericella nidulans]
21351	ENU05145	ANI61C8490: 40-59 139..1775	773-792		NAP	ANI61C8490: 40-59 139..1775	g112984	1245	158	3.00E-70	68	53	"aspartate aminotransferase, mitochondrial precursor (Transaminase A) (glutamate oxaloacetate transaminase-2) [Mus musculus]" (AL031523) hypothetical protein [Schizosaccharomyces pombe]
21352	ENU05146	ANI61C1856: 22-46 563..95	449-476		NAP	ANI61C1856: 22-46 563..95	g3560223	121	66	1.00E-10	29	48	(AL023776) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]
21353	ENU05147	ANI61C33:86 22-47 9..1	718-744		NAP	ANI61C33:86 22-47 9..1	g3184060	578	123	6.00E-50	49	26	[Schizosaccharomyces pombe] (AF064069) aryl-alcohol oxidase precursor [Pleurotus eryngii] (AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
21354	ENU05148	ANI61C726:6 22-46 82..1	562-581		NAP	ANI61C726:6 22-46 82..1	g3851524	190	97	1.00E-19	30	32	(AL031824) putative transcriptional regulator [Schizosaccharomyces pombe]
21355	ENU05149	ANI61C2963: 32-59 1..501	331-354		NAP	ANI61C2963: 32-59 1..501	g3850084	156	75	3.00E-13	32	46	hypothetical 33.7 KD protein in ISC10 3-region [Saccharomyces cerevisiae]
21356	ENU05150	ANI61C8811: 49-68 2796..2412	336-356		NAP	ANI61C8811: 49-68 2796..2412	g3702632	300	128	2.00E-29	48	18	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]
21357	ENU05151	ANI61C2538: 53-73 1..457	410-434		NAP	ANI61C2538: 53-73 1..457	g731385	165	72	2.00E-12	34	48	"(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]"
21358	ENU05152	ANI61S1367: 1..720			NAP	ANI61S1367: 1..720	g82698	210	45	0.0008	32	70	glucose oxidase precursor (glucose oxyhydrase) (GOD) (beta-D-glucose:oxygen 1-oxido-reductase) [Talaromyces flavus]
21359	ENU05153	ANI61C6372: 554..1			NAP	ANI61C6372: 554..1	g1805261	169	67	9.00E-11	33	9	hypothetical 68.5 KD protein in SCS3-SUP44 intergenic region [Saccharomyces cerevisiae]
21360	ENU05154	ANI61C1057 22-44 7:1534..2318	700-719		NAP	ANI61C1057 22-44 7:1534..2318	g3287841	828	187	8.00E-47	63	43	
21361	ENU05155	ANI61C7117: 25-48 2458..2946	375-398		NAP	ANI61C7117: 25-48 2458..2946	g1723913	499	209	1.00E-53	63	27	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21362	ENU05156	ANI61C3955: 120-138 617..1	120-138	486-505	NAP		g731968	486	203	1.00E-51	50	61	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region [Saccharomyces cerevisiae]
21363	ENU05157	ANI61C4224: 22-43 1..1762	22-43	803-826	NAP		g4557481	761	148	4.00E-35	31	18	canalicular multispecific organic anion transporter [Homo sapiens]
21364	ENU05158	ANI61C7037: 4408..5216			NAP		g4154078	195	93	7.00E-26	37	26	(AL035161) putative efflux protein [Streptomyces coelicolor]
21365	ENU05159	ANI61C856:2 57-76 108..1613	57-76	451-470	NAP		g1170131	209	103	7.00E-22	37	35	glucarate dehydratase subunit (GDH) [Pseudomonas putida]
21366	ENU05160	ANI61C8308: 26-46 7120..5761	26-46	806-829	NAP		g1351678	130	43	0.003			hypothetical 41.5 KD protein C1F5.03C in chromosome I [Schizosaccharomyces pombe]
21367	ENU05161	ANI61C1012 26-53 3:1048..1	26-53	723-749	NAP		g82798	844	197	4.00E-71	55	15	DNA-directed RNA polymerase (EC 2.7.7.6) I 189K chain - fission yeast (Schizosaccharomyces pombe)
21368	ENU05162	ANI61S395:5 105-126 19..1	105-126	442-461	NAP		g4574121	146	85	4.00E-16	32	30	[Schizosaccharomyces pombe] (AF009415) choline dehydrogenase [Staphylococcus xylosus]
21369	ENU05163	ANI61C9793: 22-48 1..5711	22-48	781-803	NAP		g2342601	1701	158	4.00E-38	30	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21370	ENU05164	ANI61C7505: 69-88 2078..1	69-88	774-796	NAP		g1363761	598	73	6.00E-15			probable membrane protein YPR194c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21371	ENU05165	ANI61C2147: 33-52 576..1	33-52	455-477	NAP		g1723578	296	130	2.00E-30	48	53	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
21372	ENU05166	ANI61C1526: 46-64 2630..1517	46-64	803-822	NAP		g4456821	1167	306	5.00E-99	76	56	(AL035548) casein kinase i homolog cki1 [Schizosaccharomyces pombe]
21373	ENU05167	ANI61C8658: 22-43 2074..3488	22-43	761-780	NAP		g3183368	810	191	7.00E-59	58	41	hypothetical 64.0 KD protein C20G4.05C in chromosome I [Schizosaccharomyces pombe]
21374	ENU05168	ANI61S2442: 1..533			NAP		g1805261	251	94	5.00E-19	43	9	"(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]"
21375	ENU05169	ANI61C8742: 22-47 940..1	22-47	728-749	NAP		g4106669	791	225	1.00E-69	73	57	(AL035064) protein kinase skp1p [Schizosaccharomyces pombe]
21376	ENU05170	ANI61C6713: 49-68 719..1	49-68	638-657	NAP		g3402279	415	152	9.00E-40	61	48	(AJ000999) putative beta-subunit of K+ channels [Solanum tuberosum]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21377	ENU05171	ANI61C4226: 1..3006	25-52	808-829	NAP		g2492658	5056	455	e-148	98	13	putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emericella nidulans]
21378	ENU05172	ANI61S3081: 1..584			NAP		g100210	184	41	0.009	34	59	extensin precursor (clone Tom L-4) - tomato [Lycopersicon esculentum]
21379	ENU05173	ANI61C2460: 494..1	103-122	457-479	NAP		g3560221	161	58	8.00E-13	35	42	(AL031523) hypothetical protein [Schizosaccharomyces pombe]
21380	ENU05174	ANI61C8889: 687..1625	38-57	789-808	NAP		g1800044	187	83	2.00E-15	32	56	(D90890) similar to [Escherichia coli]
21381	ENU05175	ANI61C3669: 765..1	46-71	677-695	NAP		g731763	576	245	3.00E-64	51	40	hypothetical 66.7 KD protein in EGD2-SUN1 intergenic region
21382	ENU05176	ANI61C1049 9:1..646			NAP		g4218005	136	60	0.000000 02	19	30	[Saccharomyces cerevisiae] (AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
21383	ENU05177	ANI61S2866: 1..310			NAP		g854065	247	34	0.009	38	24	(X83413) U88 [Human herpesvirus 6]
21384	ENU05178	ANI61C2024: 14..515			NAP		g3646479	202	56	0.000000 2	36	100	(AJ010981) putative transposase [Talaromyces stipitatus]
21385	ENU05179	ANI61C9308: 2975..3549	45-64	492-511	NAP		g3878825	354	166	1.00E-40	50	47	(Z70782) similar to sorbitol dehydrogenase; cDNA EST EMBL:T00701 comes from this gene [Caenorhabditis elegans]
21386	ENU05180	ANI61C8487: 1558..1	22-44	717-744	NAP		g3135994	689	142	4.00E-35	39	18	(AL023589) hypothetical protein [Schizosaccharomyces pombe]
21387	ENU05181	ANI61C518:8 31..1	48-67	706-730	NAP		g1706695	303	114	9.00E-25	36	54	phosphomevalonate kinase [Saccharomyces cerevisiae]
21388	ENU05182	ANI61S4173: 553..1	215-233	416-435	NAP		g1351673	322	129	1.00E-29	45	53	hypothetical 37.7 KD protein C1F7.12 in chromosome I
21389	ENU05183	ANI61C1188: 1..1389	22-41	791-815	NAP		g631954	1952	362	e-119	99	28	[Schizosaccharomyces pombe] chitin synthase (EC 2.4.1.16) chsB - Emericella nidulans [Emericella nidulans]
21390	ENU05184	ANI61C3528: 1..462	25-46	414-441	NAP		g2981719	252	106	7.00E-23	38	20	Crystal Structures Of The Copper-Containing Amine Oxidase From Arthrobacter Globiformis In The Holo- And Apo-Forms: Implications For The Biogenesis Of Topa Quinone []

Seq num	Seq id	Config source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21391	ENU05185	ANI61C6380: 2296..234	33-52	797-817	NAP		g2342601	653	101	9.00E-21	25	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21392	ENU05186	ANI61S2843: 528..1			NAP		g1352946	366	136	1.00E-31	49	60	hypothetical 32.6 KD protein in DAL5-TH11 intergenic region [Saccharomyces cerevisiae]
21393	ENU05187	ANI61C5497: 27-54	27-54	808-829	NAP		g2739355	2771	429	e-119	71	25	(AC003972) pNORF1 [Homo sapiens]
21394	ENU05188	ANI61C5368: 4102..1769	22-44	787-806	NAP		g1729996	139	54	9.00E-11	32	75	TOXD protein [Cochliobolus carbonum]
21395	ENU05189	ANI61C9887: 950..1	191-218	533-556	NAP		g3875727	225	65	2.00E-22	49	28	(Z70751) similar to 4-coumarate-CoA ligase; cDNA EST EMBL:C07240 comes from this gene; cDNA EST EMBL:C08540 comes from this gene [Caenorhabditis elegans]
21396	ENU05190	ANI61C8675: 1043..1	24-43	725-744	NAP		g3121988	339	112	9.00E-30	34	48	betaine aldehyde dehydrogenase (BADH) []
21397	ENU05191	ANI61C3613: 626..250	22-48	332-356	NAP		g1711469	257	116	6.00E-26	47	29	dibenzothiophene desulfurization enzyme C (DBT sulfur dioxygenase) [Rhodococcus sp.]
21398	ENU05192	ANI61C8895: 1..904	37-64	723-749	NAP		g102551	926	360	1.00E-98	65	17	kinesin-related protein unc-104 - Caenorhabditis elegans []
21399	ENU05193	ANI61C2996: 75-95	75-95	666-685	NAP		g3913980	435	157	9.00E-44	50	49	probable kynureninase (L-kynurenine hydrolase) [Saccharomyces cerevisiae]
21400	ENU05194	ANI61C5409: 797..1	71-90	265-284	NAP		g1314705	85	35	0.18	31	33	(U53863) Nopp44/46 [Trypanosoma brucei]
21401	ENU05195	ANI61C1209: 1..315	22-44	748-775	NAP		g462739	216	106	3.00E-22	35	34	NPL4 protein [Saccharomyces cerevisiae]
21402	ENU05196	ANI61S3756: 5959..6754	27-47	553-572	NAP		g3482917	544	142	1.00E-51	74	26	"(AC003970) Similar to Glucose-6-phosphate dehydrogenases, [Arabidopsis thaliana]"
21403	ENU05197	ANI61C1055: 9..4377..3549	22-41	788-808	NAP		g1352891	153	95	7.00E-19	24	69	putative glycosyltransferase HOC1 precursor [Saccharomyces cerevisiae]
21404	ENU05198	ANI61C4595: 829..292	67-87	492-516	NAP		g417308	457	94	8.00E-32			probable helicase MOT1 []
21405	ENU05199	ANI61C4356: 1608..2295	40-59	600-621	NAP		g481285	356	159	1.00E-38	36	32	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Aspergillus niger [Aspergillus niger]
21406	ENU05200	ANI61C3342: 1571..1021	22-41	476-495	NAP		g3219829	178	60	5.00E-15	36	99	Multidrug resistance-associated protein 4 [Homo sapiens]

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21407	ENU05201	ANI61C1135 7:2697..2156	22-48	497-521	NAP		g481230	148	88	5.00E-17	32	43	L-idiol 2-dehydrogenase (EC 1.1.1.14) precursor - rat [Rattus norvegicus] (X55731) COX11 (AA 1-277) [Saccharomyces cerevisiae] (D43686) L41 ribosomal protein [Candida maltosa] (D90907) sensory transduction histidine kinase [Synecocystis sp.] (Z98602) putative protein transport protein sec7 homolog [Schizosaccharomyces pombe] "(S62929) PRB1L precursor protein=basic proline rich proteins (Ps, PmF, PmS, and Pe) precursor {C-terminal} [Homo sapiens]" (AL031263) putative GTPase-activator protein for Rho-like GTPases [Schizosaccharomyces pombe] (U96090) myb-related transcription factor [Strongylocentrotus purpuratus] (U35661) colony 1 [Ophiostoma ulmi] hypothetical 72.5 KD protein C2F7.10 in chromosome I [Schizosaccharomyces pombe] (Z98977) hypothetical protein [Schizosaccharomyces pombe] (Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum] putative SEC14 cytosolic factor (phosphatidylinositol/phosphatidylcholine transfer protein) (PI/PC TP) [Schizosaccharomyces pombe] NADH-ubiquinone dehydrogenase 24 KD subunit precursor [Neurospora crassa] (M77661) putative pol polyprotein [Magnaporthe grisea]
21408	ENU05202	ANI61C7939: 22-41 591..1	22-41	519-539	NAP		g3567	217	96	2.00E-20	40	60	
21409	ENU05203	ANI61C7448: 3462..3016			NAP		g1272506	444	125	7.00E-43	87	100	
21410	ENU05204	ANI61C2343: 338..665			NAP		g1652639	52	75	3.00E-13	26	12	
21411	ENU05205	ANI61C1286: 65-84 1033..1	65-84	728-747	NAP		g2440190	606	187	1.00E-46	36	18	
21412	ENU05206	ANI61S281:1 2..632			NAP		g433011	114	66	2.00E-10	29	53	
21413	ENU05207	ANI61C5167: 221-239 2025..1345	221-239	605-624	NAP		g3417437	226	102	3.00E-21	34	64	
21414	ENU05208	ANI61C2551: 27-47 703..1628	27-47	775-795	NAP		g2072499	148	86	3.00E-16	29	31	
21415	ENU05209	ANI61C9694: 217-238 4641..3789	217-238	722-741	NAP		g998355	239	127	8.00E-29	30	33	
21416	ENU05210	ANI61C9624: 22-49 1365..1999	22-49	555-581	NAP		g1175373	390	137	6.00E-34	46	29	
21417	ENU05211	ANI61C6114: 296..1060			NAP		g2388934	189	56	0.000000	38	23	
21418	ENU05212	ANI61C7669: 24-51 1364..1	24-51	730-749	NAP		g3282044	1676	390	e-113	76	18	
21419	ENU05213	ANI61C3906: 1..632			NAP		g1710858	431	182	2.00E-45	50	65	
21420	ENU05214	ANI61C5852: 120-139 1..799	120-139	726-746	NAP		g730212	798	180	2.00E-89	72	90	
21421	ENU05215	ANI61C9289: 22-46 1..1309	22-46	807-829	NAP		g538067	523	161	6.00E-39	34	20	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21422	ENU05216	ANI61C7651: 833..1	28-51	787-806	NAP		g3978134	541	83	6.00E-32	48	24	(U65409) Sla2p [Yarrowia lipolytica]
21423	ENU05217	ANI61C320:1 102-129 654-677 .698			NAP		g2995360	481	99	6.00E-36	56	48	(AL022243) nucleosome assembly protein. [Schizosaccharomyces pombe]
21424	ENU05218	ANI61C6917: 36-57 576..182		348-374	NAP		g4758126	241	62	0.000000 001			"DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide, Y chromosome [Homo sapiens]"
21425	ENU05219	ANI61C9553: 23-44 2242..409		801-828	NAP		g1182233	452	55	2.00E-19			allantoate permease [Saccharomyces cerevisiae]
21426	ENU05220	ANI61C9720: 45-64 1..1503		810-829	NAP		g1352079	1801	289	e-107	70	30	beta-glucosidase 1 precursor (gentiobiose) (cellobiose) (beta-D-glucoside glucosylhydrolase) [Aspergillus aculeatus]
21427	ENU05221	ANI61C2169: 59-78 245..937		562-581	NAP		g4539264	662	241	4.00E-63	58	58	(AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]
21428	ENU05222	ANI61C4363: 27-50 1426..1		711-731	NAP		g417305	702	190	1.00E-47	46	41	"mannosyl-oligosaccharide alpha-1,2-mannosidase (MAN(9)-alpha-mannosidase) [Saccharomyces cerevisiae]"
21429	ENU05223	ANI61S1929: 111-134 521-544 575..1			NAP		g113314	891	356	5.00E-98	93	5	delta-(L-alpha-aminoacidipyl)-L-cysteiny-D-valine synthetase (ACV synthetase) (ACVS) [Emicella nidulans]
21430	ENU05224	ANI61C7050: 32-51 3317..4174		757-780	NAP		g2773302	270	179	2.00E-44	35	51	(AF040720) xylosidase/arabinosidase [Selenomonas ruminantium]
21431	ENU05225	ANI61C6970: 22-49 85..1015		797-824	NAP		g543961	210	85	8.00E-16			cell division control protein 14 [Schizosaccharomyces pombe]
21432	ENU05226	ANI61C784:5 24-43 61..1		428-455	NAP		g2154997	247	134	3.00E-31	40	26	(Y12503) Man9-mannosidase [Sus scrofa]
21433	ENU05227	ANI61S3090: 1..457			NAP		g100210	156	37	0.09	32	45	extensin precursor (clone Tom L-4) - tomato [Lycopersicon esculentum]
21434	ENU05228	ANI61C3808: 101-120 617-640 743..1		617-640	NAP		g1363750	204	65	5.00E-20	30	15	hypothetical protein YLR419w - yeast (Saccharomyces cerevisiae)
21435	ENU05229	ANI61C1125 67-87 7:485..1		437-456	NAP		g4557587	157	70	4.00E-14	37	32	[Saccharomyces cerevisiae] fumarylacetoacetase [Homo sapiens]
21436	ENU05230	ANI61C9186: 59-78 4850..1262		791-810	NAP		g4585936	1397	192	3.00E-48	38	21	(AC007211) putative helicase [Arabidopsis thaliana]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21437	ENU05231	ANI61C2296: 4890..5915	22-49	779-801	NAP		g1217600	149	92	3.00E-19	27	48	(D38215) tcr3 [Streptomyces aureofaciens]
21438	ENU05232	ANI61C8809: 310..1320			NAP		g416657	576	162	2.00E-42	52	73	Anti-silencing protein 1 [Saccharomyces cerevisiae]
21439	ENU05233	ANI61C1071 64-83	64-83	719-738	NAP		g2342601	1457	214	1.00E-57	40	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21440	ENU05234	ANI61C79:28 6:3239..1	22-46	630-649	NAP		g1174617	494	129	1.00E-42	64	33	"T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon) ["
21441	ENU05235	ANI61C9059: 29..3543	99-120	490-512	NAP		g31116126	93	61	0.000000	28	30	(AL023287) Sat1p [Schizosaccharomyces pombe]
21442	ENU05236	ANI61C8724: 1..533	22-47	800-827	NAP		g1546072	493	70	2.00E-11			(U68040) polyketide synthase [Cochliobolus heterostrophus]
21443	ENU05237	1944..3970	108-126	548-567	NAP		g2983756	265	119	2.00E-26	42	40	(AE000735) ATP-dependent protease ATPase subunit clpX [Aquifex aeolicus]
21444	ENU05238	ANI61C4376: 823..1527	22-45	646-673	NAP		g2347143	660	266	1.00E-70	59	99	(U48234) spU2AF23 [Schizosaccharomyces pombe]
21445	ENU05239	ANI61C4928: 1597..1	72-91	781-807	NAP		g2501339	673	207	9.00E-53	51	35	Copper amine oxidase 1 [Aspergillus niger]
21446	ENU05240	ANI61C9658: 2293..1816	72-89	434-456	NAP		g2132029	150	58	0.000000	37	56	Hypothetical protein YOR004w - yeast (Saccharomyces cerevisiae)
21447	ENU05241	ANI61C4358: 704..1569	31-49	719-738	NAP		g2842699	369	164	5.00E-40	42	50	[Saccharomyces cerevisiae] putative ubiquitin carboxyl-terminal hydrolase C6G9.08 (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]
21448	ENU05242	ANI61C4668: 1..996	38-57	726-747	NAP		g1177622	216	49	0.00004	28	27	(X89715) AOF1001 [Saccharomyces cerevisiae]
21449	ENU05243	ANI61C1134 8:618..1	22-46	524-548	NAP		g4160578	154	79	2.00E-14	31	54	(AL035218) hypothetical protein [Schizosaccharomyces pombe]
21450	ENU05244	ANI61C639:7 12..322	22-45	452-479	NAP		g731385	158	94	8.00E-19	37	50	hypothetical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae]
21451	ENU05245	ANI61C7684: 640..1399	72-91	718-739	NAP		g1175370	177	120	1.00E-26	30	39	hypothetical 68.8 KD protein C2F7.07C in chromosome I [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21452	ENU05246	ANI61C8831: 22-43 2353..2820	22-43	458-478	NAP		g2132738	460	175	2.00E-43	61	98	probable membrane protein YNL044w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21453	ENU05247	ANI61C6666: 23-44 734..1	23-44	490-514	NAP		g2894269	245	117	7.00E-26	32	49	(AL021839) myb family DNA binding protein [Schizosaccharomyces pombe]
21454	ENU05248	ANI61C5501: 23-50 605..2159	23-50	725-748	NAP		g462414	1454	123	8.00E-64	69	45	amino-acid permease INDA1 [Trichoderma harzianum]
21455	ENU05249	ANI61S150:5 74..155	110-130	376-399	NAP		g4263543	584	229	9.00E-60	85	15	(AC006250) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]
21456	ENU05250	ANI61S310:5 86..201	183-210	340-365	NAP		g3913727	496	142	8.00E-38	98	20	"glucose-6-phosphate 1- dehydrogenase, cytoplasmic isoform (G6PD) [Arabidopsis thaliana]"
21457	ENU05251	ANI61C5962: 22-48 1..1303	22-48	779-801	NAP		g1351928	292	66	3.00E-25	38	65	methionine aminopeptidase 1 precursor (METAP 1) (peptidase M 1) (MAP) [Saccharomyces cerevisiae]
21458	ENU05252	ANI61C6706: 37-54 2398..1	37-54	803-829	NAP		g1166378	515	79	2.00E-25	34	24	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
21459	ENU05253	ANI61C8887: 118-137 1..420	118-137	372-399	NAP		g2132861	92	45	0.00002	32	56	probable membrane protein YOL163w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21460	ENU05254	ANI61C1016 0:827..1	27-50	700-723	NAP		g2738309	251	98	8.00E-20	31	51	(AF002660) aflatoxin [Aspergillus parasiticus]
21461	ENU05255	ANI61C6324: 29-56 1123..1	29-56	723-742	NAP		g730431	914	258	6.00E-70	62	27	Periodic tryptophan protein 2 [Saccharomyces cerevisiae]
21462	ENU05256	ANI61C1002: 2743..3805			NAP		g2804298	532	118	3.00E-36	38	51	(AB010439) steroid monooxygenase [Rhodococcus rhodochrous]
21463	ENU05257	ANI61C4431: 56-75 2430..1926	56-75	460-484	NAP		g731809	182	91	4.00E-18	40	99	hypothetical 15.9 KD protein in GPP1- SYG1 intergenic region [Saccharomyces cerevisiae]
21464	ENU05258	ANI61C6829: 110-129 2880..2444	110-129	389-416	NAP		g3764029	318	146	6.00E-35	51	5	(AB001995) Tel1p [Schizosaccharomyces pombe]
21465	ENU05259	ANI61C1930: 1240..1			NAP		g1170566	697	172	4.00E-54	47	51	Myo-inositol-1-phosphate synthase (IPS) [Candida albicans]
21466	ENU05260	ANI61C3261: 22-47 1..3275	22-47	737-759	NAP		g2370466	2515	146	2.00E-34	29	5	(Z98951) hypothetical protein [Schizosaccharomyces pombe]
21467	ENU05261	ANI61C2859: 23-42 99..1099	23-42	785-804	NAP		g1421604	431	177	7.00E-44	40	48	Candida cylindracea []

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21468	ENU05262	ANI61C4819: 121-146 2775..2475	121-146	256-280	NAP		g3219530	226	106	5.00E-23	52	52	(AJ006688) IgE-binding protein [Aspergillus fumigatus]
21469	ENU05263	ANI61C1017 51..712	172-191	538-557	NAP		g558311	520	118	1.00E-51	57	51	(L35487) mannanase [Aspergillus aculeatus]
21470	ENU05264	ANI61C9994: 22-49 26..1083	22-49	804-829	NAP		g4507293	354	185	3.00E-46	43	81	syntaxin 5A [Homo sapiens]
21471	ENU05265	ANI61S1430: 1..745			NAP		g4218005	156	62	0.000000	21	35	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
21472	ENU05266	ANI61C746:1 ..380	122-142	337-358	NAP		g418296	268	123	5.00E-28			vacuolar ATP synthase 95 KD subunit (vacuolar ATPase 95 KD subunit) [Saccharomyces cerevisiae]
21473	ENU05267	ANI61C2820: 22-44 629..1	22-44	490-509	NAP		g3169065	219	104	4.00E-22	32	19	(AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]
21474	ENU05268	ANI61C7326: 50-75 1..356	50-75	308-335	NAP		g2499454	219	104	2.00E-22	46	34	pectinesterase precursor (pectin methyltransferase) (PE) [Aspergillus aculeatus]
21475	ENU05269	ANI61C7855: 22-43 3027..4065	22-43	801-828	NAP		g2132944	430	183	1.00E-45	40	87	probable membrane protein YOR311c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21476	ENU05270	ANI61C1495: 102-126 1..635	102-126	464-483	NAP		g3850070	575	120	1.00E-56	58	28	(AL033385) transketolase [Schizosaccharomyces pombe]
21477	ENU05271	ANI61C7628: 27-52 1..386	27-52	340-365	NAP		g2905657	323	138	1.00E-32	59	31	(AF047469) arsenite translocating ATPase [Homo sapiens]
21478	ENU05272	ANI61C7236: 22-42 1..584	22-42	541-563	NAP		g1077557	101	55	0.000000	30	26	probable membrane protein YDR061w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21479	ENU05273	ANI61C7050: 22-40 965..2783	22-40	802-829	NAP		g1929089	253	36	0.46			(Z93777) hypothetical protein Rv1215c [Mycobacterium tuberculosis]
21480	ENU05274	ANI61C5946: 39-58 1..992	39-58	789-807	NAP		g4160583	578	218	4.00E-56	50	73	(AL035218) conserved hypothetical protein [Schizosaccharomyces pombe]
21481	ENU05275	ANI61C8772: 22-45 51..569	22-45	456-475	NAP		g2133256	318	129	2.00E-30	68	39	o-pyrocatechuate decarboxylase (EC 4.1.1.46) - Aspergillus niger (fragments) []
21482	ENU05276	ANI61C1063 3:1017..1	47-66	755-780	NAP		g3130032	378	165	4.00E-40	35	48	(AL023534) major facilitator family transporter [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21483	ENU05277	ANI61S3800: 1..651			NAP		g119712	160	51	0.000009	32	78	extensin precursor (proline-rich glycoprotein) [Zea mays]
21484	ENU05278	ANI61C4389: 93-112		387-406	NAP		g1652128	102	68	5.00E-11	27	9	(D90903) hypothetical protein [Synecocystis sp.]
21485	ENU05279	ANI61S530:5 43-70		396-423	NAP		g538067	149	50	0.000000	29	13	(M77661) putative pol polyprotein [Magnaporthe grisea]
21486	ENU05280	ANI61C7970: 102-129		278-296	NAP		g442927	246	77	9.00E-17	50	18	Glucose Oxidase (E.C.1.1.3.4) []
21487	ENU05281	ANI61C255:1 32-51		776-795	NAP		g4704282	236	88	9.00E-17			(AL049728) hypothetical protein [Schizosaccharomyces pombe]
21488	ENU05282	ANI61C4337: 22-44		806-825	NAP		g3080521	391	149	9.00E-37	38	33	(AL022599) hypothetical protein [Schizosaccharomyces pombe]
21489	ENU05283	ANI61C9934: 56-75		380-399	NAP		g3123246	548	226	5.00E-59	71	28	serine-type carboxypeptidase F precursor (proteinase F) (CPD-II) [Aspergillus niger]
21490	ENU05284	ANI61C1103 22-46		771-798	NAP		g1175933	206	92	5.00E-18	33	21	hypothetical 96.7 KD protein in STE2-FRS2 intergenic region [Saccharomyces cerevisiae]
21491	ENU05285	ANI61C565:3 347..5170		803-829	NAP		g1708073	1592	250	7.00E-66	66	45	GMP synthase (glutamine-hydrolysing) (glutamine amidotransferase) (GMP synthetase) [Saccharomyces cerevisiae]
21492	ENU05286	ANI61C12:18 22-42		714-735	NAP		g4758416	281	121	6.00E-27			golgi-specific brefeldin A-resistance factor 1 [Homo sapiens]
21493	ENU05287	ANI61C7103: 54-73		623-650	NAP		g3114278	698	281	3.00E-75	70	99	"Chain J, Crystal Structure Of The 20s Proteasome From Yeast At 2.4 Angstroms Resolution []"
21494	ENU05288	ANI61C7913: 22-49		515-534	NAP		g3043626	81	34	0.85			(AB011123) KIAA0551 protein [Homo sapiens]
21495	ENU05289	ANI61C5607: 70-89		778-801	NAP		g2267601	244	59	1.00E-19	31	44	(AF009417) cytochrome P450 [Myrothecium roridum]
21496	ENU05290	ANI61C9702: 22-48		802-828	NAP		g5022	2884	429	e-119	68	36	(X60499) rad15 [Schizosaccharomyces pombe]
21497	ENU05291	ANI61C1121 28-47		759-784	NAP		g1708195	892	136	2.00E-31	50	22	HFM1 protein [Saccharomyces cerevisiae]
21498	ENU05292	ANI61C3793: 102-126		388-413	NAP		g1805251	143	52	0.000002	31	25	(U58946) transposase [Aspergillus awamori]
21499	ENU05293	ANI61C3447: 33-60		722-741	NAP		g3915963	503	154	6.00E-37	36	15	ATP-dependent bile acid permease [Saccharomyces cerevisiae]

Seq num	Seq id	Primer	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21500	ENU05294	Contig source ANI61C9040: 31-58 1009..1	3 pos 723-749 NAP	ANI61C9040: 31-58 1009..1	g3915067	362	100	1.00E-38	41	43	aspartyl-TRNA synthetase (aspartate--TRNA ligase) (ASPRS) [Aquifex aeolicus]
21501	ENU05295	ANI61C1022 66-87 2:1219..667	513-532 NAP	ANI61C1022 66-87 2:1219..667	g1168269	278	123	1.00E-27	37	50	"arabian endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabananASE A) (ABN A) [Aspergillus niger]"
21502	ENU05296	ANI61C9143: 145-164 322..1	454-479 NAP	ANI61C9143: 145-164 322..1	g4731167	173	88	3.00E-17			(AFI08357) c-myc binding protein MM-1 [Mus musculus]
21503	ENU05297	ANI61C7822: 44-63 3976..4512	477-502 NAP	ANI61C7822: 44-63 3976..4512	g4519181	863	188	2.00E-75	98	16	(AB023911) chitin synthase [Emicella nidulans]
21504	ENU05298	ANI61C9203: 54-73 3211..802	778-797 NAP	ANI61C9203: 54-73 3211..802	g2147662	718	116	2.00E-25	28	12	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium [Colletotrichum lagenarium]
21505	ENU05299	ANI61C8314: 22-45 136..1241	808-829 NAP	ANI61C8314: 22-45 136..1241	g2501437	432	115	1.00E-27	30	79	DNA damage tolerance protein RHC31 (RAD31 homolog) [Saccharomyces cerevisiae]
21506	ENU05300	ANI61C9664: 22-47 520..4543	724-746 NAP	ANI61C9664: 22-47 520..4543	g2065438	1877	178	4.00E-71	48	19	(Y11989) Wak1 protein [Schizosaccharomyces pombe]
21507	ENU05301	ANI61S3836: 1..901	NAP	ANI61S3836: 1..901	g4760549	100	69	3.00E-11			(AB019494) IDN3 [Homo sapiens]
21508	ENU05302	ANI61C7667: 54-73 217..840	537-554 NAP	ANI61C7667: 54-73 217..840	g1171737	199	76	3.00E-19	43	16	Nonsense-mediated mRNA decay protein 2 (up-frameshift suppressor 2) [Saccharomyces cerevisiae]
21509	ENU05303	ANI61C1021 1:1..493	108-130 447-469 NAP	ANI61C1021 1:1..493	g4210942	537	222	9.00E-58	65	60	(AF069518) 17beta-hydroxysteroid dehydrogenase [Cochliobolus lunatus]
21510	ENU05304	ANI61C7952: 25-44 1472..966	463-485 NAP	ANI61C7952: 25-44 1472..966	g1723793	212	105	2.00E-22			putative 3 beta-hydroxysteroid dehydrogenase/delta 5-->4-isomerase (3beta-HSD) (3-beta-hydroxy-delta(5)-steroid dehydrogenase (3-beta-hydroxy-5-ene steroid dehydrogenase) (progesterone reductase) / steroid delta-isomerase.. [Saccharomyces cerevisiae]
21511	ENU05305	ANI61C3186: 35-62 4376..4770	369-396 NAP	ANI61C3186: 35-62 4376..4770	g1723781	83	64	6.00E-10	31	45	hypothetical 34.3 KD protein in TAF145-YOR1 intergenic region [Saccharomyces cerevisiae]

Seq num	Seq id	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21512	ENU05306	ANI61C1003 2:14..595	63-82	495-512	NAP	g3024443	201	89	2.00E-18	38	52	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) [Zalerion arboricola]
21513	ENU05307	ANI61C378:4 116..2992	22-47	784-803	NAP	g416820	164	75	5.00E-13	22	74	para-hydroxybenzoate-- polyprenyltransferase precursor (PHB:polyprenyltransferase) [Saccharomyces cerevisiae]
21514	ENU05308	ANI61C3805: 1..1904	67-86	780-799	NAP	g1706176	1345	138	3.00E-32	44	26	cutinase transcription factor 1 alpha [Fusarium solani f. sp. pisi]
21515	ENU05309	ANI61C3630: 6980..5626	22-47	803-829	NAP	g538067	790	203	1.00E-51	37	20	(M77661) putative pol polyprotein [Magnaporthe grisea]
21516	ENU05310	ANI61C1203: 112..571	102-122	387-406	NAP	g1001163	600	137	8.00E-34	81	45	(D64001) hypothetical protein [Synechocystis sp.]
21517	ENU05311	ANI61C1698: 352..1311	22-44	781-807	NAP	g3121995	388	159	5.00E-48	39	26	DOM34 interacting protein 2 [Saccharomyces cerevisiae]
21518	ENU05312	ANI61C9662: 741..193	36-55	477-496	NAP	g3879850	270	98	6.00E-20	43	100	(Z81592) predicted using GeneFinder [Caenorhabditis elegans]
21519	ENU05313	ANI61C1070 0:1822..483	45-64	769-788	NAP	g2959374	712	148	4.00E-35	45	47	(AL022117) putative pre-mrna splicing factor [Schizosaccharomyces pombe]
21520	ENU05314	ANI61S1429: 1..610			NAP	g2996650	121	54	0.000000	24	11	(AC004493) KIAA0324 [Homo sapiens]
21521	ENU05315	ANI61C2295: 696..1	26-45	576-595	NAP	g3411013	484	213	1.00E-54	49	24	(AF000232) protein mannosyltransferase 1 [Candida albicans]
21522	ENU05316	ANI61C8866: 1887..4165	63-82	745-765	NAP	g173384	2075	429	e-119	74	26	(L07734) DNA polymerase delta [Schizosaccharomyces pombe]
21523	ENU05317	ANI61C8004: 2211..880	22-48	700-721	NAP	g3080532	404	120	1.00E-26	39	62	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
21524	ENU05318	ANI61C914:4 406..3538	22-47	805-826	NAP	g3878905	180	121	7.00E-27	28	65	(Z46794) similarity to enoyl CoA hydratase. Amino terminus shows similarity to acyl-CoA binding domains; cDNA EST EMBL:C08977 comes from this gene; cDNA EST EMBL:C09386 comes from this gene; cDNA EST yk447c11.5 comes from this... []
21525	ENU05319	ANI61C5448: 30..818	22-48	625-644	NAP	g786117	73	48	0.00007	20	52	(L41834) nuclear protein [Ensis minor]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21526	ENU05320	ANI61C1071 7.6793..7839	22-45	790-809	NAP		g549602	195	50	0.000002	32	75	hypothetical 32.0 KD protein in SAP190-SPO14 intergenic region [Saccharomyces cerevisiae]
21527	ENU05321	ANI61C2481: 61-80 250..1826	61-80	806-829	NAP		g1654028	262	49	0.000005			(Z81360) hypothetical protein Rv1726 [Mycobacterium tuberculosis]
21528	ENU05322	ANI61S2482: 77..598			NAP		g2465144	86	58	0.000000	32	63	(Z99753) hypothetical protein [Schizosaccharomyces pombe]
21529	ENU05323	ANI61C7829: 211-235 1..670	211-235	626-649	NAP		g2266908	143	86	3.00E-16	38	70	(AE001274) PXNC; L4171.2 [Leishmania major]
21530	ENU05324	ANI61C2803: 29-53 571..130	29-53	386-405	NAP		g1711410	106	64	4.00E-10	27	34	Pristinamycin IIA synthase subunit A (PIIA synthase subunit A)
21531	ENU05325	ANI61C1039 2:1946..990	22-42	728-751	NAP		g1706694	601	238	3.00E-63	52	34	[Streptomyces pristinaespiralis] "lanosterol synthase (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene—lanosterol cyclase) (OSC) [Schizosaccharomyces pombe]"
21532	ENU05326	ANI61C5507: 25-44 1456..2907	25-44	802-829	NAP		g3219811	312	77	2.00E-13	32	70	HUS1 protein [Schizosaccharomyces pombe]
21533	ENU05327	ANI61C8456: 27-48 2215..1	27-48	611-638	NAP		g3560150	2216	359	1.00E-98	65	34	(AL031534) Chaperonin hsp78p [Schizosaccharomyces pombe]
21534	ENU05328	ANI61S1345: 1..703			NAP		g135153	105	52	0.000004	26	32	Synapsins IA and IB []
21535	ENU05329	ANI61C1768: 70-89 1148..1	70-89	721-740	NAP		g584806	1414	492	e-138	83	51	"ATP synthase alpha chain, mitochondrial precursor [Neurospora crassa]"
21536	ENU05330	ANI61C5226: 22-49 2380..1	22-49	804-823	NAP		g1723540	910	61	3.00E-13	36	27	hypothetical 100.5 KD protein C1B9.04 in chromosome I [Schizosaccharomyces pombe]
21537	ENU05331	ANI61C3227: 22-47 1..1072	22-47	732-755	NAP		g2501559	681	142	5.00E-61	45	38	hypothetical 77.8 KD protein in MRPS28-HXT7 intergenic region [Saccharomyces cerevisiae]
21538	ENU05332	ANI61C2826: 67-87 728..24	67-87	651-672	NAP		g63628	107	40	0.000000	35	79	(X14612) myb protein [Gallus gallus]
21539	ENU05333	ANI61C991:1 ..340	46-70	280-299	NAP		g1945500	98	59	0.000000	30	25	(U13644) F56D2.2 gene product [Caenorhabditis elegans]
21540	ENU05334	ANI61C1082 8:704..1	22-41	577-603	NAP		g3249039	245	120	1.00E-26	36	53	(AF071221) N-carbamyl-L-amino acid amidohydrolase [Arthrobacter aureus]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21541	ENU05335	ANI61C1043: 22-45 1228..2077	22-45	803-822	NAP		g3687510	372	123	2.00E-27	58	65	(AL031788) ubiquitin-conjugating enzyme [Schizosaccharomyces pombe]
21542	ENU05336	ANI61C4716: 22-41 3207..3737	22-41	313-332	NAP		g1084771	445	183	7.00E-46	70	77	ribosomal protein L18a.e.c13 - yeast (Saccharomyces cerevisiae)
21543	ENU05337	ANI61C2614: 39-62 1522..1	39-62	724-749	NAP		g543806	1224	299	2.00E-80	58	40	[Saccharomyces cerevisiae] "glucoamylase precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) [Aspergillus oryzae]"
21544	ENU05338	ANI61C1067 36-55 3:1..1254	36-55	802-829	NAP		g4884474	624	121	7.00E-49			(Z99163) WD repeat protein [Schizosaccharomyces pombe]
21545	ENU05339	ANI61C7406: 41-62 1100..398	41-62	645-664	NAP		g2076715	737	288	2.00E-78	67	46	(Y11322) SEC61 protein [Yarrowia lipolytica]
21546	ENU05340	ANI61C1013 1:2643..3799			NAP		g1834315	855	217	1.00E-55	52	67	(D78351) nuclease O [Aspergillus oryzae]
21547	ENU05341	ANI61S2200: 23-45 1..459	23-45	415-438	NAP		g3738162	502	180	6.00E-45	70	32	(AL031856) putative involvement in protein glycosylation in the golgi [Schizosaccharomyces pombe]
21548	ENU05342	ANI61C9766: 46-65 4104..4449	46-65	375-398	NAP		g3913082	99	53	0.000000	33	38	Aquaporin 9 [Homo sapiens]
21549	ENU05343	ANI61C8029: 45-72 1..315	45-72	265-284	NAP		g485111	168	73	6.00E-13	36	26	(U00050) similar to enoyl-CoA hydratases; highest similarity to YKRS_YEAST [Caenorhabditis elegans]
21550	ENU05344	ANI61S1642: 22-49 1..369	22-49	327-348	NAP		g1335873	264	108	2.00E-23	50	24	(U46690) ATP-dependent RNA helicase [Mus musculus]
21551	ENU05345	ANI61C659:1 174-193 412..1029	174-193	342-361	NAP		g4581500	133	64	4.00E-10	33	18	(AL034352) putative oxalyl-CoA decarboxylase [Schizosaccharomyces pombe]
21552	ENU05346	ANI61C2064: 40-59 1484..1	40-59	726-751	NAP		g458284	1502	269	1.00E-94	85	37	(U05811) serine/threonine protein kinase [Trichoderma reesei]
21553	ENU05347	ANI61C4060: 1116..1			NAP		g3023651	435	172	3.00E-42	37	48	D-lactate dehydrogenase [Kluveromyces lactis]
21554	ENU05348	ANI61S4097: 1..331			NAP		g2499312	127	57	0.000000	36	22	NADH-ubiquinone oxidoreductase 51 KD subunit precursor (complex I-51KD) (CI-51KD) [Aspergillus niger]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21555	ENU05349	ANI61C2044: 488..893			NAP		g2851654	219	110	7.00E-24	46	22	2-dehydro-3-deoxyphosphogalactonate aldolase (6-phospho-2-dehydro-3-deoxygalactonate aldolase) (2-oxo-3-deoxygalactonate 6-phosphate aldolase) / galactonate dehydratase [Escherichia coli]
21556	ENU05350	ANI61C9912: 22-47 1396..2092		480-505	NAP		g1125833	569	167	3.00E-55	80	78	(U43283) Similar to ras-related protein; coded for by C. elegans cDNA CEESK32F; coded for by C. elegans cDNA yk82h5.3; coded for by C. elegans cDNA yk82h5.5; coded for by C. elegans cDNA yk168c1.3; coded for by C. elegans cDNA yk168c1.5 [Cae...
21557	ENU05351	ANI61C55:78 24-47 1..1323		498-520	NAP		g4895135	87	78	4.00E-14			(AF127374) MmcR [Streptomyces lavendulae]
21558	ENU05352	ANI61C8078: 37-59 450..4089		722-749	NAP		g3355628	1981	267	6.00E-71	48	17	(X91867) CPC3 protein [Neurospora crassa]
21559	ENU05353	ANI61C806:2 22-43 543..1		725-745	NAP		g3114719	1435	217	1.00E-67	50	16	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
21560	ENU05354	ANI61C2673: 58-83 850..36		729-746	NAP		g547901	760	262	6.00E-78	64	70	"MAlate dehydrogenase, mitochondrial precursor [Saccharomyces cerevisiae]"
21561	ENU05355	ANI61C1129 103-122 4:1..562		516-535	NAP		g2497072	315	96	3.00E-32	47	18	hypothetical 103.0 KD protein in RAD10-PRS4 intergenic region [Saccharomyces cerevisiae]
21562	ENU05356	ANI61C1032 108-127 7:1..1791		727-748	NAP		g2673947	1501	272	2.00E-72	52	21	(U62931) multidrug resistance protein 1 [Aspergillus flavus]
21563	ENU05357	ANI61C949:5 22-47 42..1402		787-814	NAP		g1938424	293	94	3.00E-22	35	25	(U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases [Caenorhabditis elegans]
21564	ENU05358	ANI61C7361: 37-56 1583..2751		773-800	NAP		g1077257	282	111	8.00E-24	27	27	hypothetical protein YPL009c - yeast (Saccharomyces cerevisiae)
21565	ENU05359	ANI61C179:1 22-44 ..1794		755-780	NAP		g3288709	1767	377	e-104	63	19	[Saccharomyces cerevisiae] (AB010442) PMR1 [Penicillium digitatum]
21566	ENU05360	ANI61C9217: 31-56 135..888		707-733	NAP		g3183391	118	78	7.00E-14	29	97	hypothetical 27.3 KD protein C9G1.08C in chromosome I [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21567	ENU05361	ANI61C1120 5:9406..10373	22-45	786-805	NAP		g3702641	498	124	9.00E-28	41	86	(AL031825) similar to human 75k autoantigen [Schizosaccharomyces pombe]
21568	ENU05362	ANI61C1045 7:2607..1	34-55	728-747	NAP		g2342601	1392	174	8.00E-43	32	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21569	ENU05363	ANI61C8576: 3269..4146	23-41	802-829	NAP		g586858	223	81	1.00E-14	42	94	hypothetical 21.4 KD protein in DACA-SERS intergenic region [Bacillus subtilis]
21570	ENU05364	ANI61C258:1 399..1	46-65	773-792	NAP		g2132903	436	73	2.00E-12	24	33	probable membrane protein YOR165w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21571	ENU05365	ANI61C1091 7:2457..3107			NAP		g2144323	357	143	1.00E-33	46	14	xanthine dehydrogenase (EC 1.1.1.204) / xanthine oxidase (EC 1.1.3.22) - rat [
21572	ENU05366	ANI61S4059: 575..1	183-208	527-554	NAP		g1020096	596	252	1.00E-66	76	41	(D49832) stearyl-acyl carrier protein desaturase [Sesamum indicum]
21573	ENU05367	ANI61C1047 9:862..1762	63-82	806-825	NAP		g2506150	325	101	5.00E-21	35	88	Versicolorin reductase (VER-1) [Aspergillus parasiticus]
21574	ENU05368	ANI61C7245: 546..1367	22-41	596-618	NAP		g2493389	343	159	2.00E-38	35	53	probable sterigmatocystin biosynthesis P450 MONOOxygenase STCF (cytochrome P450 60A2) [Emericella nidulans]
21575	ENU05369	ANI61S3950: 1..807			NAP		g1572721	143	40	0.022	27	18	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
21576	ENU05370	ANI61C5314: 861..1576	22-44	666-693	NAP		g2245026	104	78	6.00E-14	35	100	(Z97341) hypothetical protein [Arabidopsis thaliana]
21577	ENU05371	ANI61C4173: 676..1	24-43	629-652	NAP		g2624405	163	98	6.00E-20	27	30	(X92655) gluconate [Schizosaccharomyces pombe]
21578	ENU05372	ANI61C1147 2:1..2042	22-46	669-688	NAP		g731806	1647	347	6.00E-95	63	23	probable calcium-transporting ATPase 7 [Saccharomyces cerevisiae]
21579	ENU05373	ANI61C5508: 855..1			NAP		g2511761	1185	458	e-128	86	34	(AF023156) carnitine acetyl transferase FacC [Emericella nidulans]
21580	ENU05374	ANI61C8155: 1..398	104-123	352-371	NAP		g1073534	165	75	2.00E-15	38	36	incB protein - Escherichia coli [Escherichia coli]
21581	ENU05375	ANI61S365:5 25..1	182-204	462-484	NAP		g131154	895	364	e-100	94	23	Photosystem I P700 chlorophyll A apoprotein A2 [Nicotiana tabacum]
21582	ENU05376	ANI61C4338: 667..1	38-57	550-573	NAP		g2239236	674	255	3.00E-67	66	16	(Z97211) probable involvement in ergosterol synthesis [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21583	ENU05377	ANI61C2934: 27-46 335..1201	748-768	NAP			g1345571	376	104	2.00E-40	47	25	(X80010) starch branching enzyme II [Pisum sativum]
21584	ENU05378	ANI61C403:1 71-90 ..2381	806-824	NAP			g2842700	1133	155	4.00E-56	41	15	hypothetical 192.5 KD protein C6G9.10C in chromosome I [Schizosaccharomyces pombe]
21585	ENU05379	ANI61C196:1 22-44 130..2491	764-790	NAP			g538067	809	227	7.00E-59	43	20	(M77661) putative pol polyprotein [Magnaporthe grisea]
21586	ENU05380	ANI61S822:6 215-234 60..160	414-433	NAP			g3913995	217	63	0.000000	39	19	ATP-dependent protease LA [Azospirillum brasilense]
21587	ENU05381	ANI61C2843: 72-91 533..1	409-428	NAP			g120609	238	93	9.00E-20			uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTase) [Saccharomyces cerevisiae]
21588	ENU05382	ANI61C9743: 26-45 2636..1864	731-752	NAP			g1730032	230	89	4.00E-17	32	99	2-deoxy-D-gluconate 3-dehydrogenase (2-keto-3-deoxygluconate oxidoreductase) [Escherichia coli]
21589	ENU05383	ANI61C1137: 1..333		NAP			g83727	544	218	1.00E-56	96	33	hypothetical nox3 protein - Emericella nidulans mitochondrion (SGC3) [Emericella nidulans]
21590	ENU05384	ANI61C3195: 40-59 68..609	468-487	NAP			g1168269	223	95	3.00E-22	38	53	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) [Aspergillus niger]"
21591	ENU05385	ANI61C966:6 37-62 8..566	390-417	NAP			g3288709	623	245	5.00E-66	78	11	(AB010442) PMR1 [Penicillium digitatum]
21592	ENU05386	ANI61C3723: 162-182 1163..494	621-648	NAP			g2493388	228	107	6.00E-27	39	49	probable aflatoxin biosynthesis P450 monooxygenase ORD1 (cytochrome P450 60A1) [Aspergillus parasiticus]
21593	ENU05387	ANI61C2144: 103-122 1..645	520-540	NAP			g1168269	189	103	1.00E-21	31	64	"arabinan endo-1,5-alpha-L-arabinosidase A precursor (endo-1,5-alpha-L-arabinanase A) (ABN A) [Aspergillus niger]"
21594	ENU05388	ANI61S1049: 1..735		NAP			g3153821	127	50	0.00001	23	27	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
21595	ENU05389	ANI61C6621: 26-45 621..1	497-520	NAP			g1709097	286	121	2.00E-29	37	50	mitochondrial respiratory function protein homolog [Schizosaccharomyces pombe]

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21596	ENU05390	ANI61C5111: 108-127 885..1782	108-127	654-673	NAP		g3560142	252	123	1.00E-27	36	29	(AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
21597	ENU05391	ANI61C7295: 22-45 928..1	22-45	800-827	NAP		g3139137	259	98	2.00E-26	41	22	(AF063864) essential nuclear protein Mcm3p [Schizosaccharomyces pombe]
21598	ENU05392	ANI61C5341: 22-49 1491..1	22-49	766-787	NAP		g3395584	868	273	8.00E-73	52	24	(AL031179) importin beta subunit [Schizosaccharomyces pombe]
21599	ENU05393	ANI61C6532: 118-137 1..494	118-137	448-473	NAP		g2388906	396	183	6.00E-46	57	54	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
21600	ENU05394	ANI61C986:1 ..646	113-139	476-503	NAP		g3023676	495	187	5.00E-49	48	31	probable translation initiation factor EIF-2B epsilon subunit (EIF-2B GDP-GTP exchange factor) [Schizosaccharomyces pombe]
21601	ENU05395	ANI61C7272: 54-73 4101..4547	54-73	372-399	NAP		g1723230	305	123	6.00E-28	45	58	hypothetical 28.5 KD protein C1D4.08 in chromosome I [Schizosaccharomyces pombe]
21602	ENU05396	ANI61C1104: 107-129 5:1..681	107-129	609-628	NAP		g3978466	567	215	2.00E-55	51	31	(AF086822) dihydroxyacetone synthase [Candida boidinii]
21603	ENU05397	ANI61C1017: 137-156 3:859..1	137-156	722-749	NAP		g1546072	249	118	6.00E-26	34	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
21604	ENU05398	ANI61C6174: 39-57 1218..1848	39-57	555-574	NAP		g731878	197	105	3.00E-22	29	25	AXL2 protein precursor (SRO4 protein) [Saccharomyces cerevisiae]
21605	ENU05399	ANI61S1311: 1..713			NAP		g190504	97	45	0.0004			(K03205) salivary proline-rich protein precursor [Homo sapiens]
21606	ENU05400	ANI61C9864: 54-73 455..2549	54-73	803-822	NAP		g1169823	368	33	3.1			regulatorY protein GAL4 [Saccharomyces cerevisiae]
21607	ENU05401	ANI61C1033: 24-41 0:1..4071	24-41	625-645	NAP		g2342601	2035	119	1.00E-42	43	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21608	ENU05402	ANI61C9342: 36-55 2795..2015	36-55	703-723	NAP		g4689350	727	298	3.00E-80			(AF132563) BcDNA.LD14392 [Drosophila melanogaster]
21609	ENU05403	ANI61C4212: 23-48 1230..2470	23-48	707-730	NAP		g585446	660	180	9.00E-45	33	45	Maltose permease MAL3T (maltose transport protein MAL3T) [Saccharomyces cerevisiae]
21610	ENU05404	ANI61C6072: 26-47 1..926	26-47	803-829	NAP		g3834343	1545	436	e-121	97	17	(X05204) arom polypeptide [Emericella nidulans]
21611	ENU05405	ANI61C3958: 126-149 1437..1101	126-149	287-306	NAP		g3219962	210	88	2.00E-17	46	33	putative mitochondrial carrier C17H9.08 [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21612	ENU05406	ANI61C937:1 .486	102-127	440-465	NAP		g4587971	772	277	2.00E-74	96	12	(AF082072) ABC transporter protein AtcC [Emericella nidulans]
21613	ENU05407	ANI61C2980: 56-77 586..1	527-546		NAP		g2462911	321	105	9.00E-32	42	28	(Z83832) UDP-glucose:sterol glucosyltransferase [Avena sativa]
21614	ENU05408	ANI61S3826: 146-165 1..664	507-524		NAP		g2327063	174	45	0.0005	22	23	(AF001305) protease 1 [Pneumocystis carinii f. sp. carinii]
21615	ENU05409	ANI61C9451: 41-61 4893..5790	625-649		NAP		g2076715	914	231	6.00E-91	76	51	(Y11322) SEC61 protein [Yarrowia lipolytica]
21616	ENU05410	ANI61C199:6 32..198			NAP		g539218	106	42	0.003	20	25	hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []
21617	ENU05411	ANI61C1002 25-52 5:4341..3161	807-829		NAP		g1586814	736	205	3.00E-52	48	63	glycerol-3-phosphate dehydrogenase [Schizosaccharomyces pombe]
21618	ENU05412	ANI61C3264: 22-45 1240..2489	766-783		NAP		g2414609	1146	354	4.00E-97	69	53	(Z99295) citrate lyase [Schizosaccharomyces pombe]
21619	ENU05413	ANI61C7483: 22-46 1457..719	691-718		NAP		g584766	537	173	2.00E-42	66	99	ADP-ribosylation factor-like protein 1 [Saccharomyces cerevisiae]
21620	ENU05414	ANI61C9092: 54-73 1..1170	765-782		NAP		g4581500	838	252	2.00E-66	50	47	(AL034352) putative oxalyl-CoA decarboxylase [Schizosaccharomyces pombe]
21621	ENU05415	ANI61C3548: 1816..1030			NAP		g126791	816	233	2.00E-73	88	42	MRNA maturase B11 (COBA intron protein) []
21622	ENU05416	ANI61C2656: 87-114 1..644	562-581		NAP		g731288	474	175	3.00E-43	43	27	hypothetical 87.5 KD protein in ACS1- GCV3 intergenic region [Saccharomyces cerevisiae]
21623	ENU05417	ANI61C1514: 1..1308			NAP		g2493965	1869	244	e-108	84	20	xanthine dehydrogenase (purine hydroxylase I) [Emericella nidulans]
21624	ENU05418	ANI61C305:2 22-44 799..1	723-749		NAP		g2459997	1553	144	3.00E-49	45	20	(AF012898) protein phosphatase Ssd1 homolog [Candida albicans]
21625	ENU05419	ANI61C9125: 22-44 1..431	378-397		NAP		g3646447	92	53	0.000001	35	69	"(AL031603) peroxisomal membrane protein pmp20p, Ahpc-TSA family protein [Schizosaccharomyces pombe]"
21626	ENU05420	ANI61C5598: 100-118 513..1	462-481		NAP		g1805262	292	131	3.00E-30	49	7	"(U75347) fatty acid synthase, beta subunit [Emericella nidulans]"
21627	ENU05421	ANI61C2807: 109-130 844..335	465-487		NAP		g4262222	299	105	2.00E-22	39	30	"(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]"
21628	ENU05422	ANI61C8964: 108-127 6972..6519	375-394		NAP		g2493143	335	72	3.00E-23	74	66	vacuolar ATP synthase 16 KD proteolipid subunit [Candida tropicalis]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21629	ENU05423	ANI61C9643: 34-53 1704..1	724-743	NAP			g1723575	515	83	2.00E-15			hypothetical protein C26F1.01 in chromosome I [Schizosaccharomyces pombe]
21630	ENU05424	ANI61C4970: 22-46 1460..125	795-822	NAP			g699196	560	141	8.00E-33	42	52	(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]
21631	ENU05425	ANI61C1099 22-49 1:1..1013	766-785	NAP			g3114719	588	196	1.00E-49	48	15	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
21632	ENU05426	ANI61C5574: 59-86 556..1	410-437	NAP			g3947855	244	67	2.00E-20	45	60	(AL034381) putative Golgi membrane protein [Schizosaccharomyces pombe]
21633	ENU05427	ANI61C9448: 22-48 4363..3345	806-829	NAP			g403179	367	114	3.00E-42	34	55	(L24441) kinesin light chain [Loligo pealii]
21634	ENU05428	ANI61S991:1..576		NAP			g3329623	165	57	0.000000	21	57	(AF078790) No definition line found [Caenorhabditis elegans]
21635	ENU05429	ANI61C9118: 25-47 1..1241	802-824	NAP			g3163927	1659	187	e-106	99	63	(AJ001157) hymA [Emericella nidulans]
21636	ENU05430	ANI61C1327: 804..1520		NAP			g3850093	228	124	7.00E-28	30	47	(AL033389) putative allantoin permease [Schizosaccharomyces pombe]
21637	ENU05431	ANI61C9639: 122-141 9628..9095	489-513	NAP			g2137308	66	42	0.003	23	47	G protein beta subunit like - mouse [Mus musculus]
21638	ENU05432	ANI61C1236: 36-60 3252..1	714-736	NAP			g1805261	1628	259	1.00E-68	48	15	"(U75347) fatty acid synthase, alpha subunit [Emericella nidulans]"
21639	ENU05433	ANI61C1001 79-98 1:314..1	275-294	NAP			g2612805	142	80	1.00E-14	37	21	(AL008883) glmA4 [Mycobacterium tuberculosis]
21640	ENU05434	ANI61C2961: 31-50 1431..2728	770-789	NAP			g2342601	645	152	4.00E-36	41	4	(X89442) peptidase synthetase [Metarhizium anisopliae]
21641	ENU05435	ANI61C1258: 53-75 1..467	398-417	NAP			g732372	90	50	0.000000	37	38	hypothetical oxidoreductase in PTA-ROCC intergenic region [Bacillus subtilis]
21642	ENU05436	ANI61C2743: 22-49 1213..1800	542-567	NAP			g2707191	124	36	0.22	38	53	(U94186) glutamine rich protein similar to glutenins [Glomerella cingulata]
21643	ENU05437	ANI61C3684: 28-55 1985..2821	784-811	NAP			g4502229	435	122	7.00E-40	53	100	ADP-ribosylation factor-like 2 [Homo sapiens]
21644	ENU05438	ANI61C9235: 106-128 1..631	561-580	NAP			g549795	384	161	4.00E-39			GTP-binding protein YPT51/VPS21 [Saccharomyces cerevisiae]

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21645	ENU05439	ANI61C6976: 23-45 768..1	23-45	638-657	NAP		g2706459	179	85	5.00E-16	26	75	(AL021046) hypothetical PHD finger domain protein [Schizosaccharomyces pombe]
21646	ENU05440	ANI61C8570: 6404..8745			NAP		g2408082	806	96	1.00E-27	37	28	(Z99167) putative helicase [Schizosaccharomyces pombe]
21647	ENU05441	ANI61C1109 4:1..910			NAP		g1709159	449	120	2.00E-49	42	39	putative methylenetetrahydrofolate reductase [Saccharomyces cerevisiae]
21648	ENU05442	ANI61C4289: 24-44 3522..2514	24-44	803-829	NAP		g238482	269	135	4.00E-31	36	73	"long chain alpha-hydroxy acid oxidase=FMN-dependent alpha-hydroxy acid-oxidizing enzyme [EC 1.1.3.15] [rats, kidney, Peptide, 352 aa]"
21649	ENU05443	ANI61C1038 27-49 3:2142..1	27-49	722-749	NAP		g3123262	1765	341	e-115	73	33	DNA repair protein RHP54 [Schizosaccharomyces pombe]
21650	ENU05444	ANI61C5267: 222-241 2181..1622	222-241	503-530	NAP		g2266427	229	99	1.00E-21	43	67	(Y13917) yngF [Bacillus subtilis]
21651	ENU05445	ANI61C1038 22-43 6:3257..1601	22-43	802-829	NAP		g3929362	648	92	4.00E-36	42	45	Pisatin demethylase (cytochrome P450 57A1) [Nectria haematococca mpVI]
21652	ENU05446	ANI61C7643: 22-45 1203..1	22-45	760-779	NAP		g3878874	351	124	9.00E-28	34	49	(Z67993) R03A10.3 [Caenorhabditis elegans]
21653	ENU05447	ANI61S4583: 405..1			NAP		g101813	585	141	1.00E-33	91	99	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - Emericella nidulans mitochondrion (SGC3) []
21654	ENU05448	ANI61C1798: 120-141 1..300	120-141	260-279	NAP		g3130015	75	50	0.000005	27	19	(AL023517) putative iron-sulfur binding oxidoreductase [Streptomyces coelicolor]
21655	ENU05449	ANI61C9805: 186-213 3895..3285	186-213	551-570	NAP		g547935	581	106	1.00E-47	72	41	26S protease regulator Y subunit 4 homolog (MTS2 protein) [Schizosaccharomyces pombe]
21656	ENU05450	ANI61C1029 72-91 6:2784..1	72-91	717-736	NAP		g2330803	2374	353	1.00E-96	58	19	(Z98560) hypothetical protein [Schizosaccharomyces pombe]
21657	ENU05451	ANI61C617:8 96-120 45..1	96-120	700-727	NAP		g1834342	1276	472	e-139	97	18	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
21658	ENU05452	ANI61C1022 27-48 9:876..8	27-48	810-829	NAP		g418426	594	233	1.00E-60	54	59	putative 60S ribosomal protein YEL050C [Saccharomyces cerevisiae]
21659	ENU05453	ANI61S4056: 358..1			NAP		g2117435	101	64	5.00E-10	27	33	probable membrane protein YDL246c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21660	ENU05454	ANI61C9713: 98-118 1..383	873..377	336-362	NAP	ANI61C9713: 98-118 1..383	g2995374	273	120	6.00E-27	53	56	(AL022245) hypothetical 21.5 kd protein [Schizosaccharomyces pombe]
21661	ENU05455	ANI61C6683: 110-129	451-471		NAP	ANI61C6683: 110-129	g1565203	151	92	2.00E-18	32	41	(D87894) chitinase [Rhizopus microsporus var. oligosporus]
21662	ENU05456	ANI61C1044 28-48 2:1202..1	686-710		NAP	ANI61C1044 28-48 2:1202..1	g2132863	600	238	4.00E-62	45	38	probable membrane protein YOR001w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21663	ENU05457	ANI61C5918: 42-61 863..1	765-784		NAP	ANI61C5918: 42-61 863..1	g416900	422	115	6.00E-25	42	46	probable aldehyde dehydrogenase [Pseudomonas sp.]
21664	ENU05458	ANI61S1481: 84..985			NAP	ANI61S1481: 84..985	g1334398	166	32	6.9	29	75	(X15081) MURF2 protein (AA 1-348) [Cnithidia fasciculata]
21665	ENU05459	ANI61C9981: 42-62 336..2698	724-749		NAP	ANI61C9981: 42-62 336..2698	g3023272	2834	458	e-128	76	28	alpha-glucosidase precursor (maltase) (AGL) [Aspergillus oryzae]
21666	ENU05460	ANI61C1118 31-50 3:742..1	616-641		NAP	ANI61C1118 31-50 3:742..1	g2308977	977	100	2.00E-52	99	11	(AB000125) chitin synthase [Emicella nidulans]
21667	ENU05461	ANI61C6359: 23-50 1003..1	803-829		NAP	ANI61C6359: 23-50 1003..1	g3021303	1362	359	e-127	100	10	(Y15996) acetyl-CoA carboxylase [Emicella nidulans]
21668	ENU05462	ANI61C540:1 104-123 100..1	722-741		NAP	ANI61C540:1 104-123 100..1	g3947883	562	215	4.00E-55	44	55	(AL034382) putative Trp-Asp repeat protein [Schizosaccharomyces pombe]
21669	ENU05463	ANI61C1212: 53-76 8468..8970	463-482		NAP	ANI61C1212: 53-76 8468..8970	g4505739	119	45	0.0003	26	100	prefoldin 1 [Homo sapiens]
21670	ENU05464	ANI61C739:6 33-54 90..1	626-650		NAP	ANI61C739:6 33-54 90..1	g4210899	68	54	0.000001	22	48	(AF045609) OrdL [Sinorhizobium meliloti]
21671	ENU05465	ANI61C3278: 108-131 825..1	701-724		NAP	ANI61C3278: 108-131 825..1	g3116113	454	212	3.00E-54	53	29	(AL023286) probable atp-dependent rna helicase [Schizosaccharomyces pombe]
21672	ENU05466	ANI61C2706: 65-84 1..385	317-343		NAP	ANI61C2706: 65-84 1..385	g1168403	183	81	4.00E-15	41	15	regulatory protein ALCR []
21673	ENU05467	ANI61C1097 90-114 1:1..430	370-389		NAP	ANI61C1097 90-114 1:1..430	g731385	147	68	4.00E-11	35	46	hypothetical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae]
21674	ENU05468	ANI61C558:3 26-46 433..5023	803-829		NAP	ANI61C558:3 26-46 433..5023	g522302	959	143	8.00E-45	39	23	(L35053) endonuclease [Magnaporthe grisea]
21675	ENU05469	ANI61C2976: 23-47 1157..228	805-826		NAP	ANI61C2976: 23-47 1157..228	g3868931	342	125	9.00E-37	39	66	(AB014769) glutamyl cyclase [Bothrops jararaca]
21676	ENU05470	ANI61C4309: 48-67 1..3926	762-781		NAP	ANI61C4309: 48-67 1..3926	g1654096	1237	78	4.00E-50	54	8	(Y09076) RAD3 [Schizosaccharomyces pombe]
21677	ENU05471	ANI61S1014: 335..931			NAP	ANI61S1014: 335..931	g3037018	170	33	0.011	27	92	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21678	ENU05472	ANI61S1690: 1..793			NAP		g786117	159	49	0.00003	17	52	(L41834) nuclear protein [Ensis minor]
21679	ENU05473	ANI61C1127: 63-90		551-575	NAP		g3006175	448	191	3.00E-48	53	33	(AL022305) putative transcription factor [Schizosaccharomyces pombe]
21680	ENU05474	ANI61C6111: 22-44		810-829	NAP		g117619	450	122	4.00E-27	34	41	Choline transport protein [Saccharomyces cerevisiae]
21681	ENU05475	ANI61C3619: 41-60		616-635	NAP		g4033411	533	222	3.00E-57	44	27	putative importin beta-2 subunit (karyopherin beta-2 subunit) (importin 104) (transportin) (TRN) [Schizosaccharomyces pombe]
21682	ENU05476	ANI61C4102: 112-131		321-343	NAP		g416963	402	171	2.00E-42			C-5 sterol desaturase [Saccharomyces cerevisiae]
21683	ENU05477	ANI61C1696: 70-89		625-644	NAP		g2501730	328	92	5.00E-18	29	75	Peroxisome assembly protein PER8 (peroxin-10) [Pichia angusta]
21684	ENU05478	ANI61C1763: 22-45		748-767	NAP		g4160581	644	227	2.00E-61	48	67	(AL035218) possible involvement in nuclear protein localisation [Schizosaccharomyces pombe]
21685	ENU05479	ANI61C7954: 24-44		807-826	NAP		g2833327	329	100	2.00E-20	33	54	Hexokinase [Schistosoma mansoni]
21686	ENU05480	ANI61C5158: 22-48		695-714	NAP		g140925	419	144	3.00E-37	37	99	hypothetical oxidoreductase in INLA 5'region (ORFA) [Listeria monocytogenes]
21687	ENU05481	ANI61C3007: 23-46		714-741	NAP		g1916927	769	286	2.00E-76	55	48	(U87965) putative G-protein [Mus musculus]
21688	ENU05482	ANI61C9656: 40-59		495-520	NAP		g2330829	307	123	8.00E-28	35	13	(Z98530) hypothetical protein [Schizosaccharomyces pombe]
21689	ENU05483	ANI61C4620: 183-203		528-548	NAP		g2780359	448	194	3.00E-49	49	34	(AB010110) ascorbate oxidase [Acremonium sp.]
21690	ENU05484	ANI61C7917: 28-55		724-749	NAP		g1077412	376	136	3.00E-31	42	22	hypothetical protein YLR187w - yeast (Saccharomyces cerevisiae)
21691	ENU05485	ANI61C1002 38-56		764-784	NAP		g2492658	1339	111	6.00E-24	27	14	[Saccharomyces cerevisiae] putative sterigmatocystin biosynthesis fatty acid synthase beta subunit [Emericella nidulans]
21692	ENU05486	ANI61C3789: 221-240		738-764	NAP		g4481951	583	243	8.00E-64	41	11	(AL035637) putative alpha-glucan synthase [Schizosaccharomyces pombe]
21693	ENU05487	ANI61C1946: 53-75		515-534	NAP		g113701	422	185	2.00E-46	46	38	Acetamidase [Emericella nidulans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21694	ENU05488	ANI61C2383: 22-45 558..1	22-45	438-457	NAP		g417567	136	84	8.00E-16			protein-tyrosine phosphatase 2 (PTPase 2) [Schizosaccharomyces pombe]
21695	ENU05489	ANI61C8573: 22-47 5799..4734	22-47	798-825	NAP		g4836505	296	64	0.000000 002			(AF124929) putative deacetylcephalosporin C acetyltransferase [Streptomyces clavuligerus]
21696	ENU05490	ANI61C1008 65-84 7:33..887	65-84	806-829	NAP		g559964	194	102	3.00E-21	40	74	(J05282) insect-type dehydrogenase [Pseudomonas cepacia]
21697	ENU05491	ANI61C513:1 102-129 ..729	102-129	617-640	NAP		g4557525	590	208	2.00E-53	54	44	dihydrolipoamide dehydrogenase precursor [Homo sapiens]
21698	ENU05492	ANI61C8488: 68-86 759..1235	68-86	435-453	NAP		g1723495	168	61	0.000000 007	39	23	hypothetical 63.2 KD protein C1F3.09 in chromosome I
21699	ENU05493	ANI61C9883: 25-44 1642..3323	25-44	661-687	NAP		g2326833	704	200	9.00E-51	38	33	[Schizosaccharomyces pombe] (Z73502) ORF YPL147w
21700	ENU05494	ANI61C1003: 23-49 2456..953	23-49	802-829	NAP		g1653242	559	70	2.00E-11	28	53	[Saccharomyces cerevisiae] (D90912) hypothetical protein [Synechocystis sp.]
21701	ENU05495	ANI61C855:1 128-147 ..585	128-147	408-428	NAP		g1749490	138	82	4.00E-15	31	69	"(D89141) similar to Saccharomyces cerevisiae hypothetical 27.6KD protein in chromosome VII, SWISS-PROT Accession Number P46948
21702	ENU05496	ANI61C1018 22-48 2:872..1324	22-48	365-392	NAP		g1437475	134	64	8.00E-10	30	38	[Schizosaccharomyces pombe]" (D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii]"
21703	ENU05497	ANI61C1003 51-70 9:1..557	51-70	515-534	NAP		g4049543	131	60	0.000000 01	33	39	(AL034564) putative protease; endopeptidase [Schizosaccharomyces pombe]
21704	ENU05498	ANI61C1042 22-43 1:156..1036	22-43	804-829	NAP		g2995339	199	91	8.00E-18	27	32	(AL022244) hypothetical protein [Schizosaccharomyces pombe]
21705	ENU05499	ANI61C1057 41-60 0:1..2533	41-60	788-807	NAP		g113314	4339	538	e-152	99	7	delta-(L-alpha-aminoadipyl)-L-cysteinyl-D-valine synthetase (ACV synthetase) (ACVS) [Emericella nidulans]
21706	ENU05500	ANI61C5776: 206-225 1424..697	206-225	681-701	NAP		g4826880	94	62	0.000000 004			oxidase (cytochrome c) assembly 1-like [Homo sapiens]
21707	ENU05501	ANI61C6356: 22-49 998..1	22-49	725-749	NAP		g3702200	717	252	2.00E-66	47	43	(AJ011686) methylenetetrahydrofolate reductase [Schizosaccharomyces pombe]

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21708	ENU05502	ANI61C4103: 42-61 987..1		795-814	NAP		g1346660	464	145	5.00E-34	37	58	Salicylate hydroxylase (salicylate 1-monooxygenase) [Pseudomonas putida]
21709	ENU05503	ANI61C1102: 25-46 1..1.483		390-413	NAP		g133356	258	115	2.00E-25			DNA-directed RNA polymerase III largest subunit (C160) [Saccharomyces cerevisiae]
21710	ENU05504	ANI61C9104: 45-64 4840..5692		762-781	NAP		g1173383	328	163	1.00E-39	37	66	SCN1 protein [Schizosaccharomyces pombe]
21711	ENU05505	ANI61C1296: 22-43 1318..1		728-749	NAP		g4500377	415	143	6.00E-38	36	47	(AL035439) putative NADPH cytochrome reductase [Schizosaccharomyces pombe]
21712	ENU05506	ANI61C6074: 1430..1			NAP		g1805262	2017	391	e-108	77	13	"(U75347) fatty acid synthase, beta subunit [Emmericella nidulans]"
21713	ENU05507	ANI61C9521: 37-57 1556..843		661-679	NAP		g2826168	235	106	2.00E-22	39	49	(AB010714) salicylate hydroxylase [Pseudomonas putida]
21714	ENU05508	ANI61C4432: 40-66 892..547		303-325	NAP		g1790870	191	90	7.00E-18	38	44	(U32622) toluenesulfonate zinc-independent alcohol dehydrogenase [Comamonas testosteroni]
21715	ENU05509	ANI61C7537: 23-42 1247..2374		740-765	NAP		g67385	736	154	7.00E-52	42	52	alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]
21716	ENU05510	ANI61C8019: 178-195 1..467		422-446	NAP		g113701	170	81	5.00E-15	28	28	Acetamidase [Emmericella nidulans]
21717	ENU05511	ANI61C3497: 61-80 1..606		388-413	NAP		g3122272	717	261	4.00E-69	70	37	Importin alpha subunit (karyopherin alpha subunit) (serine-rich RNA polymerase I suppressor protein) [Schizosaccharomyces pombe]
21718	ENU05512	ANI61C2554: 42-66 778..1		730-749	NAP		g2244898	254	132	3.00E-30	29	26	"(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]"
21719	ENU05513	ANI61C3764: 23-47 587..1		494-517	NAP		g730378	502	141	4.00E-48			Proteasome component C11 (macropain subunit C11) (proteinase YSCE subunit 11) (multicatalytic endopeptidase complex subunit C11) [Saccharomyces cerevisiae]
21720	ENU05514	ANI61C7285: 23-42 541..1312		729-751	NAP		g4105147	848	175	8.00E-69	68	100	"(AF043595) xyloglucan-specific endo-beta-1,4-glucanase precursor [Aspergillus aculeatus]"

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21721	ENU05515	ANI61C3973: 37-64 2126..1	713-737	NAP			g730881	1645	210	1.00E-87	64	33	"threonyl-tRNA synthetase, cytoplasmic (threonine--tRNA ligase) (THRRS) [Saccharomyces cerevisiae]" emopamil-binding protein - human [Homo sapiens]
21722	ENU05516	ANI61C3026: 22-49 589..1	392-419	NAP			g1362793	168	84	8.00E-16	35	69	(Z82021) cytochrome P450 [Agaricus bisporus]
21723	ENU05517	ANI61C4961: 121-140 1146..289	799-824	NAP			g1666269	261	83	2.00E-29	40	75	putative cysteine synthase (O-acetylserine sulphydrylase) (O-acetylserine (thiol)-lyase) (CSASE) [Schizosaccharomyces pombe]
21724	ENU05518	ANI61C7020: 23-42 9441..10859	762-780	NAP			g3219785	885	288	4.00E-77	58	65	hypothetical 119.9 KD protein C56F8.03 in chromosome I [Schizosaccharomyces pombe]
21725	ENU05519	ANI61S2922: 22-45 1..466	398-420	NAP			g1723436	610	221	2.00E-57	74	14	[Schizosaccharomyces pombe] glutamate dehydrogenase (NADP+) (EC 1.4.1.4) - Emericella nidulans [Emericella nidulans]
21726	ENU05520	ANI61C7675: 146-168 1..571	506-525	NAP			g538605	828	265	8.00E-88	86	41	(AL021837) hypothetical protein [Schizosaccharomyces pombe]
21727	ENU05521	ANI61C8815: 117-136 1..621	570-589	NAP			g2894300	256	90	2.00E-17	43	36	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
21728	ENU05522	ANI61C1562: 22-49 1003..1	727-747	NAP			g1834342	1513	512	e-144	96	18	DNA-directed RNA polymerase II 138 KD polypeptide (RNA polymerase II subunit 2) [Schizosaccharomyces pombe]
21729	ENU05523	ANI61C2594: 22-46 4976..1196	810-829	NAP			g401013	4308	384	e-120	73	21	(AF016850) alpha-mannosidase [Emericella nidulans]
21730	ENU05524	ANI61C8067: 62-81 1..1111	780-799	NAP			g2407176	1822	553	e-157	98	27	(AB020652) KIAA0845 protein [Homo sapiens]
21731	ENU05525	ANI61S775:1. 984		NAP			g4240179	204	39	0.029	26	29	(AF070937) gibberellin 3 beta-hydroxylase [Arabidopsis thaliana]
21732	ENU05526	ANI61C3351: 22-43 4228..4741	468-493	NAP			g3982753	86	70	1.00E-11	32	37	(X95073) Translin associated protein X [Homo sapiens]
21733	ENU05527	ANI61C1027 4:2881..3490	482-509	NAP			g1770576	154	51	8.00E-14	31	54	GTPase-activating protein [Schizosaccharomyces pombe]
21734	ENU05528	ANI61C5396: 24-43 1061..3386	805-829	NAP			g462156	1450	172	2.00E-42			triacylglycerol lipase (EC 3.1.1.3) I-yeast (Geotrichum candidum) (strain CBS 178.71) []
21735	ENU05529	ANI61C1028 0:2033..475	809-829	NAP			g2117970	341	71	1.00E-11			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21736	ENU05530	ANI61S302:1..41-60.500	41-60	438-457	NAP		g2245050	599	172	1.00E-63	72	6	(Z97342) resistance gene homolog [Arabidopsis thaliana]
21737	ENU05531	ANI61C6674: 31-50.321..887	31-50	487-507	NAP		g1906796	349	133	2.00E-32	44	70	(D85181) fungal sterol-C5-desaturase homolog [Homo sapiens]
21738	ENU05532	ANI61S1332: 1..724			NAP		g4759100	115	45	0.0004			"splicing factor, arginine/serine-rich 11 [Homo sapiens]"
21739	ENU05533	ANI61C2473: 48-67.1146..1	48-67	658-677	NAP		g226788	501	178	6.00E-44	37	14	erythrocyte ankyrin [Homo sapiens]
21740	ENU05534	ANI61C3738: 107-126.1..767	107-126	546-565	NAP		g2924771	126	95	6.00E-19	27	53	(AC002334) putative dimethylalanine monooxygenase [Arabidopsis thaliana]
21741	ENU05535	ANI61C3590: 32-51.3551..3072	32-51	427-448	NAP		g1749552	224	72	8.00E-28	33	35	"(D89172) similar to Saccharomyces cerevisiae transketolase 2(TK2), SWISS-PROT Accession Number P33315 [Schizosaccharomyces pombe]"
21742	ENU05536	ANI61C8544: 25-44.5873..7240	25-44	804-828	NAP		g2791647	454	110	8.00E-35	33	47	(AL021287) hypothetical protein Rv3049c [Mycobacterium tuberculosis]
21743	ENU05537	ANI61S3134: 551..1			NAP		g4558826	242	106	2.00E-22	42	41	(AF076691) aureobasidin-resistance protein; AurA [Emericella nidulans]
21744	ENU05538	ANI61C4840: 34-53.1..1000	34-53	770-797	NAP		g3914984	432	181	5.00E-45	39	7	Ferrichrome siderophore peptide synthetase [Ustilago maydis]
21745	ENU05539	ANI61C1550: 41-60.662..198	41-60	423-442	NAP		g4456808	130	52	0.000002	33	22	(AJ236923) ifc3 protein [Shewanella frigidimarina]
21746	ENU05540	ANI61C9547: 118-138.598..1	118-138	478-503	NAP		g3136025	165	104	4.00E-22	33	62	(AL023587) putative DNA repair protein [Schizosaccharomyces pombe]
21747	ENU05541	ANI61C5119: 734..1			NAP		g2909514	88	47	8.00E-10	34	48	(AL021932) hypothetical protein Rv0439c [Mycobacterium tuberculosis]
21748	ENU05542	ANI61C6475: 166-185.1..580	166-185	369-388	NAP		g121649	389	115	2.00E-42	52	14	GRR1 protein [Saccharomyces cerevisiae]
21749	ENU05543	ANI61C1044: 39-58.6:3192..6141	39-58	803-822	NAP		g1708621	930	231	1.00E-67	57	23	serine/threonine-protein kinase PMK1 [Schizosaccharomyces pombe]
21750	ENU05544	ANI61C6941: 62-81.2788..1663	62-81	804-829	NAP		g1171738	809	240	1.00E-62	48	52	nonsense-mediated mRNA decay protein 3 [Saccharomyces cerevisiae]
21751	ENU05545	ANI61C1198: 83-109.820..1	83-109	692-719	NAP		g1652509	1338	520	e-147	96	72	(D90906) poly(3-hydroxyalkanoate) synthase [Synechocystis sp.]
21752	ENU05546	ANI61C3622: 22-47.1..3057	22-47	803-829	NAP		g538067	1959	143	1.00E-33	38	16	(M77661) putative pol polyprotein [Magnaporthe grisea]

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21753	ENU05547	ANI61C7101: 38-57 1816..452	802-829		NAP		g82865	231	99	4.00E-20	28	23	regulatory protein LAC9 - yeast (Kluyveromyces marxianus var. lactis)
21754	ENU05548	ANI61C7111: 102-120 430..1	444-471		NAP		g731968	281	100	6.00E-21	47	43	hypothetical 35.9 KD protein in HXT8-CRT1 intergenic region [Saccharomyces cerevisiae]
21755	ENU05549	ANI61S878:1. 187-206 .614	408-431		NAP		g2494125	468	172	1.00E-48	48	44	(AC002376) Strong similarity to Cucumis acetyl-CoA acyltransferase (gb D70895). [Arabidopsis thaliana]
21756	ENU05550	ANI61C1047 22-41 2:1..1931	772-795		NAP		g2342601	1299	244	5.00E-64	45	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21757	ENU05551	ANI61C4808: 1813..2678			NAP		g3219304	463	131	3.00E-36	58	26	(AB009461) MUS38 [Neurospora crassa]
21758	ENU05552	ANI61C3351: 102-121 420..1	437-456		NAP		g2408015	200	73	2.00E-12	36	42	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
21759	ENU05553	ANI61C1065 24-51 5:1469..1894	391-410		NAP		g1363742	442	182	2.00E-45	61	51	probable membrane protein YLR243w - yeast [Saccharomyces cerevisiae]
21760	ENU05554	ANI61S835:1. .787			NAP		g3097062	168	72	4.00E-12	32	50	[Saccharomyces cerevisiae] (Y17145) putative betaine transporter [Eubacterium acidaminophilum]
21761	ENU05555	ANI61C3157: 111-130 1..418	370-397		NAP		g1172532	521	183	4.00E-46	72	39	Penicillolysin precursor (deuterolysin) [Penicillium citrinum]
21762	ENU05556	ANI61C18:1.. 767	716-736		NAP		g2330791	188	83	5.00E-20	32	35	(Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]
21763	ENU05557	ANI61C8494: 22-48 3514..3060	455-479		NAP		g1304227	167	91	5.00E-18	32	44	(D63781) Epoxide hydrolase [Glycine max]
21764	ENU05558	ANI61C9184: 219-237 3881..3418	382-401		NAP		g129766	316	69	8.00E-19			methylene-fatty-acyl-phospholipid synthase (unsaturated phospholipid methyltransferase) [Saccharomyces cerevisiae]
21765	ENU05559	ANI61C9126: 22-44 1..1738	765-789		NAP		g127736	1164	141	5.00E-33	28	18	Myosin-2 isoform [Saccharomyces cerevisiae]
21766	ENU05560	ANI61C9707: 22-48 4373..1505	785-811		NAP		g3646452	569	93	2.00E-18	28	19	(AL031603) BTB domain and Ankyrin repeat containing protein. [Schizosaccharomyces pombe]
21767	ENU05561	ANI61C6194: 60-85 1239..1	780-802		NAP		g1580818	1021	201	3.00E-98	71	34	(Z69254) alpha-galactosidase [Hypocrea jecorina]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21768	ENU05562	ANI61C9491: 22-43 2485..1871	22-43	570-594	NAP		g416922	381	100	9.00E-32	53	97	Deoxyuridine 5'-triphosphate nucleotidohydrolase (DUTPase) (DUTP pyrophosphatase) (P18) [Lycopersicon esculentum] (AL023534) hypothetical protein [Schizosaccharomyces pombe] (L11574) p68 RNA helicase [Schizosaccharomyces pombe] (AL023594) amino-acid permease [Schizosaccharomyces pombe] bimD protein - Emericella nidulans [Emericella nidulans] 112.3 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae] (AB008683) alpha2(I) collagen [Bos taurus] (U65409) Sla2p [Yarrowia lipolytica] (U70136) megakaryocyte stimulating factor; MSF [Homo sapiens] (AL035707) putative salicylate hydroxylase [Streptomyces coelicolor] Choline transport protein [Saccharomyces cerevisiae] Rhamnogalacturonase B precursor (rhamnogalacturonan lyase) (RGASE B) (RHG B) [Aspergillus aculeatus] hypothetical 86.2 KD protein C4G8.04 in chromosome I [Schizosaccharomyces pombe] Potential CAAX prenyl protease 1 (prenyl protein-specific endoprotease 1) (PPSEP 1) [Schizosaccharomyces pombe] 60S ribosomal protein L27A (L29) (CRP1) [Neurospora crassa]
21769	ENU05563	ANI61C1103: 118-143 1..548	118-143	508-527	NAP		g3130037	318	128	3.00E-29	45	45	
21770	ENU05564	ANI61C4837: 60-79 1..630	60-79	579-599	NAP		g173419	787	317	5.00E-86	70	38	
21771	ENU05565	ANI61C1966: 22-46 291..871	22-46	371-389	NAP		g3150139	181	61	2.00E-19	31	32	
21772	ENU05566	ANI61C5006: 22-45 1..2511	22-45	782-801	NAP		g1078626	3748	328	e-122	97	17	
21773	ENU05567	ANI61C6675: 181-202 913..257	181-202	609-636	NAP		g1723187	397	116	4.00E-44	46	20	
21774	ENU05568	ANI61S2718: 1..561			NAP		g2967448	102	40	0.013	31	13	
21775	ENU05569	ANI61C4825: 76-95 1..1071	76-95	728-747	NAP		g3978134	779	256	2.00E-67	52	26	
21776	ENU05570	ANI61S4379: 1..838			NAP		g1572721	254	50	0.00002	29	19	
21777	ENU05571	ANI61C7082: 22-41 397..1485	22-41	805-829	NAP		g4490992	219	61	3.00E-11	31	55	
21778	ENU05572	ANI61C5323: 23-42 1..1242	23-42	726-744	NAP		g117619	215	56	0.000000	32	38	
21779	ENU05573	ANI61C1707: 35-62 796..1929	35-62	718-744	NAP		g2494820	518	134	1.00E-45	46	48	
21780	ENU05574	ANI61C8098: 22-49 1..602	22-49	550-575	NAP		g1351596	221	98	7.00E-20	32	19	
21781	ENU05575	ANI61C1069 5:940..306			NAP		g1351689	297	85	1.00E-22	44	36	
21782	ENU05576	ANI61C1129 9:784..1565	23-42	720-739	NAP		g132845	598	137	1.00E-31	78	100	

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21783	ENU05577	ANI61C6931: 1..396			NAP		g1877482	65	53	0.000000 9	32	39	(U89271) short-chain alcohol dehydrogenase [Tripsacum dactyloides]
21784	ENU05578	ANI61C7468: 69-88 1494..592		776-795	NAP		g2213907	1272	438	e-122	81	93	(AF004837) putative vacuolar protein sorting homolog [Aspergillus fumigatus]
21785	ENU05579	ANI61S4063: 90-109 1..645		528-548	NAP		g3929649	463	167	6.00E-41	84	36	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]
21786	ENU05580	ANI61C1014 102-121 468-494 0..1..515			NAP		g1806234	120	63	6.00E-14	31	61	(Z84498) hypothetical protein Rv1928c [Mycobacterium tuberculosis]
21787	ENU05581	ANI61C1014 34-61 726-749 8..1981..1			NAP		g4185560	3327	571	e-162	99	12	(AF112473) PyrABCN [Emericella nidulans]
21788	ENU05582	ANI61C6750: 34-53 625-644 1851..2553			NAP		g4759160	252	69	5.00E-17			small nuclear ribonucleoprotein D3 polypeptide (18kD) [Homo sapiens]
21789	ENU05583	ANI61C4308: 117-136 584-603 1..641			NAP		g4262650	245	98	5.00E-26	38	31	(AF125969) contains similarity to GTP-binding proteins [Caenorhabditis elegans]
21790	ENU05584	ANI61C1086 43-64 395-422 1..1263..821			NAP		g3023956	101	69	2.00E-11	34	9	Vegetable incompatibility protein HET-E-1 [Podospora anserina]
21791	ENU05585	ANI61C9585: 22-48 502-521 637..1			NAP		g1175439	599	258	3.00E-68	57	22	hypothetical 107.1 KD protein C24H6.11C in chromosome I [Schizosaccharomyces pombe]
21792	ENU05586	ANI61C4157: 102-127 562-588 3992..3384			NAP		g1723926	248	130	1.00E-29	40	24	hypothetical 78.1 KD protein in TIP20-MRF1 intergenic region [Saccharomyces cerevisiae]
21793	ENU05587	ANI61C3304: 56-75 699-717 827..1			NAP		g729611	371	122	3.00E-27			Vanadate resistance protein GOG5/VRG4/VAN2 [Saccharomyces cerevisiae]
21794	ENU05588	ANI61C8348: 22-42 447-472 1658..2190			NAP		g3560147	263	122	2.00E-27	38	24	"(AL031534) ribosomal processing, ma binding, nucleolar protein [Schizosaccharomyces pombe]"
21795	ENU05589	ANI61C700:1 122-141 712-731 ..887			NAP		g1580818	1013	312	5.00E-90	64	37	(Z69254) alpha-galactosidase [Hypocrea jecorina]
21796	ENU05590	ANI61C6928: 25-52 680-707 775..1			NAP		g2342691	167	68	8.00E-14	29	33	(AC000106) F7G19.26 [Arabidopsis thaliana]
21797	ENU05591	ANI61C1019 27-46 563-582 2..1383..2024			NAP		g544013	143	64	7.00E-16	35	28	endochitinase precursor [Manduca sexta]

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21798	ENU05592	ANI61C1575: 22-49 535..1227	594-614	NAP	NAP	g3004863	530	214	4.00E-55	54	27	27	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis]"
21799	ENU05593	ANI61C9237: 64-83 1..2437	806-825	NAP	NAP	g1723929	1819	261	6.00E-69	51	17	17	hypothetical 171.5 KD helicase in NUT1-ARO2 intergenic region [Saccharomyces cerevisiae]
21800	ENU05594	ANI61C1582: 22-45 936..1	725-748	NAP	NAP	g2500542	247	105	4.00E-22	31	19	19	putative ATP-dependent RNA helicase YMR128W [Saccharomyces cerevisiae]
21801	ENU05595	ANI61C7665: 69-88 278..1134	761-780	NAP	NAP	g586486	508	178	4.00E-44	37	41	41	hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region [Saccharomyces cerevisiae]
21802	ENU05596	ANI61C2116: 1..964		NAP	NAP	g2105430	687	216	2.00E-55	48	24	24	(U97079) U5-116kD [Mus musculus]
21803	ENU05597	ANI61C3561: 95-114 1230..568	609-630	NAP	NAP	g1437475	194	105	4.00E-22	38	57	57	"(D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii]"
21804	ENU05598	ANI61C5947: 58..1380		NAP	NAP	g2924313	552	120	1.00E-26	34	25	25	"(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum]"
21805	ENU05599	ANI61C431:8 32..1303	452-471	NAP	NAP	g4803936	138	80	1.00E-17				(AC006264) unknown protein [Arabidopsis thaliana]
21806	ENU05600	ANI61C374:1 ..592	380-399	NAP	NAP	g2117310	70	39	0.032	22	63	63	(Z95620) hypothetical protein [Schizosaccharomyces pombe]
21807	ENU05601	ANI61C6452: 27-54 22..1176	805-829	NAP	NAP	g3810847	471	192	3.00E-48	37	41	41	(AL032684) zinc finger protein [Schizosaccharomyces pombe]
21808	ENU05602	ANI61C9353: 72-90 1..539	496-518	NAP	NAP	g3851530	195	59	4.00E-17	41	32	32	(AF065435) nodulin [Glycine max]
21809	ENU05603	ANI61C32:1.. 573	522-549	NAP	NAP	g3929312	145	51	0.000007	34	7	7	(AF100426) fimbriae-associated protein Fap1 [Streptococcus parasanguis]
21810	ENU05604	ANI61S133:1. 407		NAP	NAP	g2804455	274	79	3.00E-23	47	10	10	(AF043699) similar to a human orf (GB:D13642) and human UV-damaged DNA binding factor (GB:U32986) in separate non-overlapping regions [Caenorhabditis elegans]
21811	ENU05605	ANI61S618:5 73..1	212-232	456-476	NAP	g136600	886	360	3.00E-99				transcriptional regulator Y protein TYRR [Escherichia coli]
21812	ENU05606	ANI61C1008 6:1023..1	70-89	727-746	NAP	g1708982	810	143	4.00E-62	53	54	54	Ammonium transporter MEP3 [Saccharomyces cerevisiae]
21813	ENU05607	ANI61S2221: 308..1		NAP	NAP	g1708463	131	78	5.00E-14	28	37	37	IAA-amino acid hydrolase [Arabidopsis thaliana]

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21814	ENU05608	ANI61C6473: 22-46 898..1	727-749	NAP		g2408055	154	59	3.00E-11	28	35		(Z99164) hypothetical protein [Schizosaccharomyces pombe]
21815	ENU05609	ANI61C9354: 2362..1688		NAP		g2565275	361	146	1.00E-34	68	81		(AF023611) Dim1p homolog [Homo sapiens]
21816	ENU05610	ANI61C5269: 37-58 1428..2452	712-730	NAP		g550452	766	154	1.00E-65	57	39		"(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]"
21817	ENU05611	ANI61C8323: 164-183 1803..1397	361-386	NAP		g1084969	612	190	2.00E-58	94	23		sulfate adenylyltransferase (EC 2.7.7.4) - Emericella nidulans [Emericella nidulans]
21818	ENU05612	ANI61C3094: 98-125 1..854	805-829	NAP		g1652620	459	96	1.00E-47	55	45		(D90907) pyridine nucleotide transhydrogenase beta subunit [Synecocystis sp.]
21819	ENU05613	ANI61C2132: 22-41 2849..3354	425-446	NAP		g3878950	252	80	2.00E-23	44	98		(Z32683) similar to RNA binding domain; cDNA EST EMBL:D74891 comes from this gene; cDNA EST EMBL:D75208 comes from this gene; cDNA EST EMBL:D72347 comes from this gene; cDNA EST EMBL:D75552 comes from this gene; cDNA EST EMBL:D... []
21820	ENU05614	ANI61C8419: 28-46 1..2319	805-827	NAP		g4539278	553	81	2.00E-15				(AL049498) hypothetical rho1 gdp-gtp exchange protein [Schizosaccharomyces pombe]
21821	ENU05615	ANI61S2455: 33-52 462..1	413-438	NAP		g586361	127	62	0.000000	30	32		hypothetical 51.7 KD protein in CTPI-SUL2 intergenic region [Saccharomyces cerevisiae]
21822	ENU05616	ANI61S2364: 61-87 426..1	427-452	NAP		g290544	730	234	1.00E-74	98	72		(L10328) o197 [Escherichia coli]
21823	ENU05617	ANI61C1143 22-47 5:351..1918	803-829	NAP		g2239185	1187	253	1.00E-66	45	45		(Z97208) hypothetical protein [Schizosaccharomyces pombe]
21824	ENU05618	ANI61S4374: 1..547		NAP		g91210	117	61	0.000000	30	73		proline-rich protein MP3 - mouse (fragment) []
21825	ENU05619	ANI61C6626: 22-48 1..2628	780-807	NAP		g2507347	1984	48	0.00008	56	14		DNA-directed RNA polymerase II largest subunit (B220) [Saccharomyces cerevisiae]
21826	ENU05620	ANI61C7149: 28-50 320..3018	770-790	NAP		g3417430	359	90	1.00E-17	31	30		(AL031262) hypothetical protein [Schizosaccharomyces pombe]

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21827	ENU05621	ANI61C2318: 1..1219	88-108	368-390	NAP		g2267008	195	112	4.00E-24	32	10	(AF006827) adenylate cyclase [Magnaporthe grisea]
21828	ENU05622	ANI61C1143 6:8708..8293	88-108	368-390	NAP		g3978466	217	103	5.00E-22	42	19	(AF086822) dihydroxyacetone synthase [Candida boidinii]
21829	ENU05623	ANI61C1455: 122-143 491-510 537..1	122-143	491-510	NAP		g3738169	289	92	3.00E-18	41	41	(AL031856) putative mitochondrial protein import protein - DNAI protein [Schizosaccharomyces pombe]
21830	ENU05624	ANI61C1069: 23-46 4657..5330	23-46	590-612	NAP		g2967835	661	214	1.00E-61	66	54	(AF052061) polygalacturonase [Ophiostoma novo-ulmi]
21831	ENU05625	ANI61C4657: 3615..6275			NAP		g1703456	1367	231	3.00E-68	53	23	Cation-transporting ATPase PAT1 [Dictyostelium discoideum]
21832	ENU05626	ANI61C1004 51-71 5:1472..2568	51-71	641-660	NAP		g1352388	377	173	1.00E-42	38	32	"Lanosterol synthase (oxidosqualene--lanosterol cyclase) (2,3-epoxysqualene-lanosterol cyclase) (OSC) [Rattus rattus]"
21833	ENU05627	ANI61C1035: 118-138 381-400 1..422	118-138	381-400	NAP		g4150918	263	109	7.00E-24	51	55	(Z50728) putative acetyltransferase [Schizosaccharomyces pombe]
21834	ENU05628	ANI61C9868: 29-49 805-824 1119..1	29-49	805-824	NAP		g2133268	1616	457	e-128	91	32	DNA-binding protein amdA - Emericella nidulans [Emericella nidulans]
21835	ENU05629	ANI61C9030: 22-45 720-739 939..1	22-45	720-739	NAP		g2414578	251	68	2.00E-20	39	60	(Z99292) hypothetical protein [Schizosaccharomyces pombe]
21836	ENU05630	ANI61C1122 7:1..469	116-142	423-448	NAP		g84160	98	64	8.00E-10	32	40	fragmin - slime mold (Physarum polycephalum) (fragments) []
21837	ENU05631	ANI61C1120 5:381..1235	25-48	808-828	NAP		g2133293	814	154	8.00E-84	72	98	pectate lyase (EC 4.2.2.2) C - fungus (Fusarium solani) []
21838	ENU05632	ANI61C5075: 22-49 1762..3768	22-49	720-745	NAP		g3738146	528	75	7.00E-13			"(AL031852) putative cleavage and polyadenylation specificity factor subunit, yeast pre-mRNA 3'-end processing factor CF II homolog [Schizosaccharomyces pombe]"
21839	ENU05633	ANI61C5115: 60-85 1287..495	60-85	727-750	NAP		g4539609	279	101	9.00E-21	39	100	(AL049522) WD repeat protein [Schizosaccharomyces pombe]
21840	ENU05634	ANI61C7762: 24-45 584..1	24-45	540-561	NAP		g2408044	695	287	5.00E-77	65	24	(Z99164) hypothetical protein [Schizosaccharomyces pombe]
21841	ENU05635	ANI61C6096: 202-223 368..710	202-223	454-479	NAP		g3242653	155	55	0.000000	45	26	[Schizosaccharomyces pombe] (AB015510) FIL-CMCase [Aspergillus aculeatus]

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21842	ENU05636	ANI61C3621: 22-45 68..522	22-45	419-440	NAP		g2664240	476	199	1.00E-50	59	47	(AL009227) electron transfer flavoprotein alpha-subunit precursor [Schizosaccharomyces pombe]
21843	ENU05637	ANI61C2544: 22-43 1437..346	22-43	805-824	NAP		g3287941	210	101	5.00E-21	45	26	hypothetical 44.3 KD protein C25H2.15 in chromosome II [Schizosaccharomyces pombe]
21844	ENU05638	ANI61C6113: 44-71 1..1001	44-71	806-826	NAP		g1723894	806	238	6.00E-67	56	40	hypothetical GTP-binding protein in SEH1-PRP20 intergenic region [Saccharomyces cerevisiae]
21845	ENU05639	ANI61C2481: 22-42 5870..6582	22-42	581-600	NAP		g1787798	482	206	2.00E-52	43	91	(AE000249) putative enzyme [Escherichia coli]
21846	ENU05640	ANI61C8019: 38-58 3034..2507	38-58	485-507	NAP		g4106657	466	189	2.00E-47	57	46	(AL035064) activator 1 subunit (replication factor subunit) [Schizosaccharomyces pombe]
21847	ENU05641	ANI61C8982: 22-42 632..2053	22-42	762-780	NAP		g1346661	337	74	1.00E-12	47	10	NAM9 protein precursor [Saccharomyces cerevisiae]
21848	ENU05642	ANI61C1079 24-45 5:122..1260	24-45	775-794	NAP		g3133101	832	215	1.00E-64	56	72	(AL023554) conserved hypothetical protein. [Schizosaccharomyces pombe]
21849	ENU05643	ANI61C1061 43-62 6:1506..1	43-62	709-734	NAP		g2133034	385	151	7.00E-36	26	45	probable membrane protein YPR156c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21850	ENU05644	ANI61C1799: 40-67 590..22	40-67	464-489	NAP		g1524045	165	63	1.00E-12	39	37	(X96943) Geranylgeranylpyrophosphate Synthetase [Gibberella fujikuroi]
21851	ENU05645	ANI61S1588: 339..1098			NAP		g340613	112	41	0.007	25	68	(L07545) A 'c' was inserted after nt 369 (=nt 10459 in genomic sequence (M10126)) to correct -1 frameshift probably due to gel compression [Leishmania tarentolae]
21852	ENU05646	ANI61C1255: 22-45 521..1	22-45	297-321	NAP		g4867840	299	137	5.00E-32			(Z99091) putative exocyst complex component [Schizosaccharomyces pombe]
21853	ENU05647	ANI61C1043 119-136 3:288..1	119-136	453-479	NAP		g732284	99	52	0.000002	30	31	hypothetical 29.7 KD protein in RPL1-CPDB intergenic region (F286) [Escherichia coli]
21854	ENU05648	ANI61S2100: 81-100 482..1	81-100	388-405	NAP		g4539261	197	61	0.000000	42	66	(AL049495) putative synaptobrevin-type protein transport protein [Schizosaccharomyces pombe]

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21855	ENU05649	ANI61C5945: 221-240 1471..1055	221-240	373-396	NAP		g549725	90	50	5.00E-12			NADH-cytochrome B5 reductase precursor (P34/P32) [Saccharomyces cerevisiae]
21856	ENU05650	ANI61C1909: 71-92 1..546	71-92	504-525	NAP		g1827509	203	100	9.00E-21	33	24	(D83993) similar to pir: S52731 (23.4% identity in 273 aa overlap) [Schizosaccharomyces pombe]
21857	ENU05651	ANI61C1058 62-81 2:545..1	62-81	470-487	NAP		g2494052	138	57	0.000000 09	41	45	purine nucleoside phosphorylase (inosine phosphorylase) (PNP) [Bacillus stearothermophilus]
21858	ENU05652	ANI61C5888: 22-44 2738..1935	22-44	731-750	NAP		g3121767	72	49	0.00003	31	99	ARP2/3 complex 16 KD subunit (P16-ARC) [Homo sapiens]
21859	ENU05653	ANI61C7786: 222-244 1..843	222-244	795-822	NAP		g2131466	205	55	5.00E-10	30	35	hypothetical protein YDR398w - yeast (Saccharomyces cerevisiae)
21860	ENU05654	ANI61S4503: 777..1			NAP		g2330699	356	104	2.00E-28	39	53	[Saccharomyces cerevisiae] (Z98529) putative rna polymerase ii transcription factor b subunit
21861	ENU05655	ANI61C4705: 22-40 1..1508	22-40	792-811	NAP		g2133259	2209	485	e-136	77	48	[Schizosaccharomyces pombe] tannase (EC 3.1.1.20) - Aspergillus oryzae [Aspergillus oryzae]
21862	ENU05656	ANI61C1133: 22-47 6948..6145	22-47	756-783	NAP		g953179	189	85	4.00E-16	28	98	(Z37980) ORF14 [Escherichia coli]
21863	ENU05657	ANI61C1141: 1350..2351			NAP		g3411013	412	97	1.00E-37	46	27	(AF000232) protein mannosyltransferase 1 [Candida albicans]
21864	ENU05658	ANI61C1090 35-57 1:1..499	35-57	436-460	NAP		g1351919	184	103	9.00E-22	37	24	Copper amine oxidase precursor (MAOXI) [Arthrobacter sp.]
21865	ENU05659	ANI61S1834: 1..670			NAP		g4757882	344	167	8.00E-41			bystin-like [Homo sapiens]
21866	ENU05660	ANI61C6155: 107-130 3059..2512	107-130	504-527	NAP		g731763	318	109	8.00E-32	47	27	hypothetical 66.7 KD protein in EGD2-SUN1 intergenic region [Saccharomyces cerevisiae]
21867	ENU05661	ANI61C1098 22-42 4:966..1386	22-42	421-440	NAP		g134039	337	71	7.00E-16	64	100	Small nuclear ribonucleoprotein SM D1 (SNRNP core protein D1) (SM-D1) (SM-D autoantigen) [Mus musculus]
21868	ENU05662	ANI61C7744: 24-44 8689..8335	24-44	313-334	NAP		g2959371	315	95	2.00E-29	63	18	(AL022117) asparagine synthetase [Schizosaccharomyces pombe]
21869	ENU05663	ANI61C6500: 41-60 632..1	41-60	495-512	NAP		g1020413	120	57	8.00E-11	32	33	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]

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21870	ENU05664	ANI61C6591: 34-52 1145..2267		808-827	NAP		g2132842	532	237	6.00E-62	51	87	probable membrane protein YOL077c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21871	ENU05665	ANI61C1112 0-799..1	117-136	670-697	NAP		g3859709	344	176	2.00E-43	37	44	(AL033497) nucleotide phosphodiesterase [Candida albicans]
21872	ENU05666	ANI61C1213: 43-62 864..2097	43-62	715-742	NAP		g2133333	215	50	9.00E-17	27	37	probable reverse transcriptase Mars1 (clone pCGC20) - fungus (Ascobolus immersus) (fragment) [Ascobolus immersus]
21873	ENU05667	ANI61C1105 7-851..1	50-69	755-781	NAP		g2293196	397	176	2.00E-43	34	65	(AF008220) YteT [Bacillus subtilis]
21874	ENU05668	ANI61C3631: 1..879			NAP		g2244802	208	101	5.00E-21	33	16	(Z97336) retrovirus-related polypeptide homolog [Arabidopsis thaliana]
21875	ENU05669	ANI61C4225: 71-90 2092..1609	71-90	437-456	NAP		g1653493	403	153	2.00E-40	63	66	(D90914) hypothetical protein [Synecocystis sp.]
21876	ENU05670	ANI61C8023: 40-66 1..1115	40-66	738-765	NAP		g2342601	463	168	6.00E-41	33	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21877	ENU05671	ANI61C6494: 22-44 2741..1905	22-44	787-813	NAP		g1078030	294	79	2.00E-30	42	94	hypothetical protein YOR021c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21878	ENU05672	ANI61C246:7 23-44 71..1	23-44	723-750	NAP		g585856	415	164	8.00E-40	43	60	mitochondrial carrier protein RIM2 [Saccharomyces cerevisiae]
21879	ENU05673	ANI61C6363: 23-42 1281..1	23-42	718-737	NAP		g2133259	1584	467	e-131	78	48	tannase (EC 3.1.1.20) - Aspergillus oryzae [Aspergillus oryzae]
21880	ENU05674	ANI61C7430: 36-62 3318..2845	36-62	430-453	NAP		g2967691	453	108	5.00E-46	68	45	"(AF038596) beta-1,3-glucanase [Aspergillus fumigatus]"
21881	ENU05675	ANI61S1195: 1..938			NAP		g283032	192	64	0.000000	27	78	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]
21882	ENU05676	ANI61C8808: 22-48 3399..4931	22-48	809-829	NAP		g3925779	177	42	0.005	24	48	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21883	ENU05677	ANI61C9823: 2105..910			NAP		g2492940	1531	200	e-127	95	77	Arginase [Emmericella nidulans]
21884	ENU05678	ANI61C8194: 24-48 1..2472	24-48	779-801	NAP		g742559	1859	200	1.00E-50	41	10	TOR2(DRR2) gene [Saccharomyces cerevisiae]
21885	ENU05679	ANI61C3566: 48-67 2989..526	48-67	805-829	NAP		g3661614	1985	242	2.00E-63	50	35	(AF093142) aconitase [Aspergillus terreus]

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21886	ENU05680	ANI61C1218: 28-55 1644..1003	28-55	601-621	NAP		g1339938	428	185	2.00E-46	51	25	(D50430) glycerol-3-phosphate dehydrogenase [Mus musculus]
21887	ENU05681	ANI61S2611: 27-46 1..368	27-46	244-261	NAP		g2500536	283	79	5.00E-26	50	20	probable ATP-dependent RNA helicase DBP9 [Saccharomyces cerevisiae]
21888	ENU05682	ANI61C6784: 61-80 3114..2036	61-80	792-811	NAP		g1168351	198	49	0.00005	29	76	Alcohol dehydrogenase (ADH) [Bacillus stearothermophilus]
21889	ENU05683	ANI61S1114: 1..857			NAP		g2947228	184	39	0.054	25	16	(AF031886) erythrocyte binding protein [Plasmodium yoelii yoelii]
21890	ENU05684	ANI61C4594: 22-41 1477..1	22-41	804-824	NAP		g1730777	1772	367	e-109	72	26	hypothetical 119.3 KD protein in FPR1-TOM22 intergenic region [Saccharomyces cerevisiae]
21891	ENU05685	ANI61C4238: 102-125 1..382	102-125	335-361	NAP		g2132680	166	81	3.00E-15	40	3	probable membrane protein YLR087c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
21892	ENU05686	ANI61C1030 22-49 2:484..2062	22-49	801-828	NAP		g4007758	666	139	2.00E-32	53	55	(AL034433) conserved hypothetical protein [Schizosaccharomyces pombe]
21893	ENU05687	ANI61C6614: 23-44 1648..159	23-44	784-803	NAP		g2104465	627	87	2.00E-16			(Z95397) unknown [Schizosaccharomyces pombe]
21894	ENU05688	ANI61C1031 22-47 5:1412..1739	22-47	457-479	NAP		g1353100	176	91	4.00E-18	43	45	hypothetical 24.6 KD protein in MCK1-RP55B intergenic region [Saccharomyces cerevisiae]
21895	ENU05689	ANI61C6286: 27-46 706..1089	27-46	450-477	NAP		g730430	239	116	1.00E-25	49	22	delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) [Saccharomyces cerevisiae]
21896	ENU05690	ANI61C2164: 22-41 68..1154	22-41	772-799	NAP		g67385	673	114	4.00E-66	45	55	alpha-amylase (EC 3.2.1.1) 3 precursor - Aspergillus oryzae [Aspergillus oryzae]
21897	ENU05691	ANI61C1147 22-47 3:1..1399	22-47	792-819	NAP		g2493479	1035	201	4.00E-51	36	21	"dynactin, 150 KD isoform (150 KD dynein-associated polypeptide) (DP-150) (DAP-150) (P150-glued) [Neurospora crassa]"
21898	ENU05692	ANI61C8423: 22-49 2330..1180	22-49	768-787	NAP		g1914859	814	282	2.00E-75	56	75	(Y10542) homologous to 40kD subunit of RNA-polymerase I and III [Cricetulus griseus]
21899	ENU05693	ANI61C7771: 4940..5391			NAP		g2498970	539	202	6.00E-52	78	54	putative sterigmatocystin biosynthesis protein STCQ [Emmericella nidulans]
21900	ENU05694	ANI61S4257: 1..892			NAP		g4138732	194	55	0.000000	23	71	(Y17332) proline-rich protein [Zea mays]

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21901	ENU05695	ANI61C7923: 23-44 605..1	23-44	456-483	NAP		g1805251	184	61	0.000000	31	36	(U58946) transposase [Aspergillus awamori]
21902	ENU05696	ANI61C8749: 122-141 1..490	122-141	352-371	NAP		g3135990	365	157	4.00E-38	53	27	(AL023589) membrane transporter [Schizosaccharomyces pombe]
21903	ENU05697	ANI61C1122 35-62 4:8141..7555	35-62	537-564	NAP		g3925779	138	68	7.00E-11	32	27	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21904	ENU05698	ANI61C1033 23-42 9:1..929	23-42	786-813	NAP		g4583552	1171	327	e-103	74	75	"(AJ012316) arabinogalactan endo-1,4-beta-galactosidase [Aspergillus tubingensis]"
21905	ENU05699	ANI61C7064: 22-43 2540..1	22-43	720-743	NAP		g113314	4318	575	e-163	98	7	delta-(L-alpha-aminoadipyl)-L-cysteiny-D-valine synthetase (ACV synthetase) (ACVS) [Emicella nidulans]
21906	ENU05700	ANI61C9189: 75-98 1466..994	75-98	426-449	NAP		g1174433	146	78	4.00E-14	42	40	Signal recognition particle 19 KD protein homolog [Yarrowia lipolytica]
21907	ENU05701	ANI61C3701: 27-46 1333..1834	27-46	446-465	NAP		g3219956	168	44	0.0008	45	98	hypothetical protein C57A7.01 in chromosome I [Schizosaccharomyces pombe]
21908	ENU05702	ANI61C1058 36-63 8:1..587	36-63	531-556	NAP		g4160397	299	134	5.00E-31	39	53	(AL035210) halotolerance protein [Schizosaccharomyces pombe]
21909	ENU05703	ANI61C7089: 22-42 1104..733	22-42	320-347	NAP		g2501094	96	52	0.000001	24	48	Syntaxin 6 [Rattus norvegicus]
21910	ENU05704	ANI61C908:1 22-42 778..2087	22-42	363-382	NAP		g1085674	414	135	2.00E-31	75	79	blasticidin S deaminase - Aspergillus terreus [Aspergillus terreus]
21911	ENU05705	ANI61C1584: 92-111 4315..4806	92-111	391-413	NAP		g730406	106	46	0.0001	36	84	Profilin []
21912	ENU05706	ANI61C5748: 46-65 1..512	46-65	448-467	NAP		g3293344	150	77	7.00E-14	29	16	(AF059614) transportin; TRN [Xenopus laevis]
21913	ENU05707	ANI61C8295: 22-48 1..1117	22-48	775-802	NAP		g2342601	436	92	8.00E-30	31	5	(X89442) peptide synthetase [Metarhizium anisopliae]
21914	ENU05708	ANI61C9805: 24-45 2499..885	24-45	805-829	NAP		g4512702	567	121	7.00E-27	30	41	(AC006569) hypothetical protein [Arabidopsis thaliana]
21915	ENU05709	ANI61C8160: 1976..3983			NAP		g3885836	414	69	8.00E-19	30	34	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
21916	ENU05710	ANI61C1615: 74-93 734..1516	74-93	660-679	NAP		g4499837	276	88	2.00E-27	30	57	(AJ011963) dimethyl-allyl-tryptophan synthase [Claviceps purpurea]
21917	ENU05711	ANI61C6187: 35-54 1366..1	35-54	722-749	NAP		g585965	1184	371	e-102	67	37	Vesicular-fusion protein SEC18 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21918	ENU05712	ANI61C8757: 121-140 1724..1329	121-140	332-351	NAP		g5560215	203	77	5.00E-14	36	28	"(AL031536) yeast reduced viability upon starvation protein rvs167 homolog, SH3 domain containing [Schizosaccharomyces pombe]"
21919	ENU05713	ANI61C1104 24-43 1..1964	24-43	802-821	NAP		g4176546	284	50	0.00003			(AL035259) possible RanBP7-importin-beta-Cse1p superfamily [Schizosaccharomyces pombe]
21920	ENU05714	ANI61C2656: 2041..2589			NAP		g1360017	117	70	1.00E-11	45	62	(X96767) U1 snRNP-specific protein C [Mus musculus]
21921	ENU05715	ANI61S3099: 1..507			NAP		g82698	220	36	0.14	36	49	hydroxyproline-rich glycoprotein precursor - maize [Zea mays]
21922	ENU05716	ANI61C8555: 42-66 1..331	42-66	284-310	NAP		g1707880	154	84	3.00E-16			aminomethyltransferase precursor (glycine cleavage system T protein) [Saccharomyces cerevisiae]
21923	ENU05717	ANI61S1431: 1..746			NAP		g2246532	170	46	0.0002	21	22	"(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]"
21924	ENU05718	ANI61C3881: 96-115 801..1	96-115	681-698	NAP		g1351710	415	203	2.00E-51	43	18	hypothetical 138.8 KD protein C11D3.14C in chromosome I [Schizosaccharomyces pombe]
21925	ENU05719	ANI61S2549: 73..645			NAP		g91206	110	60	0.000000	29	96	proline-rich protein - mouse (fragment) [Mus musculus]
21926	ENU05720	ANI61C4525: 102-127 662..1	102-127	605-631	NAP		g550429	592	233	9.00E-61	53	20	(X81635) RAD26 [Saccharomyces cerevisiae]
21927	ENU05721	ANI61C5834: 64-83 446..2035	64-83	785-804	NAP		g731689	1635	491	e-138	61	7	hypothetical 433.2 KD protein in HXT5-NRK1 intergenic region [Saccharomyces cerevisiae]
21928	ENU05722	ANI61C117:1 23-45 ..1174	23-45	722-749	NAP		g4185560	1852	534	e-151	97	12	[Saccharomyces cerevisiae] (AF112473) PyrABCN [Emericella nidulans]
21929	ENU05723	ANI61C9675: 24-43 2354..1	24-43	786-813	NAP		g3913155	1105	101	5.00E-21	30	22	beta-galactosidase (lactase) [Arthrobacter sp.]
21930	ENU05724	ANI61C4143: 86-111 1..818	86-111	693-712	NAP		g3650382	253	115	5.00E-25	30	26	(AL031740) putative calcium dependant serine-threonine protein kinase. [Schizosaccharomyces pombe]
21931	ENU05725	ANI61C1116 22-43 3:21..1728	22-43	807-829	NAP		g3184098	1329	173	1.00E-85	64	50	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]
21932	ENU05726	ANI61C4422: 26-45 1470..2350	26-45	720-739	NAP		g3150262	167	58	2.00E-14	31	65	(AL023634) hypothetical protein [Schizosaccharomyces pombe]

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21933	ENU05727	ANI61C2800: 94-113 1..622		420-445	NAP		g4539248	339	132	2.00E-30	48	41	(AL049489) conserved hypothetical TBC domain-containing protein [Schizosaccharomyces pombe]
21934	ENU05728	ANI61C8872: 22-43 1796..1		760-780	NAP		g2909783	511	187	1.00E-46	33	17	(AF020289) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]
21935	ENU05729	ANI61C1089 33-54 5:988..1		728-747	NAP		g3850091	199	73	1.00E-15	30	46	(AL033389) putative aminotransferase [Schizosaccharomyces pombe]
21936	ENU05730	ANI61C283:5 22-44 38..1		460-479	NAP		g2494072	256	127	4.00E-29	42	32	delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) [Agaricus bisporus]
21937	ENU05731	ANI61C9677: 202-223 2179..1317		804-829	NAP		g1352666	963	333	7.00E-98	82	83	"serine/threonine protein phosphatase PP2A-beta, catalytic subunit [Sus scrofa]"
21938	ENU05732	ANI61C9325: 22-43 1274..1		729-749	NAP		g1345625	423	61	5.00E-14			Biotin--protein ligase (biotin apo-protein ligase) (biotin-- [Saccharomyces cerevisiae]
21939	ENU05733	ANI61C7546: 47-66 1592..1		784-807	NAP		g3929399	1088	185	1.00E-67	46	51	proline-specific permease (proline transport protein) [Emmericella nidulans]
21940	ENU05734	ANI61C9605: 27-46 1026..1		723-742	NAP		g729007	358	56	3.00E-14	43	49	CAJ1 protein [Saccharomyces cerevisiae]
21941	ENU05735	ANI61C601:6 63-84 37..268		294-314	NAP		g284071	175	83	7.00E-16	41	56	dTMP kinase (EC 2.7.4.9) - human [Homo sapiens]
21942	ENU05736	ANI61S645:1. 39-62 .416		287-314	NAP		g2988417	43	46	0.0002	39	43	(U97573) peptidyl-prolyl cis-trans isomerase [Treponema pallidum]
21943	ENU05737	ANI61C678:8 27-46 17..1		729-747	NAP		g3914273	448	96	1.00E-34	49	65	Pectate lyase precursor [Emmericella nidulans]
21944	ENU05738	ANI61C8413: 30-49 1813..109		797-816	NAP		g125348	1078	76	3.00E-19	33	31	KEX1 protease precursor [Kluyveromyces lactis]
21945	ENU05739	ANI61C2004: 54-73 38..1648		740-759	NAP		g3088571	1869	485	e-136	86	47	(AF059523) heat shock protein 60 [Paracoccidioides brasiliensis]
21946	ENU05740	ANI61S2337: 1..550			NAP		g4325349	302	86	1.00E-24	52	43	(AF128394) contains similarity to Petunia PTTA' (GB:AF009516) [Arabidopsis thaliana]
21947	ENU05741	ANI61C5790: 104-121 1..434		361-381	NAP		g4210461	260	87	8.00E-17	49	20	(D11392) UV-endonuclease [Neurospora crassa]
21948	ENU05742	ANI61C4064: 204-227 1..828		788-807	NAP		g2342601	301	116	2.00E-32	35	4	(X89442) peptide synthetase [Metarhizium anisopliae]

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21949	ENU05743	ANI61C8506: 1137..1	22-44	720-746	NAP		g3136057	427	153	1.00E-36	38	58	(AL023592) actin-like protein [Schizosaccharomyces pombe]
21950	ENU05744	ANI61C7482: 22-47 915..1	22-47	752-771	NAP		g2388975	336	67	2.00E-25	44	69	(Z98980) phosphotyrosyl phosphatase activator [Schizosaccharomyces pombe]
21951	ENU05745	ANI61S2702: 1..589			NAP		g3157413	113	44	0.0008	26	25	(AJ001386) catalase [Claviceps purpurea]
21952	ENU05746	ANI61C1084 2:460..1			NAP		g731385	112	46	0.0002	33	49	hypothetical 33.7 KD protein in ISC10 3'region [Saccharomyces cerevisiae]
21953	ENU05747	ANI61C1087 22-45 2:1270..2819	22-45	806-825	NAP		g4176751	2421	443	e-130	92	43	(AF052391) heat shock protein 70 [Trichophyton rubrum]
21954	ENU05748	ANI61C5200: 22-42 1338..2380	22-42	780-799	NAP		g2388905	459	188	5.00E-47	48	59	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
21955	ENU05749	ANI61C21:96 37-56 5..1	37-56	728-749	NAP		g2132242	1203	379	e-104	81	56	hypothetical protein YPL235w - yeast [Saccharomyces cerevisiae]
21956	ENU05750	ANI61C7402: 22-44 1..1593	22-44	720-740	NAP		g83711	2184	314	e-135	94	34	"nitrite reductase (NADH) (EC 1.6.6.4), short form - Emericella nidulans []"
21957	ENU05751	ANI61C7966: 25-44 3747..3004	25-44	700-723	NAP		g2133240	196	50	8.00E-11	34	100	immunoreactive protein - Coccidioides immitis [Coccidioides immitis]
21958	ENU05752	ANI61C8144: 22-48 449..2530	22-48	715-734	NAP		g4106690	946	104	6.00E-48	42	36	(AL035065) putative urea active transporter [Schizosaccharomyces pombe]
21959	ENU05753	ANI61C9575: 22-41 4706..8327	22-41	749-769	NAP		g729456	2757	227	7.00E-59	44	21	exonuclease II (exo II) (P140) [Schizosaccharomyces pombe]
21960	ENU05754	ANI61C7591: 22-43 1015..1722	22-43	666-687	NAP		g3136047	385	169	1.00E-41	44	53	(AL023592) rna binding protein [Schizosaccharomyces pombe]
21961	ENU05755	ANI61C1370: 533..4			NAP		g1363749	151	89	2.00E-17	38	35	probable membrane protein YLR418c - yeast [Saccharomyces cerevisiae]
21962	ENU05756	ANI61C7297: 22-44 576..1016	22-44	375-402	NAP		g3402004	273	94	6.00E-19	58	78	[Saccharomyces cerevisiae] Mbp1 From Saccharomyces Cerevisiae []
21963	ENU05757	ANI61C543:1 34-61 ..1874	34-61	628-651	NAP		g3913210	1707	324	e-117	73	29	putative ATP-dependent RNA helicase CDC28 [Schizosaccharomyces pombe]
21964	ENU05758	ANI61C811:1 22-43 ..1042	22-43	756-781	NAP		g3417424	410	180	1.00E-44	38	10	(AL031261) putative transport protein [Schizosaccharomyces pombe]
21965	ENU05759	ANI61C1079 28-48 5:2047..3775	28-48	806-828	NAP		g626178	834	204	6.00E-52	42	28	HIR1 protein - yeast [Saccharomyces cerevisiae] [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21966	ENU05760	ANI61C9078: 4178..1	22-45	668-694	NAP		g2492604	2285	157	9.00E-38	37	15	multidrug resistance protein CDR2 [Candida albicans]
21967	ENU05761	ANI61C1585: 1..491	42-68	448-470	NAP		g2144467	267	120	6.00E-27	43	22	alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkoae) []
21968	ENU05762	ANI61C1208: 6485..8096	22-44	810-829	NAP		g2894293	295	101	7.00E-21	24	54	(AL021837) hypothetical protein [Schizosaccharomyces pombe]
21969	ENU05763	ANI61C7167: 2698..3037	41-64	424-444	NAP		g3861442	255	83	1.00E-15	50	41	(AL033505) hypothetical protein SC1E6.19c [Streptomyces coelicolor]
21970	ENU05764	ANI61C3924: 920..1	22-46	719-738	NAP		g2656007	782	183	1.00E-77	50	44	(Z99126) putative dna helicases. [Schizosaccharomyces pombe]
21971	ENU05765	ANI61C4789: 1..431	118-137	307-326	NAP		g585856	211	96	2.00E-19	40	32	mitochondrial carrier protein RIM2 [Saccharomyces cerevisiae]
21972	ENU05766	ANI61C1039 8:2329..550	35-54	803-829	NAP		g3925779	282	55	4.00E-10	23	45	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
21973	ENU05767	ANI61S3461: 1..322	28-53	272-298	NAP		g3024528	435	176	5.00E-44	80	50	RAS-related protein RAB2BV [Beta vulgaris]
21974	ENU05768	ANI61C4749: 2526..4013	22-42	780-801	NAP		g4505651	524	54	8.00E-12	36	59	"phosphate cytidylyltransferase 2, ethanolamine [Homo sapiens]"
21975	ENU05769	ANI61C1954: 710..1			NAP		g1723566	534	196	3.00E-56	52	43	putative glucosyltransferase C17C9.07 [Schizosaccharomyces pombe]
21976	ENU05770	ANI61C4887: 1785..1260	105-123	396-415	NAP		g2244629	415	120	6.00E-32	58	94	(Z82019) septin [Agaricus bisporus]
21977	ENU05771	ANI61C1913: 2849..1	31-50	806-829	NAP		g2492657	4813	558	e-158	98	18	putative sterigmatocystin biosynthesis fatty acid synthase alpha subunit [Emmericella nidulans]
21978	ENU05772	ANI61S1288: 1..553	47-70	350-369	NAP		g442927	133	54	0.000000	33	28	Glucose Oxidase (E.C.1.1.3.4) []
21979	ENU05773	ANI61C7281: 1246..1	28-46	716-735	NAP		g4539286	849	213	9.00E-55	44	47	(AL049498) activator of Hsp70 and Hsp90 chaperones
21980	ENU05774	ANI61C243:3 559..4334	23-50	692-712	NAP		g2132889	228	163	1.00E-39	32	22	[Schizosaccharomyces pombe] probable membrane protein YOR109w - yeast (Saccharomyces cerevisiae)
21981	ENU05775	ANI61C7816: 1..546	46-65	498-525	NAP		g4502887	198	94	9.00E-19	40	28	[Saccharomyces cerevisiae] "ceroid-lipofuscinosis, neuronal 2, late infantile [Jansky-Bielschowsky disease] [Homo sapiens]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
21982	ENU05776	ANI61C525:7 159..2357	22-47	799-818	NAP		g1077042	3207	122	9.00E-54	61	14	cadmium resistance protein YCF1 - yeast [Saccharomyces cerevisiae]
21983	ENU05777	ANI61C1705: 22-45 5289..6343		802-829	NAP		g586361	733	153	2.00E-36	45	54	[Saccharomyces cerevisiae] hypothetical 51.7 KD protein in CTP1-SUL2 intergenic region
21984	ENU05778	ANI61S4513: 35-57 377..75		317-334	NAP		g136232	115	68	6.00E-11	30	18	[Saccharomyces cerevisiae] "potassium transport protein, low-affinity [Saccharomyces cerevisiae]"
21985	ENU05779	ANI61C1142 48-67 7:3870..2510		784-803	NAP		g171124	411	101	7.00E-21	25	48	(M20319) aminotriazole resistance protein [Saccharomyces cerevisiae]
21986	ENU05780	ANI61C9782: 49-70 505..1		446-465	NAP		g2131764	128	73	9.00E-13	33	40	hypothetical protein YLR063w - yeast [Saccharomyces cerevisiae]
21987	ENU05781	ANI61C5615: 1694..1			NAP		g3021303	2839	531	e-150	95	12	[Saccharomyces cerevisiae] (Y15996) acetyl-CoA carboxylase [Emicella nidulans]
21988	ENU05782	ANI61C8296: 24-43 2054..49		804-828	NAP		g3417424	791	39	0.000000			(AL031261) putative transport protein [Schizosaccharomyces pombe]
21989	ENU05783	ANI61C8795: 22-47 1067..1		807-826	NAP		g1175379	428	151	7.00E-36	30	36	hypothetical 88.2 KD protein C2F7.18C in chromosome I []
21990	ENU05784	ANI61C3558: 1569..916			NAP		g1709924	491	214	5.00E-55	50	15	phosphoribosylformylglycinamide synthase (FGAM synthase) (formylglycinamide ribotide amidotransferase) (FGARAT) [Saccharomyces cerevisiae]
21991	ENU05785	ANI61C4915: 39-58 2886..1		711-731	NAP		g2104421	1647	139	2.00E-32	34	23	[Z95395] putative taf; transcription factor TFIIID complex component [Schizosaccharomyces pombe]
21992	ENU05786	ANI61C2010: 29-50 1..1196		720-744	NAP		g2493011	732	254	8.00E-67	47	17	probable calcium-transporting ATPase 8 [Saccharomyces cerevisiae]
21993	ENU05787	ANI61C6994: 27-49 783..1393		563-590	NAP		g4584493	174	101	4.00E-21	35	58	(AL049587) putative transcriptional regulator [Streptomyces coelicolor]
21994	ENU05788	ANI61S1378: 41-59 1..327		219-239	NAP		g243989	474	192	5.00E-49	90	5	"sodium channel alpha subunit [human, skeletal muscle, Peptide, 1836 aa]"
21995	ENU05789	ANI61C385:4 30-57 068..4993		808-829	NAP		g1723752	242	91	2.00E-23	35	99	hypothetical 25.6 KD protein in SM11-PHO81 intergenic region [Saccharomyces cerevisiae]
21996	ENU05790	ANI61C4905: 1..545			NAP		g4107343	436	175	1.00E-43	62	23	(AJ224922) ATP citrate lyase [Sordaria macrospora]

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21997	ENU05791	ANI61C3311: 1.428	103-124	388-407	NAP		g4680709	322	97	3.00E-32	30	33	(AF132969) CGL-35 protein [Homo sapiens]
21998	ENU05792	ANI61C7708: 22-43	802-821		NAP		g3005587	326	33	2.3	30	33	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]
21999	ENU05793	ANI61C8066: 41-60	715-742		NAP		g1710663	1183	111	5.00E-69	58	22	putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) [Schizosaccharomyces pombe]
22000	ENU05794	ANI61C8202: 34-53	724-743		NAP		g553118	646	132	2.00E-54	38	53	(M27081) alkane hydroxylating cytochrome P-450 [Candida maltosa]
22001	ENU05795	ANI61C1091 1852..3080	43-62	780-799	NAP		g3024986	265	142	3.00E-33			hypothetical zinc-type alcohol dehydrogenase-like protein in AHPF-RNK intergenic region [Escherichia coli]
22002	ENU05796	ANI61C3211: 22-43	714-733		NAP		g3183035	1559	159	1.00E-41	41	27	importin beta-1 subunit (karyopherin beta-1 subunit) (importin 95) [Schizosaccharomyces pombe]
22003	ENU05797	ANI61C1633: 22-46	442-463		NAP		g1706221	211	62	3.00E-17	43	100	cytochrome B5 [Saccharomyces cerevisiae]
22004	ENU05798	ANI61C8674: 102-125	263-290		NAP		g409547	127	66	8.00E-11	33	19	(L07492) sugar transport protein [Saccharomyces cerevisiae]
22005	ENU05799	ANI61C1106 1.311	500-527		NAP		g2131422	184	83	2.00E-15	34	38	hypothetical protein YDR306c - yeast (Saccharomyces cerevisiae)
22006	ENU05800	ANI61C5670: 7:1..558			NAP		g83726	714	280	4.00E-75	97	42	[Saccharomyces cerevisiae] hypothetical nox2 protein - Emericella nidulans mitochondrion (SGC3) [Emericella nidulans]
22007	ENU05801	ANI61C7760: 29-56	306-331		NAP		g631806	233	104	3.00E-22	41	26	"beta2-chimerin, cerebellar - rat (fragment) []"
22008	ENU05802	ANI61C6462: 29-54	804-824		NAP		g1805251	924	159	6.00E-60	44	50	(U58946) transposase [Aspergillus awamori]
22009	ENU05803	ANI61C7280: 43-62	793-820		NAP		g2956768	400	122	4.00E-27	37	71	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22010	ENU05804	ANI61C4923: 39-60	804-823		NAP		g2507441	1041	135	4.00E-80	63	53	"T-complex protein 1, delta subunit (TCP-1-delta) (CCT-delta) [Saccharomyces cerevisiae]"
22011	ENU05805	ANI61C2862: 105-124	580-602		NAP		g4158188	147	74	1.00E-12	37	49	(AL035206) putative alcohol dehydrogenase [Streptomyces coelicolor]

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22012	ENU05806	ANI61C1129 9:1..489	119-146	443-465	NAP		g2408082	398	169	8.00E-42	52	17	(Z99167) putative helicase [Schizosaccharomyces pombe]
22013	ENU05807	ANI61C9103: 32-50 3387..4733	776-802		NAP		g2673955	1266	357	6.00E-98	87	32	(U62935) multidrug resistance protein 2 [Aspergillus fumigatus]
22014	ENU05808	ANI61C6282: 112-135 853..3152	711-738		NAP		g731262	220	125	4.00E-28	24	23	vacuolar protein sorting-associated protein VPS8 [Saccharomyces cerevisiae]
22015	ENU05809	ANI61C6738: 57-76 5525..4473	810-829		NAP		g731597	300	94	2.00E-18	31	70	hypothetical 36.1 KD protein in YLF2-PRPS4 intergenic region [Saccharomyces cerevisiae]
22016	ENU05810	ANI61C1129 23-47 8:981..1	788-808		NAP		g1352980	778	300	1.00E-85	64	24	ATP-dependent RNA helicase DOB1 (MRNA transport regulator MTR4) [Saccharomyces cerevisiae]
22017	ENU05811	ANI61C850:7 22-46 95..1499	601-626		NAP		g1706480	212	87	8.00E-18	34	19	DNA ligase I (polydeoxyribonucleotide synthase (ATP)) [Xenopus laevis]
22018	ENU05812	ANI61C3634: 22-45 1..3043	804-823		NAP		g1546072	1105	147	8.00E-35	32	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22019	ENU05813	ANI61C5125: 22-47 2091..4346	770-797		NAP		g731899	947	280	6.00E-75	49	18	putative membrane glycoprotein in SDL1 5' region precursor [Saccharomyces cerevisiae]
22020	ENU05814	ANI61C5245: 31-58 2005..1327	604-631		NAP		g3738163	347	94	1.00E-18	38	99	(AL031856) putative DNA J domain containing protein [Schizosaccharomyces pombe]
22021	ENU05815	ANI61S1152: 118-145 572..1	505-524		NAP		g2498506	271	85	3.00E-25	42	26	proline-rich protein LAS17 [Saccharomyces cerevisiae]
22022	ENU05816	ANI61C1643: 78-97 1060..1	720-740		NAP		g1261823	684	229	1.00E-59	48	25	(L77234) glycine rich protein [Neurospora crassa]
22023	ENU05817	ANI61S3304: 52-71 1..522	285-312		NAP		g4097158	162	94	6.00E-19	37	7	(U46488) NrpS [Proteus mirabilis]
22024	ENU05818	ANI61C8526: 4623..5636			NAP		g3004634	798	113	6.00E-53	59	81	(U96385) GATA transcription factor [Penicillium chrysogenum]
22025	ENU05819	ANI61C4111: 27-46 1..1163	807-826		NAP		g1076802	134	38	0.12			extensin-like protein - maize [Zea mays]
22026	ENU05820	ANI61C3323: 32-59 483..1136	603-622		NAP		g401335	526	114	1.00E-42	77	99	vacuolar ATP synthase 16 KD proteolipid subunit [Neurospora crassa]
22027	ENU05821	ANI61C1225: 190-211 594..1	528-548		NAP		g131768	217	87	1.00E-16	41	31	quinate permease (quinate transporter) [Emericella nidulans]

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22028	ENU05822	ANI61C9283: 325..1	107-126	444-463	NAP		g871830	113	39	0.017	35	60	(D30747) mini-collagen [Acropora donei]
22029	ENU05823	ANI61C2431: 77-96	719-737		NAP		g3319315	977	290	7.00E-78	54	33	(AF074951) cellobiose dehydrogenase [Thielavia heterothallica]
22030	ENU05824	ANI61C1512: 26-53	796-819		NAP		g3929395	2040	328	4.00E-89	67	32	vacuolar ATP synthase 98 KD subunit (vacuolar ATPase 98 KD subunit) [Neurospora crassa]
22031	ENU05825	ANI61C5551: 22-48	785-809		NAP		g2120666	724	241	6.00E-63	42	48	"2,4-chlorocatechol 1,2-dioxygenase (EC 1.13.11.-) ttdB - Pseudomonas putida [Pseudomonas putida]"
22032	ENU05826	ANI61S2863: 36-55	436-454		NAP		g2950458	228	88	3.00E-17	29	19	(AL022071) hypothetical protein [Schizosaccharomyces pombe]
22033	ENU05827	ANI61C5475: 22-46	792-812		NAP		g4102990	9834	578	e-164	98	12	(AF019254) DNA polymerase epsilon homolog [Emmericella nidulans]
22034	ENU05828	ANI61C4262: 22-47	806-828		NAP		g2808662	854	122	3.00E-27	30	33	(AJ223459) PrnA protein [Emmericella nidulans]
22035	ENU05829	ANI61C2219: 42-65	613-638		NAP		g4557619	1082	161	1.00E-87	66	35	"glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme) [Homo sapiens]"
22036	ENU05830	ANI61C8552: 10563..10144			NAP		g460627	92	53	0.000000	31	15	(U07187) Mlh1p [Saccharomyces cerevisiae]
22037	ENU05831	ANI61C1129	112-136	548-567	NAP		g2130466	719	290	7.00E-78	62	51	protein kinase (EC 2.7.1.37) - fission yeast [Schizosaccharomyces pombe]
22038	ENU05832	ANI61C4402: 27-48	622-649		NAP		g1351711	1351	311	4.00E-88	66	18	[Schizosaccharomyces pombe] hypothetical 143.7 KD protein C11D3.15 in chromosome I
22039	ENU05833	ANI61C1064	22-41	671-695	NAP		g1176045	1101	286	2.00E-76	50	35	[Schizosaccharomyces pombe] hypothetical 89.4 KD TRP-ASP repeats containing protein in PMT6-PCT1 intergenic region [Saccharomyces cerevisiae]
22040	ENU05834	ANI61C1036	77-96	564-590	NAP		g4539186	228	102	7.00E-23	45	51	(AL049485) probable zinc-binding alcohol dehydrogenase [Streptomyces coelicolor]
22041	ENU05835	ANI61C9204: 59-78	805-829		NAP		g2598192	900	375	e-103	67	30	(AF027687) beta glucosidase homolog [Cochliobolus heterostrophus]
22042	ENU05836	ANI61C5575: 402..1			NAP		g1705828	123	63	0.000000	32	16	chitin synthase 2 (chitin-UDP acetyl-glucosaminyl transferase 2) [Emmericella nidulans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22043	ENU05837	ANI61C1100: 5121..4463	22-49	616-638	NAP		g3695005	256	115	3.00E-25	37	49	(AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2 [Zea mays]
22044	ENU05838	ANI61S37:44 72-91	72-91	391-414	NAP		g1881271	210	78	4.00E-14	35	73	"(AB001488) function unknown, similar product in H. influenzae and synecocystis. [Bacillus subtilis]"
22045	ENU05839	ANI61C1145 102-124 455-479	102-124	455-479	NAP		g4760360	115	76	1.00E-13			"(AL035213) predicted using hexExon; L3291.5, Hypothetical protein, len: 300 aa [Leishmania major]"
22046	ENU05840	ANI61S2374: 66-86	66-86	257-276	NAP		g78837	517	205	9.00E-53	95	38	rimK protein - Escherichia coli [Escherichia coli]
22047	ENU05841	ANI61C7587: 33-55 2400..2047	33-55	294-313	NAP		g729611	286	126	5.00E-29			Vanadate resistance protein GOG5/VRG4/VAN2 [Saccharomyces cerevisiae]
22048	ENU05842	ANI61C8467: 189-208 367-388	189-208	367-388	NAP		g3059184	147	79	1.00E-14	33	40	(D88014) homologous to HpcE (HHDD isomerase) protein of E. coli [Rhodococcus erythropolis]
22049	ENU05843	ANI61C5479: 28-49 1309..2279	28-49	802-829	NAP		g114878	379	147	8.00E-35	37	83	carboxyvinyl-carboxyphosphonate phosphorylmutase (carboxyphosphonoenolpyruvate phosphonmutase) (CPEP phosphonmutase) [Streptomyces hygroscopicus]
22050	ENU05844	ANI61C1078 102-124 354-373	102-124	354-373	NAP		g4249409	111	63	4.00E-13	33	29	(AC006072) putative sugar transporter [Arabidopsis thaliana]
22051	ENU05845	ANI61C4441: 22-48 1..966	22-48	633-659	NAP		g1351645	869	324	6.00E-88	55	52	hypothetical amino-acid permease C8A4.11 [Schizosaccharomyces pombe]
22052	ENU05846	ANI61C1134 32-51 6:1472..493	32-51	774-793	NAP		g4583351	380	185	4.00E-46	41	47	(AF114167) lysosomal pepstatin insensitive protease [Canis familiaris]
22053	ENU05847	ANI61C2920: 37-56 387..1499	37-56	790-809	NAP		g1723578	381	102	1.00E-38	36	78	probable oxidoreductase C26F1.07 in chromosome I [Schizosaccharomyces pombe]
22054	ENU05848	ANI61C7166: 50-69 267..653	50-69	442-461	NAP		g3136036	128	82	2.00E-15	40	48	(AL023590) Glutathione S-transferase [Schizosaccharomyces pombe]
22055	ENU05849	ANI61C2437: 25-52 2082..3715	25-52	725-751	NAP		g728771	639	101	5.00E-42	52	23	Alanine/arginine aminopeptidase [Saccharomyces cerevisiae]
22056	ENU05850	ANI61C6823: 53-73 576..1	53-73	530-549	NAP		g2226425	124	71	6.00E-12	25	10	(Z97204) hypothetical protein [Schizosaccharomyces pombe]

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22057	ENU05851	ANI61C2391: 1406..2123	24-43	634-654	NAP		g3800835	205	67	2.00E-10	38	4	(AF079138) type I polyketide synthase [Streptomyces venezuelae]
22058	ENU05852	ANI61S1602: 316..1	49-76	439-466	NAP		g2909465	110	56	0.000000	34	38	PikAII [Streptomyces venezuelae]
22059	ENU05853	ANI61C7205: 49-71	414-434		NAP		g1588283	463	205	2.00E-52	61	12	(AL021930) hypothetical protein Rv0276 [Mycobacterium tuberculosis]
22060	ENU05854	ANI61C4233: 101-126	791-813		NAP		g600810	228	90	2.00E-17	39	99	MSH6 gene [Saccharomyces cerevisiae]
22061	ENU05855	ANI61C918:2 54-73	770-789		NAP		g731502	351	153	1.00E-36	32	25	(Z46921) unknown [Saccharomyces cerevisiae]
22062	ENU05856	ANI61C8801: 165-182	469-488		NAP		g130582	196	97	1.00E-19	35	12	importin beta-4 subunit (karyopherin beta-4 subunit) (ran binding protein YRB4) [Saccharomyces cerevisiae]
22063	ENU05857	ANI61C3205: 23-44	649-668		NAP		g3288709	1601	291	6.00E-78	52	19	Retrovirus-related pol polyprotein from transposon TNT 1-94 [Nicotiana tabacum]
22064	ENU05858	ANI61C4172: 89-108	681-700		NAP		g3413518	506	231	5.00E-60	41	16	(AB010810) phospholipase D [Candida albicans]
22065	ENU05859	ANI61C3591: 29-48	793-811		NAP		g3116147	329	64	7.00E-17	30	47	(AL023290) amino acid permease [Schizosaccharomyces pombe]
22066	ENU05860	ANI61C5426: 43-63	522-549		NAP		g1731075	306	178	4.00E-44	43	53	probable NADH-dependent flavin oxidoreductase YQJM [Bacillus subtilis]
22067	ENU05861	ANI61C1073 22-48	778-796		NAP		g3393022	397	176	2.00E-43	38	38	(AL031174) hypothetical protein [Schizosaccharomyces pombe]
22068	ENU05862	ANI61C7940: 127-145	642-664		NAP		g2498701	94	71	1.00E-11	26	46	sterigmatocystin 7-O-methyltransferase precursor [Aspergillus flavus]
22069	ENU05863	ANI61C3966: 24-46	760-781		NAP		g4539255	359	129	3.00E-29			(AL049495) hypothetical protein [Schizosaccharomyces pombe]
22070	ENU05864	ANI61S4253: 918..16			NAP		g3153821	160	47	0.0001	23	30	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22071	ENU05865	ANI61C9594: 1..503			NAP		g3282229	293	78	3.00E-14			(U68722) BcLHH [Botryotinia fuckeliana]
22072	ENU05866	ANI61C8675: 92-111	368-387		NAP		g1749656	105	73	2.00E-12	35	38	(D89224) similar to Saccharomyces cerevisiae ORF YCR028 [Schizosaccharomyces pombe]

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22073	ENU05867	ANI61C4988: 36-58 460..1074	36-58	483-510	NAP		g1351666	316	119	4.00E-27	50	30	putative ATP-dependent RNA helicase C1F7.02C [Schizosaccharomyces pombe]
22074	ENU05868	ANI61C5515: 115-134 1..506	115-134	391-410	NAP		g2501339	327	148	2.00E-35	44	24	Copper amine oxidase 1 [Aspergillus niger]
22075	ENU05869	ANI61C7746: 22-49 994..1	22-49	615-635	NAP		g2133285	298	129	3.00E-29			tryptophan dimethylallyltransferase (EC 2.5.1.34) - ergot fungus [Claviceps purpurea]
22076	ENU05870	ANI61C1105: 1..787			NAP		g135140	570	219	9.00E-63	54	22	"Leucyl-TRNA synthetase, cytoplasmic (leucine--TRNA ligase) (LEURS) [Neurospora crassa]"
22077	ENU05871	ANI61C6132: 409..1			NAP		g1730744	352	136	1.00E-31	56	45	hypothetical 33.5 KD protein in MKS1-MSK1 intergenic region [Saccharomyces cerevisiae]
22078	ENU05872	ANI61C1070: 42-61 4:918..2134	42-61	806-828	NAP		g998355	455	71	2.00E-22	31	31	(U35661) colony 1 [Ophiostoma ulmi]
22079	ENU05873	ANI61C2660: 25-44 1..1437	25-44	709-736	NAP		g2145937	415	57	7.00E-17	33	12	polyketide synthase pksE - Mycobacterium leprae [Mycobacterium leprae]
22080	ENU05874	ANI61S2794: 113-139 610..74	113-139	459-486	NAP		g3327882	453	205	1.00E-52	54	43	(AB016221) SSL1 [Schizosaccharomyces pombe]
22081	ENU05875	ANI61C8962: 31-58 3309..4653	31-58	754-773	NAP		g1407655	179	46	0.0003			(U58884) SH3P7 [Mus musculus]
22082	ENU05876	ANI61C8475: 28-47 692..1773	28-47	793-812	NAP		g4107343	1137	243	e-111	91	36	(AJ224922) ATP citrate lyase [Sordaria macrospora]
22083	ENU05877	ANI61C5331: 117-134 3094..2630	117-134	425-444	NAP		g1723448	339	124	9.00E-31	46	28	hypothetical protein C56F8.17C in chromosome 1 [Schizosaccharomyces pombe]
22084	ENU05878	ANI61S813:1 0..622			NAP		g2635194	425	173	9.00E-43	47	99	(Z99117) similar to hypothetical proteins [Bacillus subtilis]
22085	ENU05879	ANI61S617:6 51..1	216-235	527-546	NAP		g4091929	422	185	2.00E-46	47	50	"(AF069752) C5,6 desaturase [Candida albicans]"
22086	ENU05880	ANI61S564:5 39..143			NAP		g2635812	276	125	1.00E-28	46	70	(Z99120) similar to hypothetical proteins [Bacillus subtilis]
22087	ENU05881	ANI61C5372: 22-48 1805..3381	22-48	790-817	NAP		g2342601	820	242	3.00E-63	48	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22088	ENU05882	ANI61C4407: 26-45 732..1	26-45	584-606	NAP		g118239	131	42	0.000000	31	71	Dihydrodipicolinate synthase (DHDPS) [Corynebacterium glutamicum]

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22089	ENU05883	ANI61C4408: 1363..1	22-44	633-652	NAP		g3116018	679	134	1.00E-46	44	53	(Y13067) vanillin: NAD+ oxidoreductase [Pseudomonas fluorescens]
22090	ENU05884	ANI61C1974: 133-152	494-517		NAP		g83673	183	96	3.00E-19	36	34	amidase (EC 3.5.1.4) - Aspergillus oryzae [Aspergillus oryzae]
22091	ENU05885	ANI61C409:1 1..699	29-48	761-780	NAP		g114971	1192	181	6.00E-45	37	33	beta-glucosidase precursor (gentiobiase) (beta-D-glucoside glucosylhydrolase) [Kluyveromyces marxianus]
22092	ENU05886	ANI61C9938: 183-204	430-453		NAP		g3947883	172	68	3.00E-11	31	31	(AL034382) putative Trp-Asp repeat protein [Schizosaccharomyces pombe]
22093	ENU05887	ANI61C1941: 22-43	792-819		NAP		g3915963	1019	192	2.00E-48	45	14	ATP-dependent bile acid permease [Saccharomyces cerevisiae]
22094	ENU05888	ANI61C9360: 23-47	522-545		NAP		g2765195	214	101	7.00E-21	33	6	(Y12527) HMWP1 protein [Yersinia enterocolitica]
22095	ENU05889	ANI61C7355: 22-43	727-746		NAP		g2132992	120	104	9.00E-22	34	21	probable membrane protein YPL183c - yeast (Saccharomyces cerevisiae)
22096	ENU05890	ANI61C7856: 24-43	485-504		NAP		g3080368	162	91	6.00E-18	34	24	[Saccharomyces cerevisiae]
22097	ENU05891	ANI61S1700: 36-63	387-413		NAP		g2894215	104	71	6.00E-12	29	38	(AL022580) putative protein [Arabidopsis thaliana]
22098	ENU05892	ANI61C2695: 58-83	404-425		NAP		g4505499	213	119	1.00E-26	40	18	(AL021841) amiB [Mycobacterium tuberculosis]
		1..605											O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase) [Homo sapiens]
22099	ENU05893	ANI61C2136: 115-134	805-829		NAP		g266448	648	252	3.00E-66			long-chain-fatty-acid--COA ligase 1 (long-chain acyl-CoA synthetase 1) (fatty acid activator 1) [Saccharomyces cerevisiae]
22100	ENU05894	ANI61C1060 153-176	654-679		NAP		g2499125	458	196	2.00E-49	37	8	vacuolar protein sorting-associated protein VPS13 [Saccharomyces cerevisiae]
22101	ENU05895	ANI61C7807: 22-46	804-829		NAP		g32020205	166	55	0.000000			(AF054613) peroxin [Yarrowia lipolytica]
22102	ENU05896	ANI61C3104: 61-80	807-826		NAP		g4007757	1872	368	e-126	72	51	(AL034433) glucose-6-phosphate isomerase [Schizosaccharomyces pombe]

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22103	ENU05897	ANI61C6457: 314..1526	22-47	801-826	NAP		g2052244	324	92	3.00E-18	37	52	(Y12561) Cdc1 protein [Schizosaccharomyces pombe] []
22104	ENU05898	ANI61C477:1 194..1787	24-45	535-560	NAP		g3879684	151	85	4.00E-16	36	49	(Z74042) predicted using Genefinder; Similarity to Haemophilus 3-oxoacyl-(acyl-carrier protein) reductase (SW:FABG_HAEIN); cDNA EST yk470b2.3 comes from this gene; cDNA EST yk470b2.5 comes from this gene [Caenorhabditis elegans]
22105	ENU05899	ANI61C9467: 3514..72	22-42	796-819	NAP		g4115480	1564	122	2.00E-43	42	12	(AB010274) fatty acid synthetase [Schizosaccharomyces pombe]
22106	ENU05900	ANI61C9162: 1823..2453	27-49	434-456	NAP		g416716	917	254	3.00E-67	92	10	cell division-associated protein BIMB []
22107	ENU05901	ANI61C1100 4:4254..2142	50-69	795-814	NAP		g3769519	982	209	2.00E-53	45	41	(AF080217) acetoacetyl-CoA synthetase; acetoacetyl-CoA ligase; acyl-activating enzyme [Sinorhizobium meliloti]
22108	ENU05902	ANI61C4407: 4252..5353	34-54	707-730	NAP		g1653242	390	91	1.00E-23	32	58	(D90912) hypothetical protein [Synecocystis sp.]
22109	ENU05903	ANI61C1871: 684..1	22-49	640-660	NAP		g3650370	299	116	1.00E-25	37	41	(AL031741) putative membrane transporter [Schizosaccharomyces pombe]
22110	ENU05904	ANI61C1015 2:1..1341	37-54	764-790	NAP		g462768	85	41	0.008			(L10127) ORF17 [Molluscum contagiosum virus type 1]
22111	ENU05905	ANI61C9626: 607..2155	22-48	802-829	NAP		g3650405	960	216	2.00E-55	49	53	(AL031739) putative dna primase large subunit [Schizosaccharomyces pombe]
22112	ENU05906	ANI61C9067: 3953..1900	26-49	806-825	NAP		g4574121	402	100	2.00E-20	36	27	(AF009415) choline dehydrogenase [Staphylococcus xylosum]
22113	ENU05907	ANI61C7016: 4685..3207	25-48	806-825	NAP		g2257494	737	122	4.00E-27	45	41	(AB004534) cdc2 kinase homologue [Schizosaccharomyces pombe]
22114	ENU05908	ANI61C7570: 1..1423	24-50	803-822	NAP		g3169091	1112	199	4.00E-81	59	46	(AL023706) hypothetical protein [Schizosaccharomyces pombe]
22115	ENU05909	ANI61S1726: 1..791			NAP		g1572721	130	45	0.0008	25	18	(U70136) megakaryocyte stimulating factor; MSF [Homo sapiens]
22116	ENU05910	ANI61C6647: 22-41 2707..3778	22-41	803-829	NAP		g3219964	455	158	4.00E-38	46	87	putative RAS-related protein C1B3.11C [Schizosaccharomyces pombe]
22117	ENU05911	ANI61C7639: 2584..1	22-49	807-829	NAP		g4587971	3918	501	e-141	99	20	(AF082072) ABC transporter protein AtnC [Emmericella nidulans]

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22118	ENU05912	ANI61C2128: 1906..1	22-41	725-746	NAP		g1709029	1120	295	2.00E-79	56	27	MIC1 protein [Saccharomyces cerevisiae]
22119	ENU05913	ANI61C1267: 1081..1	22-42	786-805	NAP		g2133039	685	218	4.00E-56	45	17	probable membrane protein YPR184w - yeast [Saccharomyces cerevisiae]
22120	ENU05914	ANI61S4277: 1..568	69-88	527-547	NAP		g4733981	345	57	4.00E-18			[Saccharomyces cerevisiae] (AC007268) putative serine carboxypeptidase [Arabidopsis thaliana]
22121	ENU05915	ANI61S4437: 465..1	204-225	414-436	NAP		g2414610	170	53	4.00E-13	43	48	"(Z99295) oxidoreductase, possible sorbitol utilization [Schizosaccharomyces pombe]"
22122	ENU05916	ANI61C7381: 195..928	34-61	686-713	NAP		g1666269	430	90	6.00E-36	40	97	(Z82021) cytochrome P450 [Agaricus bisporus]
22123	ENU05917	ANI61C2718: 372..9	50-76	457-479	NAP		g229530	193	75	5.00E-20	43	97	cytochrome b2 1-103 [Saccharomycetales]
22124	ENU05918	ANI61S3976: 136..520			NAP		g547782	162	73	1.00E-12	36	47	"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3')I) [Plasmid NTP16]"
22125	ENU05919	ANI61C775:2 14..1041	24-51	682-709	NAP		g1730771	602	172	3.00E-42	55	25	hypothetical 110.9 KD protein in SPC98-TOM70 intergenic region [Saccharomyces cerevisiae]
22126	ENU05920	ANI61C2389: 2144..1723	72-93	375-401	NAP		g1351972	666	153	7.00E-37	95	16	Nitrogen regulatory protein area [Emicella nidulans]
22127	ENU05921	ANI61C1098 7:1221..1	91-110	738-756	NAP		g3914054	447	131	5.00E-30	32	35	MUTS protein homolog 1 [Schizosaccharomyces pombe]
22128	ENU05922	ANI61C3268: 2781..1885	22-44	802-829	NAP		g2132229	149	47	0.0002	31	94	hypothetical protein YPL199c - yeast [Saccharomyces cerevisiae]
22129	ENU05923	ANI61C1371: 1175..482	112-133	640-667	NAP		g3702646	135	72	5.00E-12	26	38	[Saccharomyces cerevisiae] (AL031825) putative membrane transport protein
22130	ENU05924	ANI61C6060: 740..1	22-47	597-624	NAP		g4495124	436	174	5.00E-43	43	62	[Schizosaccharomyces pombe] (AL035675) WD repeat protein; human U5 SNRNP-specific-like
22131	ENU05925	ANI61C679:2 506..1	22-45	721-748	NAP		g2131263	2782	396	e-109	66	13	[Schizosaccharomyces pombe] GLT1 protein - yeast [Saccharomyces cerevisiae] [Saccharomyces cerevisiae]

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22132	ENU05926	ANI61C1134; 52-71 6666..8397	781-800	781-800	NAP		g2132124	1978	445	e-124	75	25	hypothetical protein YOR304w - yeast (Saccharomyces cerevisiae)
22133	ENU05927	ANI61C2187: 24-47 1719..1	680-702	680-702	NAP		g2144167	351	70	7.00E-26	32	34	[Saccharomyces cerevisiae] beta-glucosidase (EC 3.2.1.21) - yeast (Candida molischiana) [Pichia capsulata]
22134	ENU05928	ANI61C7216: 22-48 214..1063	793-815	793-815	NAP		g4033486	238	56	6.00E-20	33	51	putative tartrate transporter [Agrobacterium vitis]
22135	ENU05929	ANI61C247:1 29-48 250..2139	797-816	797-816	NAP		g3133104	154	61	0.000000	34	74	(AL023554) conserved hypothetical protein [Schizosaccharomyces pombe]
22136	ENU05930	ANI61C8055: 22-47 2141..227	765-784	765-784	NAP		g117298	1073	194	9.00E-49			cytochrome P450(BM-3) / NADPH-cytochrome P450 reductase [Bacillus megaterium]
22137	ENU05931	ANI61C8057: 91-110 1..467	417-444	417-444	NAP		g586797	112	61	0.000000	26	28	hypothetical 59.1 KD protein ZK637.1 in chromosome III []
22138	ENU05932	ANI61S1712: 22-41 1..453	395-420	395-420	NAP		g114971	415	173	5.00E-43	53	17	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Kluyveromyces marxianus]
22139	ENU05933	ANI61C7085: 26-45 2078..3434	803-829	803-829	NAP		g1352079	1500	357	e-126	77	32	beta-glucosidase 1 precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Aspergillus aculeatus]
22140	ENU05934	ANI61S2736: 1..906			NAP		g786117	236	48	0.0001	19	55	(L41834) nuclear protein [Ensis minor]
22141	ENU05935	ANI61C323:3 22-49 652..2386	808-829	808-829	NAP		g2956768	907	242	3.00E-63	47	67	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22142	ENU05936	ANI61S1621: 67-85 365..1	320-344	320-344	NAP		g3925755	110	62	0.000000	30	21	putative phosphodiesterase-nucleotide pyrophosphatase precursor
22143	ENU05937	ANI61C978:8 22-48 38..1	718-737	718-737	NAP		g2132846	275	113	2.00E-24	31	48	[Schizosaccharomyces pombe] probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae)
22144	ENU05938	ANI61C1138 26-48 7:1..552	442-461	442-461	NAP		g731462	179	94	9.00E-19	40	22	[Saccharomyces cerevisiae] hypothetical 74.0 KD protein in CAJ1-HOM3 intergenic region [Saccharomyces cerevisiae]

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22145	ENU05939	ANI61C1146 7:3408..4913	22-45	714-732	NAP		g3810838	429	88	7.00E-17	37	38	"(AL032684) putative DNA polymerase epsilon, subunit b [Schizosaccharomyces pombe]"
22146	ENU05940	ANI61C1098 8:1704..2552	26-45	721-743	NAP		g3451448	195	80	3.00E-14	35	80	(AL031350) putative dehydrogenase [Streptomyces coelicolor]
22147	ENU05941	ANI61C1053 1:3372..1	22-43	710-734	NAP		g3914984	1047	72	4.00E-12	22	7	Ferrichrome siderophore peptide synthetase [Ustilago maydis] (X89442) peptide synthetase [Metarhizium anisopliae]
22148	ENU05942	ANI61C9561: 32-51 288..1649	32-51	758-785	NAP		g2342601	674	128	6.00E-43	39	5	nitrate transport protein crnA - Emericella nidulans []
22149	ENU05943	ANI61C2459: 3409..4341	22-49	788-812	NAP		g101795	1373	406	e-112	98	51	(AF053764) NADP-dependent mannitol dehydrogenase [Agaricus bisporus]
22150	ENU05944	ANI61C1143 6:5110..4334	24-46	735-756	NAP		g3869276	296	138	4.00E-32	33	97	chitin synthase (EC 2.4.1.16) chsB - Emericella nidulans [Emericella nidulans]
22151	ENU05945	ANI61S973:1. ..511			NAP		g631954	402	145	2.00E-34	53	18	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
22152	ENU05946	ANI61C8446: 34-53 608..1	34-53	480-506	NAP		g3850084	308	105	2.00E-29	44	52	Copper amine oxidase 1 [Aspergillus niger]
22153	ENU05947	ANI61C6254: 58-77 1232..2582	58-77	768-787	NAP		g2501339	541	161	2.00E-47	49	37	(L31778) alkaline protease [Aspergillus nidulans]
22154	ENU05948	ANI61C3968: 22-42 789..1	22-42	712-739	NAP		g470731	1194	269	e-126	97	60	threonine dehydratase precursor (threonine deaminase) [Arxula adenivorans]
22155	ENU05949	ANI61S75:52 7..1	215-232	463-482	NAP		g3915105	430	189	9.00E-48	55	31	"(AF026291) chaperonin containing t-complex polypeptide 1, delta subunit; CCT-delta [Homo sapiens]"
22156	ENU05950	ANI61C6610: 30-50 702..1	30-50	577-601	NAP		g2559008	345	131	1.00E-32	57	30	(X98808) peroxidase ATP3a [Arabidopsis thaliana]
22157	ENU05951	ANI61S3152: 122-146 590..107	122-146	437-463	NAP		g1546698	456	111	3.00E-24	93	34	"putative dihydroxy-acid dehydratase precursor (DAD) (2,3-dihydroxy acid hydrolyase) [Schizosaccharomyces pombe]"
22158	ENU05952	ANI61C9158: 22-43 1..560	22-43	446-464	NAP		g1708464	689	171	2.00E-62	73	31	High-affinity glucose transporter SNF3 [Saccharomyces cerevisiae]
22159	ENU05953	ANI61C5582: 103-128 1..745	103-128	683-706	NAP		g1351078	107	76	3.00E-13	25	26	Nitrate reductase (NADPH) (NR) [Emericella nidulans]
22160	ENU05954	ANI61S2588: 205-232 580..188	205-232	343-370	NAP		g128192	514	209	8.00E-54	82	15	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22161	ENU05955	ANI61S4224: 997..549	22-49	810-829	NAP		g3329623	130	30	8.7	28	44	(AF078790) No definition line found [Caenorhabditis elegans]
22162	ENU05956	ANI61C6104: 1..1195	22-49	810-829	NAP		g2499716	755	217	8.00E-56	46	59	"exopolysaccharuronase precursor (exoPG) (galacturan 1,4-alpha- galacturonidase) (poly(1,4-alpha-D- galacturonide)galacturonohydrolase) [Aspergillus tubingensis]" Kinesin heavy chain []
22163	ENU05957	ANI61C4643: 1007..1	72-89	777-796	NAP		g1346380	1126	383	e-105	81	30	
22164	ENU05958	ANI61C9251: 2690..2369	23-45	408-434	NAP		g3130014	63	61	0.000000	29	40	(AL023517) putative lipoprotein [Streptomyces coelicolor]
22165	ENU05959	ANI61C1307: 317..1363	25-44	808-829	NAP		g114275	698	223	1.00E-57	46	80	L-Asparaginase precursor (L- asparagine amidohydrolase) [Erwinia chrysanthemi]
22166	ENU05960	ANI61S4270: 610..1			NAP		g3738194	192	59	0.000000	41	26	(AL031854) hypothetical protein [Schizosaccharomyces pombe]
22167	ENU05961	ANI61C1126 7..1.477	24-43	394-421	NAP		g464369	108	64	5.00E-10	32	18	Phenol 2-monooxygenase (phenol hydroxylase) [Trichosporon cutaneum]
22168	ENU05962	ANI61C1110 0.8975..10390	46-65	723-744	NAP		g3650376	720	216	1.00E-55	44	30	(AL031740) dna ligase protein [Schizosaccharomyces pombe]
22169	ENU05963	ANI61C2411: 2469..1213	22-41	803-829	NAP		g3395556	724	146	1.00E-63	58	70	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]
22170	ENU05964	ANI61C2118: 1698..2569	51-70	763-780	NAP		g2388904	528	173	8.00E-55	51	39	(Z98974) hypothetical protein [Schizosaccharomyces pombe]
22171	ENU05965	ANI61C3180: 242..753	23-42	436-455	NAP		g3036901	89	55	0.000000	28	55	(AL222715) DapA [Sinorhizobium meliloti]
22172	ENU05966	ANI61C1061 5..1250..1	94-113	732-749	NAP		g461623	522	155	4.00E-37	38	25	beta-galactosidase precursor (lactase) [Aspergillus niger]
22173	ENU05967	ANI61C5650: 327..1072	56-78	702-725	NAP		g227874	482	98	1.00E-41	50	28	Extracellular beta glucosidase [Trichoderma reesei]
22174	ENU05968	ANI61C8513: 724..1	65-86	658-677	NAP		g1498245	324	151	6.00E-36	38	29	"(X99960) putative, YGL139w [Saccharomyces cerevisiae]"
22175	ENU05969	ANI61C3470: 262..1249	22-49	806-829	NAP		g217326	396	82	3.00E-32	40	42	(D13332) Ca2+/calmodulin-dependent protein kinase II [Drosophila sp.]
22176	ENU05970	ANI61C4698: 1522..1924	92-119	375-398	NAP		g3913326	173	88	3.00E-17	31	31	Cytochrome P450 52A9 (CYP11A9) (alkane-inducible P450-ALK5-A) [Candida maltosa]

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22177	ENU05971	ANI61C7088: 928..1	108-127	719-738	NAP		g2407970	666	209	2.00E-53	63	38	(Y14750) TOM70 [Podospira anserina]
22178	ENU05972	ANI61C8560: 60-87 1528..936	60-87	519-546	NAP		g640053	144	50	2.00E-12	41	35	(U19714) 3-phosphoserine aminotransferase [Saccharomyces cerevisiae]
22179	ENU05973	ANI61C8579: 22-47 1699..344	22-47	793-820	NAP		g4586928	449	155	5.00E-37	39	5	(AB017641) polyketide synthase [Micromonospora griseorubida]
22180	ENU05974	ANI61C1021 22-48 5:1152..1	22-48	710-732	NAP		g3087842	624	152	8.00E-53	48	55	(Y08841) core protein II [Neurospora crassa]
22181	ENU05975	ANI61S557:1..750			NAP		g2213913	92	53	8.00E-10	21	9	(AF004884) neuronal calcium channel alpha 1A subunit isoform A-1 [Homo sapiens]
22182	ENU05976	ANI61C9522: 22-43 1062..1831	22-43	646-669	NAP		g4104764	293	119	2.00E-26	40	54	(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
22183	ENU05977	ANI61S3702: 140..527			NAP		g125462	90	38	0.046			"aminoglycoside 3'-phosphotransferase (kanamycin kinase, type I) (neomycin-kanamycin phosphotransferase, type I) (APH(3')I) [Cloning vector pHIND2.2]"
22184	ENU05978	ANI61C7393: 22-41 715..1	22-41	568-595	NAP		g113701	332	128	5.00E-33	48	36	Acetamidase [Emericella nidulans]
22185	ENU05979	ANI61C4935: 40-59 591..1	40-59	499-521	NAP		g4803681	131	73	2.00E-12			(AL049819) putative AraC-family transcriptional regulator [Streptomyces coelicolor]
22186	ENU05980	ANI61C5316: 47-65 1..593	47-65	533-552	NAP		g4008543	98	61	0.000000 009	29	62	(AL034492) putative deacetylase [Streptomyces coelicolor]
22187	ENU05981	ANI61C1030 22-45 1:5850..6911	22-45	633-660	NAP		g1708808	550	213	2.00E-59	47	79	Lactoylglutathione lyase (methylglyoxalase) (aldoketomutase) (glyoxalase I) (GLX I) (ketone-aldehyde mutase) (S-D-lactoylglutathione methylglyoxal lyase) [Saccharomyces cerevisiae]
22188	ENU05982	ANI61C1103 2:476..1	102-127	453-479	NAP		g3860373	466	171	4.00E-42	57	47	(AJ012668) tomatinase [Fusarium oxysporum f. sp. lycopersici]
22189	ENU05983	ANI61C2278: 39-66 879..1	39-66	721-748	NAP		g2275095	185	109	2.00E-23	26	24	(X86179) phosphoprotein [Schizosaccharomyces pombe]
22190	ENU05984	ANI61S2170: 30-49 543..159	30-49	334-361	NAP		g3183329	297	126	6.00E-29	53	26	Hypothetical aminotransferase C6B12.04C [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22191	ENU05985	ANI61C2482: 1.703	102-125	653-680	NAP		g3850151	437	115	4.00E-44	58	70	(AL033396) rehydrin-like protein [Candida albicans]
22192	ENU05986	ANI61C1048 7.6940..8616	43-70	807-829	NAP		g1805251	1078	131	4.00E-43	41	50	(U58946) transposase [Aspergillus awamori]
22193	ENU05987	ANI61C1147: 2911..4181	22-45	705-730	NAP		g1749410	711	183	5.00E-59	59	41	"(D89101) similar to Saccharomyces cerevisiae Asparagine synthetase(glutamine-hydrolyzing)2, SWISS-PROT Accession Number P49090 [Schizosaccharomyces pombe]"
22194	ENU05988	ANI61C2507: 1229..391	144-171	796-818	NAP		g2896707	511	138	4.00E-51	52	90	(AL021897) echA8 [Mycobacterium tuberculosis]
22195	ENU05989	ANI61S3763: 1..619	33-52	385-410	NAP		g4263063	213	98	7.00E-20	34	28	(AC005142) hypothetical protein [Arabidopsis thaliana]
22196	ENU05990	ANI61S1588: 1..487			NAP		g2500356	357	157	6.00E-38	54	69	60S ribosomal protein L10 (QM protein homolog) (SPQM) [Schizosaccharomyces pombe]
22197	ENU05991	ANI61C1133 2:493..1	105-125	379-398	NAP		g1749480	179	82	3.00E-15	43	26	"(D89136) similar to Saccharomyces cerevisiae BCS1 protein, SWISS-PROT Accession Number P32839 [Schizosaccharomyces pombe]"
22198	ENU05992	ANI61C4764: 971..2614	22-46	723-744	NAP		g1711623	1646	372	e-102	67	29	"alanyl-tRNA synthetase, cytoplasmic (alanine—tRNA ligase) (ALARS) [Saccharomyces cerevisiae]"
22199	ENU05993	ANI61C8670: 1371..215	35-54	793-815	NAP		g2956768	384	80	3.00E-14	27	61	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22200	ENU05994	ANI61C1074 6:1760..1442	53-78	261-288	NAP		g3850084	134	54	0.000000	36	30	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
22201	ENU05995	ANI61C487:6 04..1	114-136	474-493	NAP		g731294	247	79	3.00E-14	37	43	hypothetical zinc-type alcohol dehydrogenase-like protein in GDH3-CNE1 intergenic region [Saccharomyces cerevisiae]
22202	ENU05996	ANI61C9976: 2078..412	23-50	809-828	NAP		g3549899	332	78	6.00E-14			(Y15013) copalyl diphosphate synthase [Gibberella fujikuroi]
22203	ENU05997	ANI61C7223: 6158..5046	23-49	794-813	NAP		g1171890	885	261	3.00E-71			"pyruvate dehydrogenase E1 component, beta subunit precursor (PDHE1-B) [Schizosaccharomyces pombe]"

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22204	ENU05998	ANI61C553:2 43..745	27-46	342-361	NAP		g3378446	112	48	0.00005	30	63	(AF079317) 4-hydroxy-2-oxovalerate aldolase [Sphingomonas aromaticivorans]
22205	ENU05999	ANI61S2740: 1..354			NAP		g4218005	122	39	0.014	31	16	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
22206	ENU06000	ANI61C9901: 3907..4488			NAP		g2131340	358	127	8.00E-29	47	61	hypothetical protein YDL119c - yeast (Saccharomyces cerevisiae)
22207	ENU06001	ANI61C9014: 275..627	105-128	453-474	NAP		g1077357	232	99	4.00E-23	42	31	[Saccharomyces cerevisiae] probable membrane protein YLR359w - yeast (Saccharomyces cerevisiae)
22208	ENU06002	ANI61C3570: 331..1656	71-90	802-829	NAP		g4894182	652	183	2.00E-45			[Saccharomyces cerevisiae] (AJ242551) 12-oxophytodienoate reductase [Lycopersicon esculentum]
22209	ENU06003	ANI61C7889: 1..837	49-70	788-807	NAP		g730115	395	158	4.00E-38	38	35	Nitrate reductase [Synechococcus sp.]
22210	ENU06004	ANI61C9695: 892..1	37-56	717-744	NAP		g4507007	267	128	6.00E-29	31	37	Calcium binding mitochondrial carrier superfamily member Aralar [Homo sapiens]
22211	ENU06005	ANI61C1230: 4470..1314	22-45	805-829	NAP		g1166378	1020	101	5.00E-21			"(L76169) reverse transcriptase, RnaseH [Glomerella cingulata]"
22212	ENU06006	ANI61C2256: 1842..633	22-43	777-796	NAP		g140965	346	173	1.00E-42	40	48	Probable serine/threonine-protein kinase YKL116C [Saccharomyces cerevisiae]
22213	ENU06007	ANI61S1491: 1..981			NAP		g119714	466	36	0.38	41	43	Extensin precursor (cell wall hydroxyproline-rich glycoprotein) [Nicotiana tabacum]
22214	ENU06008	ANI61C4969: 1048..17	22-41	711-730	NAP		g119791	181	80	2.00E-14	35	63	3-oxoacyl- [Cuphea lanceolata]
22215	ENU06009	ANI61C1471: 1005..1	38-61	712-738	NAP		g4176721	683	196	1.00E-49	52	46	(AF038568) negative regulator Moe1 [Schizosaccharomyces pombe]
22216	ENU06010	ANI61C9067: 114..1174	22-46	804-824	NAP		g2290999	409	163	2.00E-43	42	85	(AF006000) unknown [Bordetella pertussis]
22217	ENU06011	ANI61C1087 5:1444..2508	25-52	798-819	NAP		g1465804	295	143	1.00E-33	32	77	(U64852) W01A11.2 gene product [Caenorhabditis elegans]
22218	ENU06012	ANI61C5251: 672..1	23-45	625-651	NAP		g113626	612	185	9.00E-56			fructose-bisphosphate aldolase [Saccharomyces cerevisiae]
22219	ENU06013	ANI61C1972: 1260..386	202-221	802-822	NAP		g416875	353	116	6.00E-30	35	41	Allantoin permease (allantoin transport protein) [Saccharomyces cerevisiae]

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22220	ENU06014	ANI61C1013 4:1072..1			NAP		g2500936	447	196	2.00E-49	40	36	High-affinity glucose transporter RGT2 [Saccharomyces cerevisiae]
22221	ENU06015	ANI61C4401: 38-57 2373..1660		672-693	NAP		g549689	352	129	9.00E-32	51	99	Hypothetical 19.7 KD protein in LHS1-NUP100 intergenic region [Saccharomyces cerevisiae]
22222	ENU06016	ANI61C6292: 22-45 1017..226		745-765	NAP		g3015626	1262	227	e-119	98	68	(AF041976) nitrogen metabolite repression regulator NmrA [Emicella nidulans]
22223	ENU06017	ANI61C2265: 72-91 1012..1		623-645	NAP		g4758416	489	201	5.00E-51			golgi-specific brefeldin A-resistance factor 1 [Homo sapiens]
22224	ENU06018	ANI61C1241: 42-61 1..3733		764-783	NAP		g1078633	5787	123	2.00E-69	97	21	myosin I myoA - Emicella nidulans [Emicella nidulans]
22225	ENU06019	ANI61C8228: 23-42 1182..1		716-734	NAP		g2293233	152	76	3.00E-13	26	49	(AF008220) YtcJ [Bacillus subtilis]
22226	ENU06020	ANI61C9644: 40-59 2543..1		725-749	NAP		g1546072	1051	144	9.00E-34	38	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22227	ENU06021	ANI61C1915: 22-47 2189..2885		642-667	NAP		g462683	320	137	7.00E-32			putative N-acetylglucosamine-6-phosphate deacetylase (GLCNAC 6-P deacetylase) [Caenorhabditis elegans] (Z99111) similar to formylmethionine deformylase [Bacillus subtilis]
22228	ENU06022	ANI61S4147: 62-81 1..360		310-329	NAP		g2633827	408	165	1.00E-40	63	65	(AB003111) actin [Humicola grisea var. thermoidea]
22229	ENU06023	ANI61S2660: 399..1			NAP		g4249564	206	61	0.000000	48	30	(AL031535) putative n-terminal acetyltransferase complex su bunit [Schizosaccharomyces pombe]
22230	ENU06024	ANI61C8071: 27-46 516..1		447-474	NAP		g3560266	248	63	6.00E-20	44	72	Octapeptide-repeat protein T2 [Mus musculus]
22231	ENU06025	ANI61S4267: 399..892			NAP		g730888	138	50	0.00001	31	85	Vesicular-fusion protein SEC18 [Saccharomyces cerevisiae]
22232	ENU06026	ANI61C1090: 197-223 1..464		417-443	NAP		g585965	230	104	5.00E-22	37	19	(AF069525) 190 kDa ankyrin isoform; AnkG190 [Rattus norvegicus]
22233	ENU06027	ANI61C4878: 634..1			NAP		g3202046	117	80	2.00E-14	30	9	(AJ012408) citrate synthase [Anabaena PCC7120]
22234	ENU06028	ANI61C6400: 39-58 1..496		433-460	NAP		g3819717	165	52	1.00E-13	31	42	Vegetatible incompatibility protein HET-E-1 [Podospora anserina]
22235	ENU06029	ANI61C532:6 105..6538			NAP		g3023956	178	80	5.00E-15	34	11	(Z68905) ATP-binding cassette multidrug transporter [Emicella nidulans]
22236	ENU06030	ANI61C3032: 84-103 885..1		720-738	NAP		g1834342	800	292	2.00E-79	54	19	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22237	ENU06031	ANI61C1134 5:1958..1415	104-131	483-510	NAP		g1711561	177	67	5.00E-17	47	18	Sugar transporter STL1 [Saccharomyces cerevisiae]
22238	ENU06032	ANI61C4015: 507..1	24-51	341-365	NAP		g1255425	86	46	0.0001	21	42	(U53154) No definition line found [Caenorhabditis elegans]
22239	ENU06033	ANI61C8048: 2217..3278	43-62	804-829	NAP		g3184558	290	82	4.00E-15	31	77	(AF052290) unknown [Synecococcus PCC7002]
22240	ENU06034	ANI61S3246: 169..616			NAP		g4204304	259	129	2.00E-29	42	24	(AC003027) lclprt_seq No definition line found [Arabidopsis thaliana]
22241	ENU06035	ANI61C1043 4:2564..3682	22-45	774-801	NAP		g1743374	143	69	5.00E-19	28	36	(Y10034) L-aminocyclopropane-1-carboxylic acid oxidase [Rumex palustris]
22242	ENU06036	ANI61C1041 1:6403..7672	22-41	808-827	NAP		g3738182	1083	287	5.00E-77	63	47	"(AL031854) probable t-complex protein 1, theta subunit [Schizosaccharomyces pombe]"
22243	ENU06037	ANI61S1333: 1..588			NAP		g3153821	140	45	0.0006	22	21	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22244	ENU06038	ANI61C6363: 3584..2480	24-43	809-828	NAP		g1890776	157	68	9.00E-11			(U88574) syringomycin biosynthesis enzyme [Pseudomonas syringae pv. syringae]
22245	ENU06039	ANI61C6186: 1283..1	23-50	802-829	NAP		g418150	726	157	7.00E-38			GABA-specific permease (GABA-specific transport protein) [Saccharomyces cerevisiae]
22246	ENU06040	ANI61C5013: 1202..1	193-220	784-808	NAP		g731276	967	314	6.00E-91	71	65	hypothetical 40.7 KD protein in PYK1-SNC1 intergenic region [Saccharomyces cerevisiae]
22247	ENU06041	ANI61C5574: 4289..4900	53-72	371-394	NAP		g115943	334	103	4.00E-30	41	58	cytochrome C heme lyase (CCHL) (holocytochrome-C synthase) [Neurospora crassa]
22248	ENU06042	ANI61C9267: 2297..2780	56-82	455-474	NAP		g1890290	51	42	0.003	25	17	(U89999) Ski2 [Xenopus laevis]
22249	ENU06043	ANI61S2314: 1..614	65-84	392-411	NAP		g3891714	155	84	9.00E-16	32	38	Gal6 (Yeast Bleomycin Hydrolase) Mutant C73a []
22250	ENU06044	ANI61C7278: 3793..4190	29-48	444-463	NAP		g267125	511	154	1.00E-46	98	99	"Thioredoxin [Aspergillus nidulans, Peptide, 109 aa]"
22251	ENU06045	ANI61C382:3 734..3027	22-41	650-675	NAP		g1171671	688	166	1.00E-71	74	100	hypothetical calcium-binding protein C18B11.04 in chromosome I [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22252	ENU06046	ANI61C9568: 37-56 1..1387		639-658	NAP		g399112	1005	242	4.00E-76	48	27	beta-galactosidase (lactase) [Kluyveromyces lactis]
22253	ENU06047	ANI61C1019 5:1..1249			NAP		g1166378	376	72	4.00E-12	34	23	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
22254	ENU06048	ANI61C431:4 516..3943	203-222	491-510	NAP		g2388991	206	69	2.00E-11	35	64	(Z98980) hypothetical protein [Schizosaccharomyces pombe]
22255	ENU06049	ANI61C4184: 22-45 569..1544		723-741	NAP		g3850071	405	170	1.00E-41	37	54	(AL033385) cadmium resistance protein [Schizosaccharomyces pombe]
22256	ENU06050	ANI61C7503: 37-56 1..2346		617-634	NAP		g1170811	2349	302	2.00E-81	53	25	putative mitochondrial ATP-dependent protease precursor
22257	ENU06051	ANI61C3397: 29-48 3028..1963		780-807	NAP		g4512354	202	71	1.00E-11			[Schizosaccharomyces pombe] (AB011836) alkyl hydroperoxide reductase large subunit [Bacillus halodurans]
22258	ENU06052	ANI61C3251: 39-58 1943..3165		804-824	NAP		g3738153	237	69	5.00E-23	39	25	(AL031852) putative cleavage and polyadenylation specificity factor
22259	ENU06053	ANI61C9170: 22-47 2863..1253		806-829	NAP		g2225983	414	34	1			[Schizosaccharomyces pombe] (Z97193) hypothetical protein Rv1877
22260	ENU06054	ANI61C2103: 111-130 1..579		456-480	NAP		g2370466	374	165	2.00E-40	46	3	[Mycobacterium tuberculosis] (Z98951) hypothetical protein
22261	ENU06055	ANI61C5199: 102-129 1587..1130		418-437	NAP		g2493134	299	50	4.00E-13	48	58	[Schizosaccharomyces pombe] vacuolar ATP synthase subunit E (V-ATPase E subunit) (V-ATPase 26 KD subunit) [Neurospora crassa]
22262	ENU06056	ANI61C3111: 102-123 1..720		660-686	NAP		g1710848	428	138	3.00E-45	45	21	SIT4-associating protein SAP190 [Saccharomyces cerevisiae]
22263	ENU06057	ANI61C466:9 50..3127		797-816	NAP		g4106672	57	37	0.16			(AL035064) hypothetical protein [Schizosaccharomyces pombe]
22264	ENU06058	ANI61C5033: 22-46 1..1089		724-749	NAP		g3560147	522	117	1.00E-40	35	41	"(AL031534) ribosomal processing, rna binding, nucleolar protein [Schizosaccharomyces pombe]"
22265	ENU06059	ANI61S4450: 26-51 1..472		338-359	NAP		g1805251	275	79	2.00E-14	39	28	(U58946) transposase [Aspergillus awamori]
22266	ENU06060	ANI61C3498: 98-119 714..1		591-613	NAP		g3242651	554	187	2.00E-58	59	20	(AB015509) beta-mannosidase [Aspergillus aculeatus]
22267	ENU06061	ANI61C7525: 36-63 1536..2125		542-569	NAP		g2182006	76	56	0.000000	32	49	(Z96072) hypothetical protein Rv2715 [Mycobacterium tuberculosis]
22268	ENU06062	ANI61C6205: 66-85 2201..1216		794-813	NAP		g730569	888	238	4.00E-91	73	92	60S ribosomal protein YL6 (L5) (RP8) [Saccharomyces cerevisiae]

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22269	ENU06063	ANI61C9151: 22-48 2755..3502	703-727	NAP		g2497499	482	125	8.00E-54	52	100		Guanylate kinase (GMP kinase) [Mus musculus]
22270	ENU06064	ANI61C1564: 50-69 1..1330	711-730	NAP		g1730729	441	79	4.00E-27	30	39		hypothetical 74.8 KD protein in ALG11-YTP3 intergenic region [Saccharomyces cerevisiae]
22271	ENU06065	ANI61C7241: 27-46 1200..1	722-748	NAP		g3006142	339	116	2.00E-25	36	43		(AL0222299) hypothetical protein [Schizosaccharomyces pombe]
22272	ENU06066	ANI61C498:7 072..6630	360-379	NAP		g1526987	117	66	3.00E-13	36	52		(U13050) pectate lyase D [Fusarium solani f. sp. pisi]
22273	ENU06067	ANI61C4158: 22-49 2015..756	799-818	NAP		g1764018	622	108	2.00E-43	44	66		(Z83760) COS41.8 [Ciona intestinalis]
22274	ENU06068	ANI61C7648: 22-48 710..1253	373-398	NAP		g4886445	209	34	0.59				(AL050269) hypothetical protein [Homo sapiens]
22275	ENU06069	ANI61C3744: 56-78 3348..4992	803-829	NAP		g118498	1074	252	3.00E-66	45	55		aldehyde dehydrogenase (ALDDH) [Emicella nidulans]
22276	ENU06070	ANI61C4669: 111-130 1..983	736-758	NAP		g3114719	1141	336	1.00E-91	64	18		(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
22277	ENU06071	ANI61C867:1 000..1	808-829	NAP		g1438951	581	115	4.00E-25	46	51		(U61842) cutinase negative acting protein [Fusarium solani f. sp. pisi]
22278	ENU06072	ANI61C1057 2:1..1132	805-829	NAP		g3880602	127	74	1.00E-12				(Z82080) cDNA EST EMBL:D66071 comes from this gene; cDNA EST yk274a10.3 comes from this gene; cDNA EST yk289f12.3 comes from this gene; cDNA EST yk289f12.5 comes from this gene; cDNA EST yk274a10.5 comes from this gene; cDNA ES... []
22279	ENU06073	ANI61C1041 6:537..1	413-432	NAP		g140338	258	106	2.00E-22				hypothetical 23.1 KD protein in DMSC-PFLA intergenic region [Escherichia coli]
22280	ENU06074	ANI61C2627: 31-50 1104..1	724-743	NAP		g2995341	190	66	4.00E-10	25	46		(AL022244) hypothetical protein [Schizosaccharomyces pombe]
22281	ENU06075	ANI61C1049 5:3803..6305		NAP		g1705915	2051	309	2.00E-83	51	16		Clathrin heavy chain [Bos taurus]
22282	ENU06076	ANI61C1002: 23-42 732..1	604-631	NAP		g3130036	389	125	4.00E-28	50	49		(AL023534) putative methionine aminopeptidase 1 [Schizosaccharomyces pombe]

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22283	ENU06077	ANI61C3365: 1394..1	23-49	721-740	NAP	g2290770	g3874563	668	78	5.00E-37	45	21	(AF002163) delta-adaptin [Homo sapiens]
22284	ENU06078	ANI61C3696: 113-132 561-581 1..671	113-132	561-581	NAP	g3874563	g3874563	276	115	1.00E-32			(Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... []
22285	ENU06079	ANI61C6044: 203-222 701-720 895..1	203-222	701-720	NAP	g4165293	g4165293	583	245	2.00E-64	59	22	(X58824) cdc21 protein [Schizosaccharomyces pombe]
22286	ENU06080	ANI61C3840: 102-119 599-618 1..659	102-119	599-618	NAP	g2500535	g2500535	206	97	1.00E-19	37	20	putative ATP-dependent RNA helicase YDL031W [Saccharomyces cerevisiae]
22287	ENU06081	ANI61C1933: 64-84 1700..1181	64-84	472-499	NAP	g3850093	g3850093	135	76	1.00E-13	28	33	(AL033389) putative allantoin permease [Schizosaccharomyces pombe]
22288	ENU06082	ANI61C6667: 1271..434			NAP	g3136096	g3136096	1016	406	e-112	83	69	(AF032988) spindle assembly checkpoint protein SLDB [Emmericella nidulans]
22289	ENU06083	ANI61C130:1 197-215 624-648 788	197-215	624-648	NAP	g4206286	g4206286	702	239	2.00E-62	63	24	(AF043332) plasma membrane H(+)-ATPase [Emmericella nidulans]
22290	ENU06084	ANI61C1055 22-46 773-792 5:1..5216	22-46	773-792	NAP	g1805261	g1805261	8541	284	e-121	95	14	"(U75347) fatty acid synthase, alpha subunit [Emmericella nidulans]"
22291	ENU06085	ANI61C3890: 32-52 1104..1	32-52	623-646	NAP	g4056558	g4056558	104	85	8.00E-16	30	28	(AL034583) related to yeast zds family proteins [Schizosaccharomyces pombe]
22292	ENU06086	ANI61C6567: 51-78 691..1	51-78	603-630	NAP	g3184109	g3184109	673	259	2.00E-71	81	28	(AL023780) ABC transporter [Schizosaccharomyces pombe]
22293	ENU06087	ANI61C6142: 35-54 1290..1	35-54	790-809	NAP	g4185560	g4185560	2042	460	e-147	99	12	(AF112473) PyrABCN [Emmericella nidulans]
22294	ENU06088	ANI61C4368: 119-138 802-827 2711..1864	119-138	802-827	NAP	g1723766	g1723766	415	158	5.00E-38	40	57	ubiquinone biosynthesis monooxygenase COQ6 [Saccharomyces cerevisiae]
22295	ENU06089	ANI61C1060 22-46 2:1542..1	22-46	718-738	NAP	g3929290	g3929290	727	190	1.00E-69	54	51	(AF094507) B-type cyclin [Candida albicans]
22296	ENU06090	ANI61C8408: 57-76 3444..1	57-76	711-730	NAP	g1597721	g1597721	1958	110	1.00E-23	36	18	(X99021) putative helicase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22297	ENU06091	ANI61C1987: 525..1	30-57	477-504	NAP		g1813523	124	45	0.0005	28	28	(U67763) PbTRAP [Plasmodium berghei]
22298	ENU06092	ANI61C9063: 7250..6175	22-42	800-827	NAP		g2266911	600	156	3.00E-46	39	78	(AF001274) L4171.5 [Leishmania major]
22299	ENU06093	ANI61C9187: 219..812	29-50	522-544	NAP		g1346405	303	88	4.00E-30	39	28	Laccase precursor (benzenediol:oxygenn oxidoreductase) (urishiol oxidase) (laccase I) [Emericella nidulans]
22300	ENU06094	ANI61C1765: 3666..4782	22-45	779-801	NAP		g543923	692	203	9.00E-61			Calnexin homolog precursor [Schizosaccharomyces pombe]
22301	ENU06095	ANI61C6158: 941..1	22-42	803-826	NAP		g2330690	184	69	3.00E-11	31	18	(Z98529) putative cytoskeleton assembly control protein [Schizosaccharomyces pombe]
22302	ENU06096	ANI61C8249: 1163..1	22-49	621-646	NAP		g193271	752	213	2.00E-65	61	62	(M59288) ferrochelatase [Mus musculus]
22303	ENU06097	ANI61C9171: 2142..588	58-76	797-816	NAP		g1706692	1173	189	3.00E-58	50	50	C-24(28) sterol reductase [Saccharomyces cerevisiae]
22304	ENU06098	ANI61C8836: 7304..6176	24-45	784-803	NAP		g3929395	1129	195	1.00E-85	61	31	vacuolar ATP synthase 98 KD subunit (vacuolar ATPase 98 KD subunit) [Neurospora crassa]
22305	ENU06099	ANI61C3681: 285..1751			NAP		g2492863	2264	409	e-124	98	58	Ornithine aminotransferase (ornithine--oxo-acid aminotransferase) [Emericella nidulans]
22306	ENU06100	ANI61C9107: 3660..5661	39-58	777-796	NAP		g1027486	805	73	3.00E-25	36	43	(D49538) dihydrogeodin oxidase [Aspergillus terreus]
22307	ENU06101	ANI61C5317: 1..395	114-133	281-300	NAP		g461830	176	86	1.00E-16	39	29	carboxypeptidase S1 [Penicillium janthinellum]
22308	ENU06102	ANI61C7469: 1114..1	115-142	725-744	NAP		g461830	436	113	2.00E-24	35	52	carboxypeptidase S1 [Penicillium janthinellum]
22309	ENU06103	ANI61C8631: 4266..2596	22-49	799-826	NAP		g4468731	698	146	9.00E-44	46	50	(AL035592) hypothetical protein [Schizosaccharomyces pombe]
22310	ENU06104	ANI61C8596: 2017..1	22-41	773-793	NAP		g1169885	1408	289	2.00E-77	51	26	putative glycine dehydrogenase (decarboxylating) precursor (glycine decarboxylase) (glycine cleavage system P-protein)
22311	ENU06105	ANI61C2944: 1..545	212-231	500-524	NAP		g2494820	321	111	1.00E-25	52	28	[Schizosaccharomyces pombe] Rhamnogalacturonase B precursor (rhamnogalacturonan lyase) (RGASE B) (RHG B) [Aspergillus aculeatus]

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22312	ENU06106	ANI61C6952: 99-118 759..1	99-118	652-673	NAP		g3549877	116	67	1.00E-10	32	37	(Y15902) nitrogen metabolite repression-(nmr)-responsible protein [Gibberella fujikuroi]
22313	ENU06107	ANI61C8294: 22-46 1154..1	22-46	611-630	NAP		g131618	1083	259	1.00E-86			phosphoribosylamine--glycine ligase (GARS) (glycinamide RIBOnucleotide synthetase) (phosphoribosylglycinamide synthetase) / phosphoribosylformylglycinamide cyclo-ligase (AIRS) (phosphoribosyl-aminimidazole synthetase) ... [Schizosaccharomyces pombe]
22314	ENU06108	ANI61C8529: 26-45 1740..2296	26-45	517-536	NAP		g3023956	369	166	8.00E-41	45	13	Vegetatible incompatibility protein HET-E-1 [Podospora anserina]
22315	ENU06109	ANI61C3904: 35-54 2002..1	35-54	714-735	NAP		g1352399	370	146	2.00E-34			"glucan 1,3-beta-glucosidase precursor (exo-beta 1,3 glucanase) (1,3-beta-D-glucanohydrolase) [Cochliobolus carbonum]"
22316	ENU06110	ANI61C60:18 40-59 74..1208	40-59	586-605	NAP		g2467274	466	127	6.00E-36	66	100	(Z99759) rna binding protein [Schizosaccharomyces pombe]
22317	ENU06111	ANI61C1057 24-45 1:1..3158	24-45	774-797	NAP		g1834342	1828	232	3.00E-60	70	15	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
22318	ENU06112	ANI61C4884: 64-91 481..1	64-91	451-478	NAP		g4456818	183	112	1.00E-24	27	47	(AL035548) meu14, ring zinc finger [Schizosaccharomyces pombe]
22319	ENU06113	ANI61C4660: 52-78 506..1	52-78	444-464	NAP		g1945094	317	126	1.00E-28	42	51	(D88802) ydhJ [Bacillus subtilis]
22320	ENU06114	ANI61C344:1 22-49 726..475	22-49	786-805	NAP		g549037	845	103	4.00E-42	44	63	"tyrosyl-TRNA synthetase, cytoplasmic (tyrosyl--TRNA ligase) (TYRRS) [Saccharomyces cerevisiae]"
22321	ENU06115	ANI61C7626: 22-48 1362..2185	22-48	595-617	NAP		g2828499	226	117	8.00E-26	28	64	hypothetical 41.8 KD protein (ORFM) []
22322	ENU06116	ANI61C2105: 22-41 257..1047	22-41	656-675	NAP		g731857	267	118	4.00E-26	37	26	hypothetical 103.6 KD protein in COX5B-PFK26 intergenic region [Saccharomyces cerevisiae]
22323	ENU06117	ANI61C346:4 106-123 053..3380	106-123	623-642	NAP		g4191500	1045	199	2.00E-50	97	49	(AF098669) pantothenate kinase [Emericella nidulans]
22324	ENU06118	ANI61S4392: 1..741			NAP		g2467272	701	275	3.00E-73	61	31	(Z99759) hypothetical protein [Schizosaccharomyces pombe]

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22325	ENU06119	ANI61C1002 0:1..602	102-121	499-526	NAP		g585377	550	220	2.00E-57	51	39	probable mannosyltransferase KTR4 [Saccharomyces cerevisiae]
22326	ENU06120	ANI61C9979: 82-101 4113..3675	82-101	394-418	NAP		g280164	63	62	0.000000	22	43	probable dehydrogenase (EC 1.-.-.-) - Vibrio cholerae [Vibrio cholerae]
22327	ENU06121	ANI61C1079 6:1764..41	22-46	766-789	NAP		g135100	1254	276	8.00E-84			"aspartyl-TRNA synthetase, cytoplasmic (aspartate--TRNA ligase) (ASPRS) [Saccharomyces cerevisiae]"
22328	ENU06122	ANI61C9357: 30-57 6603..5322	30-57	810-829	NAP		g1176581	1120	300	7.00E-81	53	31	hypothetical 101.7 KD protein in EGT2-KRE1 intergenic region [Saccharomyces cerevisiae]
22329	ENU06123	ANI61S3452: 59-86 511..1	59-86	462-489	NAP		g807674	327	99	4.00E-24	45	21	(M23385) pol protein [Simian sarcoma virus]
22330	ENU06124	ANI61C1040 0:1036..220	115-134	777-796	NAP		g3183028	370	159	2.00E-38	35	77	probable histidinol-phosphatase [Schizosaccharomyces pombe]
22331	ENU06125	ANI61C5831: 57-84 904..595	57-84	262-289	NAP		g3220154	235	107	3.00E-23	47	28	(AF022789) ubiquitin hydrolyzing enzyme I [Homo sapiens]
22332	ENU06126	ANI61C6438: 102-129 743..1	102-129	620-642	NAP		g1709240	518	175	4.00E-43	48	31	cell division control protein NDA4 []
22333	ENU06127	ANI61C8710: 57-77 389..1493	57-77	802-829	NAP		g2132227	364	96	2.00E-31	42	76	hypothetical protein YPL196w - yeast (Saccharomyces cerevisiae)
22334	ENU06128	ANI61C3623: 211-238 418..1	211-238	448-467	NAP		g1169590	164	89	3.00E-17	37	43	[Saccharomyces cerevisiae] Malonyl COA-acyl carrier protein transacylase (MCT) [Haemophilus influenzae Rd]
22335	ENU06129	ANI61C4966: 22-49 1430..1	22-49	657-684	NAP		g83673	503	78	1.00E-34	37	45	amidase (EC 3.5.1.4) - Aspergillus oryzae [Aspergillus oryzae]
22336	ENU06130	ANI61C6896: 43-62 960..223	43-62	652-671	NAP		g2226418	178	75	5.00E-13	34	53	(Z97204) hypothetical protein [Schizosaccharomyces pombe]
22337	ENU06131	ANI61C3102: 115-137 753..158	115-137	514-533	NAP		g4481949	581	226	1.00E-58	67	51	(AL035637) glycoprotein endopeptidase-like protein. [Schizosaccharomyces pombe]
22338	ENU06132	ANI61C7249: 22-42 1567..328	22-42	810-829	NAP		g731481	500	114	1.00E-24	44	42	hypothetical 58.0 KD peptidase in PTP3-ILV1 intergenic region [Saccharomyces cerevisiae]
22339	ENU06133	ANI61C651:1 23-43 825..1050	23-43	730-755	NAP		g4507711	119	49	0.00003	36	62	tetratricopeptide repeat domain 1 [Homo sapiens]
22340	ENU06134	ANI61C9781: 95-116 1060..606	95-116	403-422	NAP		g3702642	285	97	8.00E-20	52	36	(AL031825) rna binding protein - putative pre mna splicing factor [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22341	ENU06135	ANI61C1861: 1870..1	22-43	802-829	NAP		g1762781	1324	129	3.00E-29	44	27	(U65685) phosphoinositide-specific phospholipase C [Botryotinia fuckeliana]
22342	ENU06136	ANI61S2460: 1..574			NAP		g913016	107	79	2.00E-14	27	12	(S76267) Snq2 homolog=bfr1 [Schizosaccharomyces pombe]
22343	ENU06137	ANI61C6319: 34-53 4372..3430		806-825	NAP		g4539662	252	74	8.00E-22	31	27	(AF061282) polyprotein [Sorghum bicolor]
22344	ENU06138	ANI61C9871: 22-41 26..901		790-810	NAP		g141051	419	81	6.00E-32	43	53	hypothetical protein in MMSB 3'region (ORF1) [Pseudomonas aeruginosa]
22345	ENU06139	ANI61C591:7 33-52 27..1		644-662	NAP		g497653	70	38	0.058	19	11	(U09782) myosin heavy chain [Argopecten irradians]
22346	ENU06140	ANI61C4843: 86-109 625..11		514-538	NAP		g1488255	96	75	3.00E-13	26	32	(U38416) ferulate-5-hydroxylase [Arabidopsis thaliana]
22347	ENU06141	ANI61S2985: 1..591			NAP		g186396	135	38	0.058	33	15	(M94131) mucin [Homo sapiens]
22348	ENU06142	ANI61C8111: 42-61 1807..113		631-648	NAP		g2494820	1626	125	1.00E-55	85	36	Rhannogalacturonase B precursor (rhannogalacturonan lyase) (RGASE B) (RHG B) [Aspergillus aculeatus]
22349	ENU06143	ANI61C1024 24-51 2:434..1587		806-829	NAP		g1723685	925	180	4.00E-62	56	78	hypothetical 38.3 KD protein in RPL16B-PDC6 intergenic region [Saccharomyces cerevisiae]
22350	ENU06144	ANI61S3184: 1..431			NAP		g539218	149	41	0.003	25	26	hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae) []
22351	ENU06145	ANI61C2805: 68-87 1993..1481		465-484	NAP		g2131533	167	83	5.00E-16	32	29	hypothetical protein YDR501w - yeast (Saccharomyces cerevisiae)
22352	ENU06146	ANI61C8818: 69-88 3099..3485		440-459	NAP		g2492821	330	143	6.00E-34	48	100	[Saccharomyces cerevisiae] Augmenter of liver regeneration (HERV1 protein) [Homo sapiens]
22353	ENU06147	ANI61C2583: 118-137 1..783		645-663	NAP		g4033486	270	122	2.00E-27	30	58	putative tartrate transporter [Agrobacterium vitis]
22354	ENU06148	ANI61C1112 69-88 8:3194..4170		765-784	NAP		g2492491	971	167	5.00E-84	86	87	14-3-3 protein homolog (TH1433) [Trichoderma harzianum]
22355	ENU06149	ANI61C4678: 67-86 78..716		576-596	NAP		g2511761	938	215	4.00E-97	97	23	(AF023156) carnitine acetyl transferase FacC [Emeticella nidulans]
22356	ENU06150	ANI61C3182: 27-54 1847..2710		805-829	NAP		g549722	199	51	1.00E-20			DNA-directed RNA polymerase III 25 KD polypeptide (C25) [Saccharomyces cerevisiae]

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22357	ENU06151	ANI61C7398: 108..485	78-97	445-464	NAP		g3417421	266	126	8.00E-29	52	40	(AL031261) forkhead nuclear signalling domain protein
22358	ENU06152	ANI61C476:4 92-119 55..1		330-354	NAP		g4377374	113	43	0.000000 009	26	35	[Schizosaccharomyces pombe] (AE001684) Adenosylmethionine-8-Amino-7-Oxonanoate Aminotransferase [Chlamydia pneumoniae]
22359	ENU06153	ANI61C4149: 25-44 592..1281		581-601	NAP		g2497670	43	49	0.00003	39	15	Homeobox protein LIM-1 [Danio rerio]
22360	ENU06154	ANI61C9601: 30-54 6926..7975		620-644	NAP		g2494036	218	60	7.00E-13			D-amino acid oxidase (DAMOX) (DAO) (DAO) [Trigonopsis variabilis]
22361	ENU06155	ANI61C8113: 25-47 1170..2314		657-684	NAP		g729467	564	206	1.00E-52	42	48	purine-cytosine permease (PCP) (cytosine/purine transport protein) [Saccharomyces cerevisiae]
22362	ENU06156	ANI61C4412: 59-86 5991..4552		807-829	NAP		g529564	532	115	4.00E-32	36	65	"[L35343] 2,3-butanediol dehydrogenase [Pseudomonas putida]"
22363	ENU06157	ANI61C3596: 102-124 572..1		490-515	NAP		g1703372	126	83	1.00E-15	27	35	Probable sterol O-acyltransferase (sterol-ester synthase) [Schizosaccharomyces pombe]
22364	ENU06158	ANI61C1165: 22-49 1873..10		786-811	NAP		g1346405	736	181	5.00E-45	34	46	Laccase precursor (benzenediol:oxygen oxidoreductase) (urishiol oxidase) (laccase I) [Emericella nidulans]
22365	ENU06159	ANI61C508:2 22-47 561..3516		806-829	NAP		g2497175	396	92	4.00E-32	39	92	hypothetical 31.1 KD protein in SIP18-SPT21 intergenic region [Saccharomyces cerevisiae]
22366	ENU06160	ANI61C6718: 110-129 1..527		477-496	NAP		g1020413	84	55	0.000000 002	30	22	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
22367	ENU06161	ANI61C1080 24-43 2..818..1		684-703	NAP		g1723910	818	321	4.00E-87	66	33	Pre-MRNA splicing factor RNA helicase PRP43 (helicase JAI) [Saccharomyces cerevisiae]
22368	ENU06162	ANI61C9004: 95-114 1..550		423-442	NAP		g1834322	347	92	1.00E-29	45	52	(D50661) RNA polymerase II subunit 3 [Schizosaccharomyces pombe]
22369	ENU06163	ANI61C4804: 22-49 1622..1		725-749	NAP		g4102636	2457	555	e-159	99	43	(AF014812) G1/S regulator [Emericella nidulans]
22370	ENU06164	ANI61C9461: 38-57 1625..2292		576-603	NAP		g586919	198	80	1.00E-14	37	71	YSA1 protein [Saccharomyces cerevisiae]

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22371	ENU06165	ANI61C5506: 27-46 2157..3090	791-816	NAP			g1723769	261	134	6.00E-31	28	51	putative transporter YGR260W [Saccharomyces cerevisiae]
22372	ENU06166	ANI61C8552: 23-46 7660..5342	803-829	NAP			g2132019	392	70	2.00E-11			hypothetical protein YOL141w - yeast [Saccharomyces cerevisiae]
22373	ENU06167	ANI61C5975: 67-90 1..642	554-572	NAP			g3649751	421	174	5.00E-43	44	54	[Saccharomyces cerevisiae] (Z15137) esterase A [Streptomyces chrysomallus]
22374	ENU06168	ANI61C103:1 70-89 690..1074	562-582	NAP			g2414601	250	63	3.00E-21	51	20	(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
22375	ENU06169	ANI61C5302: 46-66 437..1975	802-829	NAP			g465480	283	145	3.00E-34			Dolichyl-diphosphooligosaccharide--protein glycosyltransferase beta subunit precursor (oligosaccharyl transferase beta subunit) [Saccharomyces cerevisiae]
22376	ENU06170	ANI61C1132: 25-44 3391..6926	776-796	NAP			g3136056	1918	85	8.00E-16	32	22	(AL023592) RanBP7/importin-beta/Cse1p superfamily protein [Schizosaccharomyces pombe]
22377	ENU06171	ANI61C3382: 22-44 848..1	711-733	NAP			g4584836	913	273	3.00E-99	67	37	(AJ238009) serine threonine protein kinase [Sclerotinia sclerotiorum]
22378	ENU06172	ANI61C2441: 39-58 402..1080	595-614	NAP			g1723485	403	182	2.00E-45	44	54	hypothetical 47.3 KD protein C17G8.13C in chromosome I [Schizosaccharomyces pombe]
22379	ENU06173	ANI61C9052: 122-142 1868..1473	344-363	NAP			g3581896	89	40	0.000007	34	18	(AL031543) putative amino-acid permease [Schizosaccharomyces pombe]
22380	ENU06174	ANI61C3578: 109-128 1..361	300-319	NAP			g3282044	367	159	6.00E-39	66	8	(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
22381	ENU06175	ANI61C9636: 103-121 4730..4145	521-540	NAP			g454894	354	148	1.00E-43	45	47	(Z29988) Mnt1 protein [Saccharomyces cerevisiae]
22382	ENU06176	ANI61C1147 60-79 7:922..2445	805-827	NAP			g2414593	781	186	2.00E-46	42	52	(Z99258) molybdopterin biosynthesis [Schizosaccharomyces pombe]
22383	ENU06177	ANI61C1183: 36-55 3191..3650	449-476	NAP			g1723514	180	83	9.00E-16	31	100	hypothetical 16.7 KD protein C1F12.10C in chromosome I [Schizosaccharomyces pombe]
22384	ENU06178	ANI61C7662: 22-44 261..930	628-649	NAP			g1168807	485	207	5.00E-53	55	32	probable protein-tyrosine phosphatase CDC14 [Saccharomyces cerevisiae]
22385	ENU06179	ANI61C6688: 33-60 328..873	500-525	NAP			g476389	55	42	0.003	19	9	"myosin heavy chain-B, neuronal - chicken [Gallus gallus]"

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22386	ENU06180	ANI61C8735: 24-50 865..1502	513-532	513-532	NAP		g2224699	197	102	2.00E-21	33	23	(AB002377) KIAA0379 [Homo sapiens]
22387	ENU06181	ANI61C9465: 47-66 1..3299	776-795	776-795	NAP		g3785995	2130	204	6.00E-52	53	18	(AC005499) unknown protein [Arabidopsis thaliana]
22388	ENU06182	ANI61C6501: 93-115 745..1	606-625	606-625	NAP		g3915154	142	63	1.00E-10	32	42	trichodiene oxygenase (cytochrome P450 58) [Fusarium sporotrichioides]
22389	ENU06183	ANI61C8122: 1..553			NAP		g462024	312	91	4.00E-27	42	47	delta(24)-sterol C-methyltransferase [Saccharomyces cerevisiae]
22390	ENU06184	ANI61C6703: 206-229 328..909	539-561	539-561	NAP		g3695005	350	159	2.00E-38	54	47	(AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2 [Zea mays]
22391	ENU06185	ANI61C4945: 50-73 926..486	396-420	396-420	NAP		g3282095	199	93	1.00E-18	37	48	(AJ007446) hypothetical protein [Thermotoga neapolitana]
22392	ENU06186	ANI61S920:1..784			NAP		g3005587	180	58	0.000000	21	31	(AF048977) Ser/Arg-related nuclear matrix protein [Homo sapiens]
22393	ENU06187	ANI61C8511: 64-83 544..1	409-429	409-429	NAP		g1935000	587	190	5.00E-60	80	75	(Y12314) GTPase [Schizosaccharomyces pombe]
22394	ENU06188	ANI61C7695: 74-93 943..1	727-749	727-749	NAP		g2094861	234	118	5.00E-26	25	13	(Z95334) t7i23.15 protein. [Schizosaccharomyces pombe]
22395	ENU06189	ANI61C7316: 22-47 6120..6902	732-759	732-759	NAP		g1666124	417	170	1.00E-41	32	100	(Z82098) hypothetical protein Rv3536c [Mycobacterium tuberculosis]
22396	ENU06190	ANI61C2480: 46-65 942..2979	781-800	781-800	NAP		g1098357	1116	161	4.00E-75	66	43	shk1 gene [Schizosaccharomyces pombe]
22397	ENU06191	ANI61C1054 36-54 0:1370..3393	804-829	804-829	NAP		g1764155	1012	236	1.00E-61	46	46	(U16782) chlorophenol monoxygenase [Ralstonia eutropha]
22398	ENU06192	ANI61S1352: 1..677			NAP		g3153821	118	47	0.0001	24	21	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
22399	ENU06193	ANI61C5463: 102-126 1..622	539-560	539-560	NAP		g4107315	225	116	1.00E-25	42	20	(AL035075) conserved hypothetical protein [Schizosaccharomyces pombe]
22400	ENU06194	ANI61C1114 2:1..1798			NAP		g1834340	1288	93	2.00E-42	59	15	(Z68904) ATP-binding cassette multidrug transporter [Emeritella nidulans]
22401	ENU06195	ANI61C5207: 37-56 1857..844	799-818	799-818	NAP		g1730102	781	294	6.00E-79	53	84	D-lactate dehydrogenase (D-LDH) [Escherichia coli]
22402	ENU06196	ANI61C7617: 23-44 834..1	714-735	714-735	NAP		g423973	536	227	7.00E-59	52	36	phenol 2-monoxygenase (EC 1.14.13.7) - jelly fungus (Trichosporon beigelii) []

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22403	ENU06197	ANI61C3223: 102-125 514-536 557..1			NAP		g2554598	85	62	0.000000 004	29	31	(AB00508) poly(3-hydroxybutyrate) depolymerase precursor [Comamonas testosteroni]
22404	ENU06198	ANI61C6564: 1..1142			NAP		g1351598	408	157	1.00E-37	40	44	hypothetical 59.6 KD protein C4G8.07C in chromosome I [Schizosaccharomyces pombe]
22405	ENU06199	ANI61S826:1..766			NAP		g134769	518	173	1.00E-46	50	59	Stage IV sporulation protein B [Bacillus subtilis]
22406	ENU06200	ANI61C7078: 1..466			NAP		g2245428	598	173	5.00E-43	94	15	(U91968) topoisomerase I [Emmericella nidulans]
22407	ENU06201	ANI61C8669: 3636..4884			NAP		g4007795	354	90	3.00E-23			(AL034463) putative nuclear envelope pore membrane protein [Schizosaccharomyces pombe]
22408	ENU06202	ANI61C2274: 100-127 300-327 1..352			NAP		g115943	281	128	2.00E-29	51	32	cytochrome C heme lyase (CCHL) (holocytochrome-C synthase) [Neurospora crassa]
22409	ENU06203	ANI61S42:41 48-69 277-303 3..1			NAP		g466053	164	95	3.00E-19	38	23	hypothetical 68.7 KD protein ZK757.1 in chromosome III [Caenorhabditis elegans]
22410	ENU06204	ANI61C1077 49-76 807-826 4:1..1700			NAP		g1352619	879	146	5.00E-50	73	40	Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex precursor (E2) [Saccharomyces cerevisiae]
22411	ENU06205	ANI61C3628: 72-91 661-680 1..1106			NAP		g231717	1359	259	1.00E-86	75	36	Minichromosome maintenance protein 5 (cell division control protein 46) [Saccharomyces cerevisiae]
22412	ENU06206	ANI61C2430: 102-127 430-457 1..480			NAP		g3261632	375	152	1.00E-36	45	30	(Z79700) accD2 [Mycobacterium tuberculosis]
22413	ENU06207	ANI61C5576: 49-73 809-829 1..1921			NAP		g3560142	633	109	2.00E-35	34	45	(AL031534) Major facilitator superfamily protein [Schizosaccharomyces pombe]
22414	ENU06208	ANI61C8479: 1457..1940			NAP		g347455	187	45	0.0003	39	93	(L22030) hydroxyproline-rich glycoprotein [Glycine max]
22415	ENU06209	ANI61C7459: 22-42 528-547 585..1			NAP		g4033735	286	156	1.00E-37	50	13	(AF054284) spliceosomal protein SAP 155 [Homo sapiens]
22416	ENU06210	ANI61C1134 46-73 807-829 1:3734..1823			NAP		g1175452	332	107	1.00E-22	30	25	hypothetical 85.7 KD protein C13G6.03 in chromosome I [Schizosaccharomyces pombe]

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22417	ENU06211	ANI61S1223: 1..340	157-177	311-331	NAP		g854065	401	49	0.00001	50	26	(X83413) U88 [Human herpesvirus 6]
22418	ENU06212	ANI61S3220: 157-177 311-331 541..87			NAP		g1352438	195	91	5.00E-18	36	38	eukaryotic initiation factor 4A-like protein C1F5.10
22419	ENU06213	ANI61C9889: 102-124 366-385 1..409			NAP		g112947	150	84	4.00E-16	38	28	[Schizosaccharomyces pombe] AAC-rich MRNA clone AAC3 protein [Dictyostelium discoideum]
22420	ENU06214	ANI61C8653: 1705..445			NAP		g4758510	735	195	4.00E-49			H beta 58 homolog [Homo sapiens]
22421	ENU06215	ANI61C1095 22-48 509-536 4:2671..3314			NAP		g131782	524	132	1.00E-52	63	13	DNA repair protein RAD50 (153 KD protein) [Saccharomyces cerevisiae]
22422	ENU06216	ANI61C8033: 22-47 49..978			NAP		g485111	405	159	8.00E-45	42	58	(U00050) similar to enoyl-CoA hydratases; highest similarity to YKRS_YEAST [Caenorhabditis elegans]
22423	ENU06217	ANI61C9123: 46-65 155..1095			NAP		g2493389	136	66	3.00E-10	23	55	probable sterigmatocystin biosynthesis P450 monooxygenase STCF (cytochrome P450 60A2) [Emericella nidulans]
22424	ENU06218	ANI61C6123: 22-49 705..1			NAP		g91209	108	43	0.003	38	58	proline-rich protein MP2 - mouse (fragment) []
22425	ENU06219	ANI61C6470: 22-46 6089..4759			NAP		g1791305	2018	420	e-143	98	65	(U83489) septin B [Emericella nidulans]
22426	ENU06220	ANI61S4337: 36-56 503..1			NAP		g3873862	182	89	2.00E-17	35	30	(Z35595) similar to 4-coumarate-coA ligase; cDNA EST yk455e10.3 comes from this gene; cDNA EST yk455e10.5 comes from this gene; cDNA EST comes from this gene; cDNA EST yk286h10.3 comes from this gene; cDNA EST yk286h10.5 comes from this gene [Caenorhabditis ... []
22427	ENU06221	ANI61S3166: 52-77 544..1			NAP		g3819099	300	127	6.00E-29	51	20	(AJ009825) copper amine oxidase [Cicer arietinum]
22428	ENU06222	ANI61C1129 37-56 3:1130..1			NAP		g2499576	1347	176	3.00E-89	85	21	protein kinase C-like [Aspergillus niger]
22429	ENU06223	ANI61C293:1 ..306			NAP		g1353167	126	61	0.000000	31	37	hypothetical 30.6 KD protein F52C9.4 in chromosome III [Caenorhabditis elegans]

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22430	ENU06224	ANI61C1386: 42-61 526..1	42-61	445-464	NAP		g1077342	200	66	1.00E-14	37	54	probable membrane protein YLR284c - yeast (<i>Saccharomyces cerevisiae</i>) [<i>Saccharomyces cerevisiae</i>] (X89442) peptide synthetase [<i>Metarhizium anisopliae</i>] (U79756) GTPase cRac1B [<i>Gallus gallus</i>] guanine nucleotide-binding protein alpha-1 subunit (GPI-alpha) [<i>Neurospora crassa</i>] (AF125451) contains similarity to the NIFR3/SMM1 family [<i>Caenorhabditis elegans</i>] (AF031194) S276 [<i>Triticum aestivum</i>]
22431	ENU06225	ANI61C1975: 23-42 2764..1	23-42	661-685	NAP		g2342601	1548	166	2.00E-40	36	5	
22432	ENU06226	ANI61C4494: 54-73 772..1419	54-73	524-546	NAP		g3184512	524	150	8.00E-53	73	77	
22433	ENU06227	ANI61C3323: 62-89 5084..4724	62-89	313-340	NAP		g585175	314	138	2.00E-32	57	33	
22434	ENU06228	ANI61C5753: 202-228 1..504	202-228	457-482	NAP		g4226107	372	110	7.00E-32	50	27	
22435	ENU06229	ANI61S2462: 24-46 1..570	24-46	345-372	NAP		g4104056	359	140	6.00E-33	40	38	
22436	ENU06230	ANI61C2477: 22-44 1677..3344	22-44	799-826	NAP		g120965	2511	473	e-135	99	53	4-aminobutyrate aminotransferase (gamma-amino-N-butyrate transaminase) (GABA transaminase) (GABA aminotransferase) [<i>Emericella nidulans</i>] hypothetical LACA/RPIB family protein in SPOIIR-GLYC intergenic region [<i>Bacillus subtilis</i>] (AL049608) extensin-like protein [<i>Arabidopsis thaliana</i>] "Citrate synthase, mitochondrial precursor [<i>Emericella nidulans</i>]" hypothetical 49.9 KD protein in SPO1-SIS1 intergenic region [<i>Saccharomyces cerevisiae</i>] "([L76169) reverse transcriptase, RNaseH [<i>Glomerella cingulata</i>]" "(Z98762) SPAC4A8.16c, putative nuclear transport protein, len:639aa, similar eg. to YMR309C, NIP1_YEAST, P32497, nuclear transport protein nip1, (812aa), fasta scores, op t:926, E:0.0, (34.3% identity in 581 aa overlap), ide... []"
22437	ENU06231	ANI61S1069: 331..740			NAP		g732387	196	77	3.00E-16			
22438	ENU06232	ANI61S769:1..859			NAP		g4584539	612			49	36	
22439	ENU06233	ANI61C6152: 51-69 1..682	51-69	601-620	NAP		g2493725	869	211	1.00E-84	96	39	
22440	ENU06234	ANI61C6829: 22-43 1799..286	22-43	801-828	NAP		g1730706	583	99	5.00E-20	29	55	
22441	ENU06235	ANI61C4535: 22-47 2861..1	22-47	782-800	NAP		g1166378	958	114	7.00E-25	32	23	
22442	ENU06236	ANI61C2280: 24-51 1536..1	24-51	768-795	NAP		g4490654	1064	162	2.00E-72	48	44	

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22443	ENU06237	ANI61C1032	34-53	561-587	NAP		g1723482	236	125	3.00E-28	37	67	DMA1 protein [Schizosaccharomyces pombe]
22444	ENU06238	ANI61C1064	188-207	624-650	NAP		g1077386	337	82	8.00E-30	40	40	hypothetical protein YLR345w - yeast [Saccharomyces cerevisiae]
22445	ENU06239	ANI61C5085: 23-42 2220..1	716-742		NAP		g730753	1745	249	1.00E-65			chromosome segregation protein SMC2 (DA-BOX protein SMC2) [Saccharomyces cerevisiae]
22446	ENU06240	ANI61C1135	22-48	776-801	NAP		g731834	596	159	2.00E-38	43	60	hypothetical 41.9 KD protein in SDS3-THS1 intergenic region [Saccharomyces cerevisiae]
22447	ENU06241	ANI61C3285: 117-136 1..534	446-465		NAP		g2623295	174	82	2.00E-16	39	42	(AC002409) hypothetical protein [Arabidopsis thaliana]
22448	ENU06242	ANI61S1082: 722..1			NAP		g1169440	904	309	7.00E-87	81	5	"dynein heavy chain, cytosolic (DYHC) [Emicella nidulans]"
22449	ENU06243	ANI61C9181: 27-54 795..1569	728-747		NAP		g2132141	286	80	4.00E-28	43	99	hypothetical protein YOR367w - yeast [Saccharomyces cerevisiae]
22450	ENU06244	ANI61C6586: 24-45 1527..1	723-746		NAP		g2499125	810	150	1.00E-35	28	9	vacuolar protein sorting-associated protein VPS13 [Saccharomyces cerevisiae]
22451	ENU06245	ANI61C1112	32-51	458-481	NAP		g2879853	248	78	1.00E-20	45	36	(AL021815) arginase family protein [Schizosaccharomyces pombe]
22452	ENU06246	ANI61C2339: 64-83 801..319	301-328		NAP		g1351629	109	90	1.00E-17			hypothetical 18.5 KD protein C12G12.05C in chromosome I [Schizosaccharomyces pombe]
22453	ENU06247	ANI61C4662: 109-128 623..325	251-278		NAP		g984373	313	134	2.00E-31	65	27	(U32375) tartrate dehydrogenase [Agrobacterium vitis]
22454	ENU06248	ANI61S1794: 1..468			NAP		g3810866	78	36	0.00006	42	39	hydroxyacylglutathione hydrolase [Schizosaccharomyces pombe]
22455	ENU06249	ANI61C9545: 100-119 1..682	625-644		NAP		g4927212	125	37	0.15			(AF134304) Scar2 [Homo sapiens]
22456	ENU06250	ANI61C9449: 25-42 7873..6332	803-823		NAP		g128853	1179	273	4.00E-87	70	62	NADH-ubiquinone oxidoreductase 40 KD subunit precursor (complex I-40KD) (CI-40KD) [Neurospora crassa]
22457	ENU06251	ANI61C1021	22-44	740-767	NAP		g731434	253	126	2.00E-28	37	97	hypothetical 25.1 KD protein in PM140-PAC2 intergenic region [Saccharomyces cerevisiae]

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22458	ENU06252	ANI61C8628: 102-124 1.658	102-124	610-637	NAP		g2256848	187	98	8.00E-20	41	78	(AP000002) 219aa long hypothetical protein [Pyrococcus horikoshii]
22459	ENU06253	ANI61C4897: 22-47 242..946	22-47	636-654	NAP		g1729996	127	62	8.00E-12	32	63	TOXD protein [Cochliobolus carbonum]
22460	ENU06254	ANI61C306:1 22-46 459..1	22-46	786-810	NAP		g2114323	287	35	0.73	26	32	(D88734) membrane glycoprotein [Equine herpesvirus 1]
22461	ENU06255	ANI61C5208: 31-50 2538..1	31-50	715-738	NAP		g2132688	1499	279	1.00E-74	47	5	probable membrane protein YLR106c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22462	ENU06256	ANI61C1077 23-42 1:1947..1	23-42	716-735	NAP		g1945493	1327	109	3.00E-36	44	25	"(U56965) Similar to NAD(P) transhydrogenase, mitochondrial; coded for by C. elegans cDNA yk27c1.5; coded for by C. elegans cDNA yk35b9.5; coded for by C. elegans cDNA yk161c9.3; coded for by C. elegans ... []"
22463	ENU06257	ANI61C8566: 33-60 905..1	33-60	760-783	NAP		g3393020	965	348	5.00E-95	70	47	(AL031174) t-complex protein 1 gamma subunit homolog [Schizosaccharomyces pombe]
22464	ENU06258	ANI61C9752: 32-59 1295..1	32-59	804-827	NAP		g1182038	583	153	2.00E-36	37	15	(Z69368) unknown [Schizosaccharomyces pombe]
22465	ENU06259	ANI61C7363: 22-46 1510..1	22-46	710-737	NAP		g2501011	986	224	6.00E-58	43	27	Isoleucyl-TRNA synthetase (isoleucine--TRNA ligase) (ILERS) [Synechocystis sp.]
22466	ENU06260	ANI61C1027 22-44 0:6447..7518	22-44	608-630	NAP		g2131201	420	155	3.00E-37	42	55	"Ca2+/H+-exchanging protein, vacuolar - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]"
22467	ENU06261	ANI61S4372: 544..239			NAP		g581280	444	168	5.00E-42	82	85	(V00618) unidentified reading frame [Escherichia coli]
22468	ENU06262	ANI61C3636: 22-47 7267..8447	22-47	717-744	NAP		g4914370	131	66	1.00E-20			(AC007584) putative polyprotein [Arabidopsis thaliana]
22469	ENU06263	ANI61C5734: 51-78 753..1816	51-78	696-716	NAP		g1870209	430	59	2.00E-18	34	50	(AC000133) ORF [Emericella nidulans]
22470	ENU06264	ANI61C7800: 23-42 1144..1	23-42	714-733	NAP		g2133034	228	95	3.00E-24	31	38	probable membrane protein YPR156c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]

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22471	ENU06265	ANI61C2511: 1537..238			NAP		g1351666	1401	129	6.00E-75	66	42	putative ATP-dependent RNA helicase C1F7.02C [Schizosaccharomyces pombe]
22472	ENU06266	ANI61C6518: 22-49	756-782		NAP		g2440082	235	75	9.00E-23	33	31	(Y14849) putative glucose sensor [Kluyveromyces lactis]
22473	ENU06267	ANI61C5564: 39-59	763-782		NAP		g1346390	334	149	2.00E-35	32	31	serine/threonine-protein kinase CLA4 [Saccharomyces cerevisiae]
22474	ENU06268	ANI61C6853: 120-139	496-515		NAP		g1710791	354	118	2.00E-26	48	42	probable mitochondrial 40S ribosomal protein S5 [Schizosaccharomyces pombe]
22475	ENU06269	ANI61C9440: 50-75	295-314		NAP		g416685	145	61	0.000000	36	36	ATP11 protein precursor [Saccharomyces cerevisiae]
22476	ENU06270	ANI61C2599: 52-71	512-531		NAP		g3913432	740	214	5.00E-69	78	25	putative pre-mRNA splicing factor ATP-dependent RNA helicase SPBC16H5.10C
22477	ENU06271	ANI61C2216: 102-122	751-777		NAP		g1706440	247	71	1.00E-24	38	39	[Schizosaccharomyces pombe] Spore wall maturation protein DIT1
22478	ENU06272	ANI61C686:5 22-49	804-827		NAP		g3150262	468	150	2.00E-35	35	80	[Saccharomyces cerevisiae] (AL023634) hypothetical protein
22479	ENU06273	ANI61C1185: 22-47	805-824		NAP		g133356	3156	160	6.00E-75			[Schizosaccharomyces pombe] DNA-directed RNA polymerase III largeST subunit (C160)
22480	ENU06274	ANI61C4836: 62-81	727-749		NAP		g279978	87	80	3.00E-14	24	46	[Saccharomyces cerevisiae] benzoylformate decarboxylase (EC 4.1.1.7) - Pseudomonas putida []
22481	ENU06275	ANI61C3148: 22-42	731-750		NAP		g416574	1638	550	e-156	94	75	probable formate dehydrogenase (NAD-dependent formate dehydrogenase) (FDH) [Emericella nidulans]
22482	ENU06276	ANI61C5449: 22-48	490-517		NAP		g1546072	131	66	2.00E-10	37	5	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22483	ENU06277	ANI61C8576: 72-91	541-560		NAP		g1705652	369	99	2.00E-34	56	100	20 KD nuclear CAP binding protein (NCBP) (CBP20) [Xenopus laevis]
22484	ENU06278	ANI61C1081 22-46	763-782		NAP		g1546072	1253	117	8.00E-26	33	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22485	ENU06279	ANI61C1043 112-131	726-749		NAP		g1169440	9561	541	e-153	99	6	"dynein heavy chain, cytosolic (DYHC) [Emericella nidulans]"

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22486	ENU06280	ANI61C1146: 1..705	102-129	636-656	NAP		g1362615	405	204	6.00E-52	43	22	iswi protein - fruit fly (<i>Drosophila melanogaster</i>) [<i>Drosophila melanogaster</i>]
22487	ENU06281	ANI61C9941: 107-127 1..392	107-127	350-371	NAP		g106185	174	83	1.00E-15	42	53	GTP-binding protein Rab2 - human [<i>Homo sapiens</i>]
22488	ENU06282	ANI61C1081: 30-48 173..847	30-48	606-625	NAP		g1934645	174	92	3.00E-18	37	97	(U93876) hypothetical protein YrdC [<i>Bacillus subtilis</i>]
22489	ENU06283	ANI61C6360: 115-136 3284..2430	115-136	809-828	NAP		g1790870	380	87	2.00E-29	42	97	(U32622) toluesulfonate zinc-independent alcohol dehydrogenase [<i>Comamonas testosteroni</i>]
22490	ENU06284	ANI61C711:1 56-78 .415	56-78	373-394	NAP		g2493915	184	90	9.00E-18	41	60	cutinase precursor [<i>Botryotinia fuckeliana</i>]
22491	ENU06285	ANI61S3073: 1..422			NAP		g2950476	134	46	0.00009	38	51	(AL022070) vesicle transport v-snare protein [<i>Schizosaccharomyces pombe</i>]
22492	ENU06286	ANI61C2684: 114-133 1465..957	114-133	467-487	NAP		g4506123	243	65	4.00E-21	39	44	pre-mRNA splicing factor similar to S. cerevisiae Prp18 [<i>Homo sapiens</i>]
22493	ENU06287	ANI61C4085: 22-49 4161..3302	22-49	809-828	NAP		g2649154	275	123	1.00E-27	31	98	(AE001006) membrane protein [<i>Archaeoglobus fulgidus</i>]
22494	ENU06288	ANI61C861:1 22-41 ..1021	22-41	711-730	NAP		g130155	853	162	4.00E-81	56	41	Deoxyribodipyrimidine photolyase (DNA photolyase) (photoreactivating enzyme) [<i>Neurospora crassa</i>]
22495	ENU06289	ANI61C2490: 27-53 1655..3594	27-53	807-829	NAP		g3322837	324	51	3.00E-14	31	41	(AE001229) T. pallidum predicted coding region TP0544 [<i>Treponema pallidum</i>]
22496	ENU06290	ANI61C6643: 50-69 1..1179	50-69	802-821	NAP		g2648180	292	98	6.00E-20	34	66	(AE000943) conserved hypothetical protein [<i>Archaeoglobus fulgidus</i>]
22497	ENU06291	ANI61C7691: 22-48 1017..289	22-48	686-708	NAP		g136642	433	131	6.00E-30			Ubiquitin-conjugating enzyme E2-34 KD (ubiquitin-protein ligase) (ubiquitin carrier protein) (cell division control protein 34) [<i>Saccharomyces cerevisiae</i>]
22498	ENU06292	ANI61C6883: 92-111 1584..1251	92-111	262-281	NAP		g984373	391	141	2.00E-33	72	31	(U32375) tartrate dehydrogenase [<i>Agrobacterium vitis</i>]
22499	ENU06293	ANI61C4294: 33-52 796..1	33-52	747-766	NAP		g228477	191			35	50	EC1F2 upstream ORF [saimirine herpesvirus 1]
22500	ENU06294	ANI61C7396: 6367..7884			NAP		g2117306	452	74	1.00E-14	35	39	(Z95620) dna-(apurinic or apyrimidinic site) lyase [<i>Schizosaccharomyces pombe</i>]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22501	ENU06295	ANI61C9984: 126-145	126-145	308-330	NAP		g683698	138	74	3.00E-15	29	40	(Z48229) orf1 [Saccharomyces cerevisiae]
22502	ENU06296	ANI61C316:5 46-65	804-829		NAP		g4499843	327	44	0.001			(AJ011965) oxidoreductase [Claviceps purpurea]
22503	ENU06297	ANI61C5121: 23-50	453-473		NAP		g3891484	142	37	0.0002	35	34	"Chain B, Co-Crystal Structure Of Protein Farnesyltransferase Complexed With A Farnesyl Diphosphate Substrate ["]
22504	ENU06298	ANI61C8634: 22-45	796-816		NAP		g538067	2311	123	1.00E-27	33	18	(M77661) putative pol polyprotein [Magnaporthe grisea]
22505	ENU06299	ANI61C3333: 22-49	705-732		NAP		g3004863	538	113	3.00E-57	50	30	"(AF029354) exo-beta-1,3-glucanase [Annelomyces quisqualis]"
22506	ENU06300	ANI61C5808: 22-46	725-747		NAP		g2209087	897	345	2.00E-94	62	41	(AF000309) putative serine/threonine kinase [Colletotrichum lindemuthianum]
22507	ENU06301	ANI61C343:6 49-76	558-584		NAP		g3914984	143	80	2.00E-14	31	5	Ferichrome siderophore peptide synthetase [Ustilago maydis]
22508	ENU06302	ANI61C1742: 72-93	553-577		NAP		g1652017	201	95	3.00E-19	32	65	(D90901) hypothetical protein [Synechocystis sp.]
22509	ENU06303	ANI61C4320: 22-46	805-829		NAP		g1723435	1087	350	6.00E-96	55	18	hypothetical 170.7 KD protein C56F8.02 in chromosome I [Schizosaccharomyces pombe]
22510	ENU06304	ANI61C6618: 49-68	677-699		NAP		g3080522	309	153	1.00E-36	39	36	(AL022599) hypothetical protein [Schizosaccharomyces pombe]
22511	ENU06305	ANI61C4435: 48-69	516-542		NAP		g3913154	319	145	3.00E-34	39	19	beta-galactosidase (lactase) [Enterobacter cloacae]
22512	ENU06306	ANI61C8171: 23-46	804-828		NAP		g2506360	276	108	5.00E-23	33	34	NPL1 protein (SEC63 protein) [Saccharomyces cerevisiae]
22513	ENU06307	ANI61C1086 122-141	500-519		NAP		g729747	411	155	3.00E-37	48	45	Flavohemoprotein (haemoglobin-like protein) (flavohemoglobin) [Ralstonia eutropha]
22514	ENU06308	ANI61C2206: 222-242	699-719		NAP		g171565	221	113	1.00E-24	35	56	(K01609) gal10 [Saccharomyces carlsbergensis]
22515	ENU06309	ANI61C1729: 35-54	730-749		NAP		g1703456	496	128	6.00E-29	43	21	Cation-transporting ATPase PAT1 [Dictyostelium discoideum]
22516	ENU06310	ANI61C9369: 22-43	802-820		NAP		g1351635	462	73	4.00E-23	40	70	hypothetical 35.8 KD protein C12G12.12 in chromosome I [Schizosaccharomyces pombe]

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22517	ENU06311	ANI61C8401: 36-55 355..1384		774-797	NAP		g585255	756	277	7.00E-74	56	49	Histidine biosynthesis bifunctional amidotransferase / cyclase [Saccharomyces cerevisiae] (Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
22518	ENU06312	ANI61S14:62 3..1			NAP		g3114719	542	183	8.00E-57	62	13	Biotin--protein ligase (biotin apo-protein ligase) (biotin-- [Saccharomyces cerevisiae]
22519	ENU06313	ANI61C6428: 122-141 1..789		691-714	NAP		g1345625	322	153	4.00E-46			hypothetical 107.9 KD protein in POL4-SRD1 intergenic region [Saccharomyces cerevisiae]
22520	ENU06314	ANI61C8003: 1200..1			NAP		g140464	594	99	5.00E-20	38	22	(D78573) aspartate kinase-homoserine dehydrogenase [Oryza sativa]
22521	ENU06315	ANI61C1:108 2..760			NAP		g1777375	198	92	1.00E-18	46	11	(L48074) secreted dipeptidyl peptidase [Aspergillus fumigatus]
22522	ENU06316	ANI61C8875: 24-43 1..1250		809-829	NAP		g2340046	813	334	4.00E-91	51	39	(X70694) trehalose-6-phosphate phosphatase [Saccharomyces cerevisiae]
22523	ENU06317	ANI61C796:1 850..1		709-731	NAP		g406769	921	229	2.00E-59	47	31	Coronin-like protein [Saccharomyces cerevisiae]
22524	ENU06318	ANI61C8121: 22-47 994..1		723-740	NAP		g3121873	483	192	3.00E-48	50	32	(AL031786) putative delta-1-pyrroline-5-carboxylate dehydrogenase [Schizosaccharomyces pombe]
22525	ENU06319	ANI61S4368: 1..670			NAP		g3687478	213	104	6.00E-22	34	39	(Z49130) cDNA EST EMBL:D74028 comes from this gene; cDNA EST EMBL:D71354 comes from this gene; cDNA EST EMBL:D76320 comes from this gene; cDNA EST yk486c7.3 comes from this gene; cDNA EST yk486c7.5 comes from this gene; cDNA ES... []
22526	ENU06320	ANI61C7484: 22-42 3606..4566		809-829	NAP		g3879532	213	86	3.00E-16	35	81	(AL031536) fnx1p. [Schizosaccharomyces pombe]
22527	ENU06321	ANI61C1043 23-50 1:2329..410		803-829	NAP		g3560207	234	58	0.000000 07			(U59303) glucoamylase precursor [Aspergillus awamori]
22528	ENU06322	ANI61C4967: 22-48 756..1		625-644	NAP		g1389841	559	186	1.00E-58	55	33	(AL022105) hypothetical protein [Schizosaccharomyces pombe]
22529	ENU06323	ANI61C1205: 109-128 513..1		391-417	NAP		g2956751	205	105	2.00E-22	31	45	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22530	ENU06324	ANI61C9687: 69-91 856..1	69-91	787-808	NAP		g1169870	365	185	3.00E-46	45	56	GCD14 protein [Saccharomyces cerevisiae]
22531	ENU06325	ANI61C8614: 23-48 2243..1	23-48	728-748	NAP		g4557481	325	97	2.00E-23	34	14	Canalicular multispecific organic anion transporter [Homo sapiens]
22532	ENU06326	ANI61C7926: 34-53 3645..5762	34-53	808-829	NAP		g932	188	42	0.006			(X53744) 68kDA subunit of signal recognition particle [Canis familiaris]
22533	ENU06327	ANI61C1343: 22-48 1..958	22-48	755-782	NAP		g1730639	299	136	2.00E-31	31	21	Hypothetical 141.1 KD protein in MET2-SEC2 intergenic region [Saccharomyces cerevisiae]
22534	ENU06328	ANI61C1109 51-70 6:561..884	51-70	361-380	NAP		g3914342	175	93	1.00E-18	51	17	3-phytase B precursor (myo-inositol-hexaphosphate 3-phosphohydrolase B) (3 phytase B) (myo-inositol hexakisphosphate phosphohydrolase B) [Emicella nidulans]
22535	ENU06329	ANI61C8939: 22-47 1157..39	22-47	803-829	NAP		g2132443	340	64	0.000000 30 002	30	76	probable membrane protein YDL144c - yeast (Saccharomyces cerevisiae)
22536	ENU06330	ANI61C1065 23-42 7:6536..6055	23-42	413-437	NAP		g1154950	153	96	2.00E-19	34	37	[Saccharomyces cerevisiae] (X94769) choline dehydrogenase [Rattus rattus]
22537	ENU06331	ANI61S3435: 38-65 1..574	38-65	496-518	NAP		g1176816	899	176	1.00E-81	95	28	hypothetical 72.8 KD protein in AGA1-MTR intergenic region (O678) [Escherichia coli]
22538	ENU06332	ANI61C5381: 33-60 833..1	33-60	709-728	NAP		g231551	262	83	2.00E-28	31	14	"Ankyrin, brain variant 2 (ankyrin B) (ankyrin, nonerythroid) [" (AL034463) putative single-strand polynucleotide binding protein [Schizosaccharomyces pombe]
22539	ENU06333	ANI61C6837: 118-136 476..1	118-136	454-479	NAP		g4007790	151	73	2.00E-13	39	25	[Schizosaccharomyces pombe] (U13049) pectate lyase C [Fusarium solani f. sp. pisi]
22540	ENU06334	ANI61C993:8 66..539			NAP		g595570	151	82	2.00E-15	41	54	hypothetical 20.1 KD protein in RTF1-CSE1 intergenic region [Saccharomyces cerevisiae]
22541	ENU06335	ANI61C4542: 23-42 1163..562	23-42	515-534	NAP		g1723978	212	64	1.00E-19			putative ATP-dependent RNA helicase C31A2.07C [Schizosaccharomyces pombe]
22542	ENU06336	ANI61C8821: 45-64 1679..2718	45-64	747-766	NAP		g1175401	940	371	e-102	66	33	beta-glucosidase precursor (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) [Kluyveromyces marxianus]
22543	ENU06337	ANI61C7550: 1..352			NAP		g114971	185	85	2.00E-16	40	13	

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22544	ENU06338	ANI61C1577: 1.638	102-126	583-602	NAP		g1169546	177	67	7.00E-13	35	82	putative ER lumen protein retaining receptor C28H8.4 [Caenorhabditis elegans]
22545	ENU06339	ANI61C7523: 3198..2768	65-84	378-397	NAP		g2136261	77	62	0.000000	25	31	tetracycline transporter-like protein - human [Homo sapiens]
22546	ENU06340	ANI61S4287: 22-48	22-48	446-467	NAP		g3941500	153	66	2.00E-10	36	57	(AF062904) putative transcription factor [Arabidopsis thaliana]
22547	ENU06341	ANI61C1023 22-45	22-45	375-399	NAP		g4539247	196	89	5.00E-19	48	64	(AL049489) putative actin polymerisation complex protein [Schizosaccharomyces pombe]
22548	ENU06342	ANI61C5375: 115-134	716-742		NAP		g3929399	896	153	2.00E-36	37	51	proline-specific permease (proline transport protein) [Emericella nidulans]
22549	ENU06343	ANI61C7079: 2167..620			NAP		g549674	832	101	7.00E-42	39	56	hypothetical 49.6 KD protein in ELM1-PR12 intergenic region [Saccharomyces cerevisiae]
22550	ENU06344	ANI61C8750: 29-54	790-809		NAP		g3021303	3668	554	e-157	99	12	(Y15996) acetyl-CoA carboxylase [Emericella nidulans]
22551	ENU06345	ANI61C1034 22-44	644-663		NAP		g1209391	2070	254	4.00E-67	46	31	(D83659) TPR protein [Schizosaccharomyces pombe]
22552	ENU06346	ANI61C6562: 1021..1			NAP		g3282044	1037	377	e-104	70	19	(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
22553	ENU06347	ANI61C9317: 22-45	803-829		NAP		g4581525	302	117	8.00E-26	34	47	(AL049559) putative short-chain dehydrogenase [Schizosaccharomyces pombe]
22554	ENU06348	ANI61C888:4 111-130	412-431		NAP		g3914142	36	38	0.052	25	50	Early nodulin 20 precursor (N-20) [Medicago truncatula]
22555	ENU06349	ANI61C2891: 328..3784			NAP		g2501152	660	222	2.00E-57	53	47	threonine synthase [Schizosaccharomyces pombe]
22556	ENU06350	ANI61C5514: 23-42	805-829		NAP		g2956768	664	217	1.00E-55	51	63	(AL022103) transmembrane transporter liz1p. [Schizosaccharomyces pombe]
22557	ENU06351	ANI61S3594: 435..1353			NAP		g2258414	119	52	0.000000	38	54	(AF007873) dolichol monophosphate mannose synthase [Schizosaccharomyces pombe]
22558	ENU06352	ANI61C234:1 22-42	612-635		NAP		g1077357	1063	124	1.00E-41	61	39	probable membrane protein YLR359w - yeast [Saccharomyces cerevisiae]
		575..1											[Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22559	ENU06353	ANI61C8537: 40-59 1090..1	40-59	712-731	NAP		g409547	239	86	3.00E-20	29	47	(L07492) sugar transport protein [Saccharomyces cerevisiae]
22560	ENU06354	ANI61C5810: 843..50			NAP		g544232	610	127	9.00E-29	50	59	elongation factor 1-gamma 2 (EF-1-gamma 2) [Saccharomyces cerevisiae]
22561	ENU06355	ANI61C8235: 22-49 1260..2280	22-49	786-813	NAP		g731465	818	267	9.00E-83	57	87	putative mitochondrial carrier YER053C [Saccharomyces cerevisiae]
22562	ENU06356	ANI61S1427: 1..719			NAP		g110849	161	52	0.000005	31	83	proline-rich protein - mouse [Mus musculus]
22563	ENU06357	ANI61C2541: 22-47 422..1457	22-47	741-763	NAP		g2330704	727	249	3.00E-65	49	81	(Z98529) putative transcription initiation factor TFIB subunit [Schizosaccharomyces pombe]
22564	ENU06358	ANI61C5404: 24-43 1..990	24-43	630-650	NAP		g3287946	1040	326	9.00E-89	64	25	putative helicase C6F12.16 in chromosome I [Schizosaccharomyces pombe]
22565	ENU06359	ANI61C8694: 27-50 1755..1	27-50	639-658	NAP		g3978466	1587	275	2.00E-73	50	37	(AF086822) dihydroxyacetone synthase [Candida boidinii]
22566	ENU06360	ANI61C9257: 22-46 1245..1	22-46	795-815	NAP		g2414649	827	198	6.00E-50	38	9	(Z99296) hypothetical protein [Schizosaccharomyces pombe]
22567	ENU06361	ANI61C1087 22-45 3:876..2793	22-45	800-819	NAP		g140474	576	76	4.00E-13			hypothetical 69.2 KD protein in HSP30-PMP1 intergenic region [Saccharomyces cerevisiae]
22568	ENU06362	ANI61C669:1 128..658			NAP		g1722769	225	99	1.00E-20	38	20	Phosphatidylinositol 3-kinase VPS34 (PI3-kinase) (PTDINS-3-kinase) (PI3K) (vacuolar sorting protein 34) [Schizosaccharomyces pombe]
22569	ENU06363	ANI61C1138 38-64 6:949..426	38-64	477-503	NAP		g4106669	323	120	2.00E-31	56	33	(AL035064) protein kinase skp1p [Schizosaccharomyces pombe]
22570	ENU06364	ANI61C5198: 24-43 1013..1	24-43	805-825	NAP		g129592	425	188	4.00E-47	45	35	Phenylalanine ammonia-lyase [Rhodotorula mucilaginosa]
22571	ENU06365	ANI61C445:1 44-63 ..1246	44-63	722-740	NAP		g1708850	684	134	1.00E-49	48	33	probable leukotriene A-4 hydrolase (LTA-4 hydrolase) (leukotriene A(4) hydrolase) [Saccharomyces cerevisiae]
22572	ENU06366	ANI61C7858: 23-44 5143..4521	23-44	566-585	NAP		g987116	126	52	0.000003	28	99	(X86780) cystathione synthase [Streptomyces hygroscopicus]
22573	ENU06367	ANI61C82:17 44-63 60..549	44-63	802-829	NAP		g3702638	416	127	1.00E-28	40	61	(AL031825) putative acetylornithine deacetylase [Schizosaccharomyces pombe]

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22574	ENU06368	ANI61C1781: 37-64 1..537		400-425	NAP		g1077382	275	133	7.00E-31	41	19	probable membrane protein YLR335w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22575	ENU06369	ANI61C8774: 35-54 290..2421		802-829	NAP		g3885836	517	45	0.000002			(AF091042) putative cercosporin transporter [Cercospora kikuchii]
22576	ENU06370	ANI61C5355: 40-67 391..1		441-468	NAP		g2828151	162	88	5.00E-17	39	41	(AF042386) cyclophilin-33B [Homo sapiens]
22577	ENU06371	ANI61C1843: 22-49 115..525		458-479	NAP		g3122326	348	163	8.00E-40	50	33	LEC14B protein [Lithospermum erythrorhizon]
22578	ENU06372	ANI61C1097 27-54 7:4250..5969		781-806	NAP		g3242972	1836	395	e-109	70	39	(AF069523) heat shock protein Hsp88 [Neurospora crassa]
22579	ENU06373	ANI61C1070 48-67 1:1..1037		791-814	NAP		g4521101	1136	289	e-121	79	75	(AB016540) alternative oxidase [Aspergillus niger]
22580	ENU06374	ANI61C1096: 52-71 692..161		464-483	NAP		g1766062	285	125	2.00E-28	42	99	(U82218) Ats1 [Schizosaccharomyces pombe]
22581	ENU06375	ANI61C9004: 22-41 3221..4026		684-705	NAP		g1077385	325	95	7.00E-19	47	66	hypothetical protein YLR348c - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22582	ENU06376	ANI61C4853: 43-63 1709..2856		782-801	NAP		g522302	1176	360	1.00E-98	63	23	(L35053) endonuclease [Magnaporthe grisea]
22583	ENU06377	ANI61C8573: 37-56 7384..7793		377-399	NAP		g1929333	186	90	1.00E-17	35	66	(Z93767) ywrF [Bacillus subtilis]
22584	ENU06378	ANI61C9181: 32-51 7917..8414		433-460	NAP		g4115939	407	176	8.00E-44	66	46	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]
22585	ENU06379	ANI61S1637: 95-114 154..690		296-319	NAP		g1351702	100	61	0.000000	33	31	hypothetical 61.1 KD protein C11D3.05 in chromosome I [Schizosaccharomyces pombe]
22586	ENU06380	ANI61C2866: 64-82 491..1		447-470	NAP		g140371	224	104	4.00E-22	36	29	hypothetical 58.8 KD protein in GLK1-SRO9 intergenic region [Saccharomyces cerevisiae]
22587	ENU06381	ANI61C1059 22-44 9:1..477		431-452	NAP		g4263825	301	130	5.00E-30	42	12	(AC006067) hypothetical protein [Arabidopsis thaliana]
22588	ENU06382	ANI61C5967: 22-46 8462..9284		690-717	NAP		g585175	452	104	2.00E-43	47	60	guanine nucleotide-binding protein alpha-1 subunit (GPI-alpha) [Neurospora crassa]

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22589	ENU06383	ANI61C1050 1:1298..7124			NAP		g1491929	10043	316	e-126	98	13	"(U51272) 1,3-beta-D-glucan synthase catalytic subunit [Emericella nidulans]"
22590	ENU06384	ANI61C7768: 29-48 3164..3929		633-652	NAP		g3135013	507	136	1.00E-45	51	26	(AJ005963) 100 kDa protein [Ajellomyces capsulatus]
22591	ENU06385	ANI61C1085 40-64 3:4930..4464		422-445	NAP		g1834342	444	175	1.00E-43	60	9	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
22592	ENU06386	ANI61C2190: 62-81 2788..1		722-741	NAP		g1351615	1732	235	3.00E-61	41	23	hypothetical protein C23D3.15 in chromosome I [Schizosaccharomyces pombe]
22593	ENU06387	ANI61C5726: 22-48 1..959		728-749	NAP		g3298291	535	229	9.00E-61	46	52	(AB010389) ALK2 [Yarrowia lipolytica]
22594	ENU06388	ANI61C1262: 45-66 524..1		446-465	NAP		g2625138	275	122	2.00E-27	39	10	(AF032443) ABC1 transporter; ABC-type ATPase [Magnaporthe grisea]
22595	ENU06389	ANI61C8354: 22-44 1077..1		723-743	NAP		g3861449	420	108	7.00E-23	25	26	(Z98596) SMC-family protein [Schizosaccharomyces pombe]
22596	ENU06390	ANI61C5304: 22-49 1..1908		762-780	NAP		g2660670	680	135	4.00E-31	36	22	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
22597	ENU06391	ANI61C8656: 22-45 1944..2456		470-492	NAP		g4769004	415	74	5.00E-36			(AF140598) ring-box protein 1 [Homo sapiens]
22598	ENU06392	ANI61C3866: 87-105 497..962		439-458	NAP		g1352994	132	78	2.00E-16			hypothetical 30.6 KD protein in SCP160-SMC3 intergenic region precursor [Saccharomyces cerevisiae]
22599	ENU06393	ANI61C3152: 185..3464			NAP		g4539277	2340	127	1.00E-28	27	18	(AL049498) myosin ii [Schizosaccharomyces pombe]
22600	ENU06394	ANI61C6685: 38-57 1..938		717-735	NAP		g3219947	566	244	5.00E-64	52	45	hypothetical 61.8 KD protein C16E8.13 in chromosome I [Schizosaccharomyces pombe]
22601	ENU06395	ANI61C1464: 83-108 1183..1		735-762	NAP		g3219304	443	185	4.00E-46	40	30	(AB009461) MUS38 [Neurospora crassa]
22602	ENU06396	ANI61C8385: 26-45 1400..3387		771-790	NAP		g1351714	483	83	2.00E-15	33	44	putative transporter C11D3.18C [Schizosaccharomyces pombe]
22603	ENU06397	ANI61C1122 22-41 5:1..442		395-421	NAP		g2462931	228	100	5.00E-21	42	20	(Z83833) UDP-glucose:sterol glucosyltransferase [Arabidopsis thaliana]
22604	ENU06398	ANI61C85:71 27-46 4..1		591-613	NAP		g136753	726	303	1.00E-81			"glycogen (starch) synthase, isoform 1 [Saccharomyces cerevisiae]"

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22605	ENU06399	ANI61C5996: 24-45 5587..4751	24-45	791-816	NAP		g4126481	196	100	1.00E-20	29	98	(AB015352) Akt2 [Alternaria alternata]
22606	ENU06400	ANI61C1158: 63-82 7268..8420	63-82	802-829	NAP		g127277	841	254	1.00E-69			mitochondrial phosphate carrier protein (phosphate transport protein) (mitochondrial import receptor) (P32) [Saccharomyces cerevisiae]
22607	ENU06401	ANI61C1029 22-41 4:7772..8074	22-41	413-432	NAP		g4468224	84	48	0.00004	21	33	(Y14855) tropomyosin [Helix aspersa]
22608	ENU06402	ANI61C8089: 31-53 1..970	31-53	767-784	NAP		g117178	147	86	3.00E-16	24	41	benzoate 4-monooxygenase (benzoate-para-hydroxylase) (cytochrome P450 53) [Aspergillus niger]
22609	ENU06403	ANI61C5229: 22-42 3623..1	22-42	725-744	NAP		g1351684	914	87	2.00E-16			hypothetical 420.8 KD protein C1F5.11C in chromosome I [Schizosaccharomyces pombe]
22610	ENU06404	ANI61C1135: 53-72 2415..1768	53-72	596-615	NAP		g586531	379	140	1.00E-32	46	98	hypothetical 21.1 KD protein in YMC2-CMD1 intergenic region [Saccharomyces cerevisiae]
22611	ENU06405	ANI61C100:1 22-48 209..1	22-48	802-829	NAP		g4388818	256	157	7.00E-38			(AC006528) putative pol polyprotein with a Zn-finger CCHC type domain (prosite:QDOC50158) and a DDE integrase signature motif [Arabidopsis thaliana]
22612	ENU06406	ANI61C7675: 24-43 7631..6374	24-43	809-829	NAP		g120593	192	57	0.000000			L-fucose permease [Escherichia coli]
22613	ENU06407	ANI61C29:98 38-57 3..1	38-57	714-733	NAP		g2132238	370	151	7.00E-36	39	21	hypothetical protein YPL226w - yeast (Saccharomyces cerevisiae)
22614	ENU06408	ANI61C7767: 22-46 4995..4254	22-46	694-712	NAP		g129072	68	49	0.00003	30	57	[Saccharomyces cerevisiae] pyruvate dehydrogenase protein X component precursor [Saccharomyces cerevisiae]
22615	ENU06409	ANI61C6108: 22-46 158..1950	22-46	780-799	NAP		g2342601	656	100	2.00E-20	25	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22616	ENU06410	ANI61C4919: 59-86 1..2627	59-86	628-648	NAP		g586461	272	112	3.00E-24	32	29	hypothetical 104.7 KD protein in PKC1-RTG3 intergenic region [Saccharomyces cerevisiae]
22617	ENU06411	ANI61C1116 22-48 8:402..1302	22-48	793-820	NAP		g1279693	740	287	6.00E-77	70	19	(X92971) translocation elongation factor [Saccharomyces cerevisiae]

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22618	ENU06412	ANI61C2633: 2627..2215	66-85	343-362	NAP		g1352941	348	151	3.00E-36	53	36	"branched-chain amino acid aminotransferase, cytosolic (BCAT) (TWT2 protein) [Saccharomyces cerevisiae]"
22619	ENU06413	ANI61C1352: 24-44 1761..1310	24-44	298-320	NAP		g1176707	81	52	0.000003	28	51	hypothetical 33.0 KD protein in PROB-PROA intergenic region [Corynebacterium glutamicum]
22620	ENU06414	ANI61C8273: 22-46 303..3850	22-46	804-829	NAP		g1399532	2420	113	2.00E-42	41	24	"(U51118) Neurospora crassa NUC-2 (Nuc-2) gene, complete cds. [Neurospora crassa]"
22621	ENU06415	ANI61C8911: 22-48 780..1	22-48	641-660	NAP		g3288709	506	193	1.00E-48	46	16	(AB010442) PMR1 [Penicillium digitatum]
22622	ENU06416	ANI61S1445: 1..1008			NAP		g730030	141	63	0.000000	16	44	micronuclear linker histone polypeptide (MIC LH) [Tetrahymena thermophila]
22623	ENU06417	ANI61C7533: 22-42 990..1	22-42	800-827	NAP		g418391	823	328	2.00E-89	56	75	ZRT1 protein [Saccharomyces cerevisiae]
22624	ENU06418	ANI61C9971: 25-43 3979..3681	25-43	292-310	NAP		g1655675	73	67	7.00E-11	33	32	(Z81368) lipK [Mycobacterium tuberculosis]
22625	ENU06419	ANI61C1064 39-66 6:682..1	39-66	557-581	NAP		g4176535	417	122	2.00E-38	41	66	(AL035263) putative TFIIF subunit (transcription-repair fac tor) [Schizosaccharomyces pombe]
22626	ENU06420	ANI61C3805: 102-129 4037..3580	102-129	413-437	NAP		g1834342	447	186	7.00E-47	53	10	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
22627	ENU06421	ANI61C3317: 56-75 1261..1792	56-75	397-418	NAP		g3702646	59	41	0.0009	29	27	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
22628	ENU06422	ANI61C6551: 22-46 1999..1	22-46	723-749	NAP		g3834294	156	55	0.000000			(U80846) No definition line found [Caenorhabditis elegans]
22629	ENU06423	ANI61C9287: 30-49 473..4546	30-49	802-829	NAP		g1546072	1848	103	1.00E-21			(U68040) polyketide synthase [Cochliobolus heterostrophus]
22630	ENU06424	ANI61C8021: 51-70 3552..2294	51-70	805-829	NAP		g3885836	510	125	4.00E-28	30	43	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
22631	ENU06425	ANI61S2328: 33-52 555..1	33-52	505-527	NAP		g2497183	573	131	2.00E-60	57	17	hypothetical 126.6 KD protein in RPL39-VTT1 intergenic region [Saccharomyces cerevisiae]
22632	ENU06426	ANI61C566:3 22-46 597..2493	22-46	805-828	NAP		g3395556	131	43	0.000001	31	72	(AL031180) putative 2-hydroxyacid dehydrogenase [Schizosaccharomyces pombe]

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22633	ENU06427	ANI61C7197: 23-46 1..1163		781-808	NAP		g1170186	1129	316	2.00E-85	53	36	probable ATP-dependent RNA helicase DBP4 (helicase CA4) (helicase UFI) [Saccharomyces cerevisiae]
22634	ENU06428	ANI61C6444: 24-51 1..819		752-775	NAP		g3668171	894	313	1.00E-95	66	22	(AB006052) RNA polymerase I second-largest subunit [Neurospora crassa]
22635	ENU06429	ANI61C362:1 22-44 ..1628		801-828	NAP		g2330871	430	174	2.00E-48	41	29	(Z98603) hypothetical protein [Schizosaccharomyces pombe]
22636	ENU06430	ANI61C1027 67-88 5:2528..4163		727-746	NAP		g1711561	256	50	0.00002			sugar transporter STL1 [Saccharomyces cerevisiae]
22637	ENU06431	ANI61C7202: 1217..1			NAP		g1709181	680	192	3.00E-48	47	46	high affinity methionine permease [Saccharomyces cerevisiae]
22638	ENU06432	ANI61C3971: 34-53 1149..1		726-749	NAP		g3150253	605	178	6.00E-44	39	23	(AL023634) hypothetical protein [Schizosaccharomyces pombe]
22639	ENU06433	ANI61C2161: 30-49 3504..5047		802-829	NAP		g3730	1119	197	3.00E-75	54	47	(X53424) glycolipid-anchored surface protein [Saccharomyces cerevisiae]
22640	ENU06434	ANI61C1116 27-46 4:1595..1		728-747	NAP		g131768	541	136	2.00E-31	34	46	quinate permease (quinate transporter) [Emmericella nidulans]
22641	ENU06435	ANI61C4297: 1275..1678			NAP		g553045	65	47	0.00009	32	64	(M28651) chloroperoxidase [Caldariomyces fumago]
22642	ENU06436	ANI61C1263: 22-49 1..745		696-723	NAP		g3810839	375	150	1.00E-35	41	44	(AL032684) conserved hypothetical zinc-finger protein [Schizosaccharomyces pombe]
22643	ENU06437	ANI61C8233: 24-43 1688..894		750-774	NAP		g3947877	540	91	1.00E-54	53	100	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]
22644	ENU06438	ANI61C3897: 1212..2040			NAP		g1799532	211	59	7.00E-17	30	66	(AB000564) salicylate hydroxylase [Sphingomonas sp.]
22645	ENU06439	ANI61C2901: 22-47 1060..607		411-433	NAP		g3342802	197	87	5.00E-17	30	31	(AF061838) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]
22646	ENU06440	ANI61C8881: 22-49 1327..1		725-749	NAP		g2494411	100	37	0.21	28	16	3-(3-hydroxy-phenyl)propionate hydroxylase [Escherichia coli]
22647	ENU06441	ANI61S4274: 35-62 1..635		494-519	NAP		g4733982	693	173	3.00E-61			(AC007268) hypothetical protein [Arabidopsis thaliana]
22648	ENU06442	ANI61C8550: 51-78 1..2571		802-821	NAP		g1166378	743	132	2.00E-30	32	25	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"

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22649	ENU06443	ANI61C9556: 36-55 7386..8061		632-651	NAP		g4106657	653	118	5.00E-61	79	50	(AL035064) activator 1 subunit (replication factor subunit) [Schizosaccharomyces pombe]
22650	ENU06444	ANI61C8783: 122-141 1..601	519-538		NAP		g1176982	71	59	0.000000	29	41	hypothetical metabolite transport protein in HTPG-IOLR intergenic region [] (AL031825) hypothetical protein [Schizosaccharomyces pombe]
22651	ENU06445	ANI61C4477: 103-130 1..757	659-684		NAP		g3702635	288	135	3.00E-31	32	61	cyclohexanone monooxygenase (EC 1.14.13.22) - Acinetobacter sp []
22652	ENU06446	ANI61C1099 33-52 9:5329..6029	616-633		NAP		g78100	336	113	2.00E-24	33	37	putative transporter C1B3.16C [Schizosaccharomyces pombe]
22653	ENU06447	ANI61C3891: 22-45 1..526	456-476		NAP		g3183364	236	94	6.00E-19	34	30	(AB019195) PV100 [Cucurbita maxima]
22654	ENU06448	ANI61S2827: 1..628			NAP		g3808062	134	57	0.000000	20	25	(AJ010317) Sand [Fugu rubripes]
22655	ENU06449	ANI61C6432: 23-45 8274..9352	721-741		NAP		g3928166	346	149	3.00E-35	35	42	beta-galactosidase precursor (lactase) [Aspergillus niger]
22656	ENU06450	ANI61C6774: 36-55 1..1713	789-806		NAP		g461623	350	47	2.00E-10	36	21	(AC006135) putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]
22657	ENU06451	ANI61S4263: 1..838			NAP		g4218005	300	45	0.0006	29	38	(AL034567) putative protein [Arabidopsis thaliana]
22658	ENU06452	ANI61C1061 112-131 2:790..184	535-555		NAP		g4049341	99	35	0.52	38	34	mitochondrial 60S ribosomal protein L37 precursor (YML37) [Saccharomyces cerevisiae]
22659	ENU06453	ANI61C3499: 22-41 2369..2795	460-479		NAP		g585899	97	56	0.000000	37	100	kynureninase (L-kynurenine hydrolase) [Rattus norvegicus]
22660	ENU06454	ANI61C4192: 153-178 4222..3816	360-386		NAP		g3913969	146	59	2.00E-11	37	28	hypothetical 57.3 KD protein GMC-type oxidoreductase CY50.03C [Mycobacterium tuberculosis]
22661	ENU06455	ANI61C1912: 30-49 1325..348	785-804		NAP		g1723076	270	80	2.00E-21	35	48	Hyp-rich glycoprotein [Zea mays]
22662	ENU06456	ANI61S1424: 1..649			NAP		g228937	211	37	0.11	34	64	DNA repair protein RAD3 [Schizosaccharomyces pombe]
22663	ENU06457	ANI61C3442: 50-69 740..2427	657-675		NAP		g400924	349	101	7.00E-21	24	26	(AF063864) essential nuclear protein Mcm3p [Schizosaccharomyces pombe]
22664	ENU06458	ANI61C9247: 22-41 1..1208	808-829		NAP		g3139137	592	111	8.00E-24	36	31	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22665	ENU06459	ANI61C1877: 31-51 1629..1	31-51	716-738	NAP		g3288709	1663	267	8.00E-71	54	17	(AB010442) PMR1 [Penicillium digitatum]
22666	ENU06460	ANI61C1878: 59-82 1..362	59-82	314-341	NAP		g3041855	180	85	1.00E-16	34	29	(AC004537) similar to tumor suppressor p33ING1; similar to AF044076 (PID:g2829208) [Homo sapiens]
22667	ENU06461	ANI61C7121: 35-61 1363..958	35-61	451-478	NAP		g1850540	183	56	0.000000	45	99	(U87806) ribosomal P2 phosphoprotein [Alternaria alternata]
22668	ENU06462	ANI61C1054: 28-49 832..1	28-49	700-719	NAP		g3183342	235	73	6.00E-28	38	54	hypothetical 44.5 KD protein C14C4.09 in chromosome I [Schizosaccharomyces pombe]
22669	ENU06463	ANI61C8705: 1..943			NAP		g2213552	369	163	1.00E-39	35	44	(Z97052) hypothetical protein [Schizosaccharomyces pombe]
22670	ENU06464	ANI61C4350: 1..602			NAP		g1174862	141	52	4.00E-14	41	33	putative ubiquitin carboxyl-terminal hydrolase C13A11.04C (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) [Schizosaccharomyces pombe]
22671	ENU06465	ANI61C7356: 22-48 418..2288	22-48	803-828	NAP		g231993	2396	388	e-107			succinate dehydrogenase (ubiquinone) flavoprotein subunit precursor (FP) (flavoprotein subunit of complex II) [Saccharomyces cerevisiae]
22672	ENU06466	ANI61C2512: 1..919			NAP		g2492798	485	179	9.00E-47	48	62	aryl-alcohol dehydrogenase (NADP+) (AAD) [Phanerochaete chrysosporium]
22673	ENU06467	ANI61S1309: 653..1			NAP		g2959371	670	265	4.00E-72	64	38	(AL022117) asparagine synthetase [Schizosaccharomyces pombe]
22674	ENU06468	ANI61S3208: 120-141 594..267	120-141	284-304	NAP		g117820	515	132	4.00E-42	96	50	cytochrome B6 [Spinacia oleracea]
22675	ENU06469	ANI61S3578: 1..612			NAP		g1131489	72	45	0.0005	25	58	"(U42580) Pro-rich protein; PAPK (24X); similar to Triticum PK-rich protein, corresponds to GenBank Accession Number X52472 [Paramecium bursaria Chlorella virus 1]"
22676	ENU06470	ANI61S1366: 1..686			NAP		g283032	153	60	0.000000	33	64	hydroxyproline-rich glycoprotein - perennial teosinte [Zea diploperennis]

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22677	ENU06471	ANI61C1037 7:1768..1143	22-48	549-576	NAP		g3914384	686	189	3.00E-71	84	100	probable peroxisomal membrane protein PMP20 (allergen ASP F 3) [Aspergillus fumigatus]
22678	ENU06472	ANI61C5116: 780..1	22-45	640-660	NAP		g117619	121	50	5.00E-10	27	28	choline transport protein [Saccharomyces cerevisiae]
22679	ENU06473	ANI61C1063 9:622..1	136-160	541-560	NAP		g3219959	290	87	1.00E-16	39	34	probable zinc metalloproteinase C17A5.04C precursor [Schizosaccharomyces pombe]
22680	ENU06474	ANI61C1118 7:5234..6480	89-108	730-749	NAP		g2146836	1134	270	7.00E-72	56	32	hypothetical protein YCL054w - yeast (Saccharomyces cerevisiae) [Saccharomyces cerevisiae]
22681	ENU06475	ANI61C7956: 752..1	22-46	617-644	NAP		g3929357	223	87	2.00E-16	37	34	O-methylsterigmatocystin oxidoreductase (OMST oxidoreductase) (cytochrome P450 64) [Aspergillus parasiticus]
22682	ENU06476	ANI61C8967: 4367..3128	22-48	802-829	NAP		g1168351	414	76	2.00E-13	38	71	alcohol dehydrogenase (ADH) [Bacillus stearothermophilus]
22683	ENU06477	ANI61S4000: 472..1	214-231	401-420	NAP		g1723751	446	80	4.00E-28	72	42	hypothetical 34.9 KD protein in SMI1-PHO81 intergenic region [Saccharomyces cerevisiae] (AL049769) mitochondrial 60s ribosomal protein 110 precursor [Schizosaccharomyces pombe]
22684	ENU06478	ANI61C6670: 1400..1791	87-106	380-398	NAP		g4760344	167	49	0.00002			[Schizosaccharomyces pombe] (L07492) sugar transport protein [Saccharomyces cerevisiae] (X99340) nucleic acid binding protein [Drosophila melanogaster]
22685	ENU06479	ANI61C2264: 1412..43	49-68	760-780	NAP		g409547	261	56	2.00E-16	29	47	[AB018537] elongation factor 3 [Yarrowia lipolytica]
22686	ENU06480	ANI61C4164: 1348..2131	52-71	662-683	NAP		g1770212	175	81	1.00E-21	29	59	putative long-chain-fatty-acid--coa ligase [Schizosaccharomyces pombe]
22687	ENU06481	ANI61C1984: 1..1014			NAP		g3776152	873	195	2.00E-84	62	55	dihydrolipoamide dehydrogenase precursor [Saccharomyces cerevisiae]
22688	ENU06482	ANI61C5698: 925..1	189-210	786-813	NAP		g3006179	436	139	2.00E-32	45	32	(AC007369) Similar to RNA helicases [Arabidopsis thaliana]
22689	ENU06483	ANI61C6002: 1831..1443	111-130	295-314	NAP		g118678	462	132	4.00E-46			molybdopterin biosynthesis MOEA protein [Synechococcus sp.]
22690	ENU06484	ANI61S2737: 1..928			NAP		g4836896	198	63	0.000000			
22691	ENU06485	ANI61S4388: 470..1	64-83	296-315	NAP		g2497956	114	71	4.00E-12	27	40	

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22692	ENU06486	ANI61C1404: 1463..496	22-48	629-647	NAP		g729296	180	76	2.00E-13	31	76	dihydrodipicolinate synthase (DHDDS) [Corynebacterium glutamicum]
22693	ENU06487	ANI61C4023: 37-56	22-48	621-640	NAP		g1352956	1303	381	e-105	68	43	hypothetical 75.5 KD protein in CCT3-CCT8 intergenic region
		1..1098											[Saccharomyces cerevisiae]
22694	ENU06488	ANI61S3272: 40-67	40-67	391-415	NAP		g2257528	597	209	4.00E-55	70	26	(AB004537) methionyl-tRNA synthetase [Schizosaccharomyces pombe]
22695	ENU06489	ANI61C6841: 22-46	22-46	803-829	NAP		g231361	910	308	4.00E-83	58	81	1-aminocyclopropane-1-carboxylate deaminase (ACC deaminase) [Pseudomonas sp.]
		2213..1178											phosphomevalonate kinase [Saccharomyces cerevisiae]
22696	ENU06490	ANI61S2126: 195-220	195-220	405-431	NAP		g1706695	96	34	0.48	26	31	hypothetical 33.9 KD protein C16C9.02C in chromosome I [Schizosaccharomyces pombe]
		533..63											[U68040] polyketide synthase [Cochliobolus heterostrophus]
22697	ENU06491	ANI61C7863: 107-126	107-126	725-744	NAP		g1175491	570	129	4.00E-58	51	82	(AF030425) pyruvate dehydrogenase E1 component alpha subunit [Pichia stipitis]
		2642..1821											(AL031534) 2-isopropylmalate synthase, [Schizosaccharomyces pombe]
22698	ENU06492	ANI61C1117: 22-43	22-43	360-379	NAP		g1546072	289	118	3.00E-26	40	6	NADH-ubiquinone oxidoreductase 30.4 KD subunit precursor (complex I-30KD) (CI-31KD) []
		8..1..497											(Z98981) putative sodium channel [Schizosaccharomyces pombe]
22699	ENU06493	ANI61C9611: 22-47	22-47	777-804	NAP		g2623175	982	226	2.00E-98	65	67	Hyp-rich glycoprotein [Zea mays]
		1087..189											farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (farnesyl diphosphate synthetase) (dimethylallyltransferase / geranyltransferase [Gibberella fujikuroi]
22700	ENU06494	ANI61C4200: 22-45	22-45	508-531	NAP		g3560136	534	138	4.00E-53	54	32	(U73900) 2-hydroxybiphenyl-3-monooxygenase [Pseudomonas azelaica]
		632..1											
22701	ENU06495	ANI61C8517: 89-108	89-108	412-432	NAP		g128862	354	154	4.00E-37	51	55	
		541..1											
22702	ENU06496	ANI61C2596: 22-44	22-44	724-748	NAP		g2388993	693	129	3.00E-29	34	14	
		1435..1											
22703	ENU06497	ANI61S3056: 1..536			NAP		g228937	164	53	0.000001	34	53	
		1..536											
22704	ENU06498	ANI61C2202: 57-76	57-76	770-789	NAP		g3122099	1167	433	e-121	72	81	
		1..1020											
22705	ENU06499	ANI61C7060: 43-62	43-62	412-435	NAP		g2098616	210	100	7.00E-21	38	25	
		1..456											

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22706	ENU06500	ANI61C6470: 1430..212	40-64	801-824	NAP		g2497989	681	212	4.00E-54	49	65	putative mitochondrial carrier YMR166C [Saccharomyces cerevisiae]
22707	ENU06501	ANI61C4397: 45-66 3555..4828	45-66	799-818	NAP		g2408036	655	211	5.00E-54	43	67	(Z99163) putative threonine aldolase [Schizosaccharomyces pombe]
22708	ENU06502	ANI61C7311: 31-52 1..1182	31-52	795-822	NAP		g1345823	910	202	3.00E-51	47	52	nitrate transporter (nitrate permease) [Emicella nidulans]
22709	ENU06503	ANI61C294:4 28-48 385..2303	28-48	808-827	NAP		g225924	273	51	7.00E-14			uracil transport protein [Saccharomyces cerevisiae]
22710	ENU06504	ANI61C7960: 22-45 1..2635	22-45	780-799	LINAP		g728904	1577	261	3.00E-69	50	22	calcium-transporting ATPase 2 (vacuolar CA2+-ATPase) ; Ca2+-transporting ATPase (EC 3.6.1.38) - yeast (Saccharomyces cerevisiae) ; (U03060) calcium ATPase [Saccharomyces cerevisiae] ; (Z72528) ORF YGL006w [Saccharomyces cerevisiae]
22711	ENU06505	ANI61C7336: 22-44 5205..3703	22-44	790-809	LINAP		g3915140	201	113	2.00E-24	32	45	isotrichodermin C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides]
22712	ENU06506	ANI61C3911: 42-61 1327..528	42-61	750-770	LINAP		g464369	220	64	5.00E-16	31	37	phenol 2-monooxygenase (phenol hydroxylase) ; (L04488) phenol hydroxylase [Trichosporon cutaneum]
22713	ENU06507	ANI61C7950: 22-48 2307..3026	22-48	680-699	LINAP		g3925779	125	70	1.00E-11	22	41	(AL034353) putative major facilitator family multi-drug resistance protein [Schizosaccharomyces pombe]
22714	ENU06508	ANI61C9771: 24-45 1842..2262	24-45	451-471	LINAP		g549594	41	54	0.000000	33	15	hypothetical 102.5 KD protein in YPT52-DBP7 intergenic region ; hypothetical protein YKR021w - yeast (Saccharomyces cerevisiae) ; (Z28246) ORF YKR021w [Saccharomyces cerevisiae]
22715	ENU06509	ANI61C3160: 22-48 877..260	22-48	562-581	LINAP		g1582765	59	36	0.31	36	24	YFW1 gene [Saccharomyces cerevisiae]
22716	ENU06510	ANI61C6787: 23-42 795..1	23-42	671-690	LINAP		g3116145	494	208	3.00E-53	43	41	(AL023290) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22717	ENU06511	ANI61C7358: 1835..6555	30-49	705-730	LINAP		g124211	772	34	0.98			translation initiation factor IF-2 ; (M36878) translational initiation factor IF2 [Streptococcus faecium] "
22718	ENU06512	ANI61C801:8 22-47 60..1	22-47	752-773	LINAP		g4522004	367	164	5.00E-40	37	46	"(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana] "
22719	ENU06513	ANI61C3916: 22-46 1..1021	22-46	776-795	LINAP		g2662028	577	166	2.00E-40	35	32	(Z99296) beta-transducin [Schizosaccharomyces pombe]
22720	ENU06514	ANI61C6734: 23-45 855..482	23-45	439-458	LINAP		g4464201	120	66	2.00E-10	30	24	(AL031587) dJ1039K5.2 (similar to monocarboxylate transporter (MCT3)) [Homo sapiens]
22721	ENU06515	ANI61C7353: 50-69 5597..3348	50-69	790-809	LINAP		g3184110	716	87	2.00E-16			(AL023780) putative mrna stability protein [Schizosaccharomyces pombe]
22722	ENU06516	ANI61C9768: 30-57 916..1	30-57	713-735	LINAP		g4249705	449	215	4.00E-55	38	48	(AF101074) step II splicing factor SLU7 [Homo sapiens]
22723	ENU06517	ANI61C3176: 32-55 72..911	32-55	781-800	LINAP		g4107314	191	61	8.00E-18	29	52	(AL035075) conserved hypothetical SH3 domain-containing protein [Schizosaccharomyces pombe]
22724	ENU06518	ANI61C7404: 114-133 1..1861	114-133	709-730	LINAP		g2388993	644	143	2.00E-33	29	15	(Z98981) putative sodium channel [Schizosaccharomyces pombe]
22725	ENU06519	ANI61C3918: 28-47 1..1337	28-47	803-829	LINAP		g4033414	905	110	1.00E-23	31	24	putative importin beta-4 subunit (karyopherin beta-4 subunit) ; (AL023780) putative importin beta-4 subunit [Schizosaccharomyces pombe]
22726	ENU06520	ANI61C6734: 22-48 4810..5529	22-48	632-654	LINAP		g284667	111	46	0.0002			neurofilament triplet H1 protein - rabbit (fragment) ; (M94315) neurofilament-H [Oryctolagus cuniculus]
22727	ENU06521	ANI61C3180: 50-69 1499..2664	50-69	798-817	LINAP		g2262189	91	64	0.000000			(U56098) FacB [Aspergillus oryzae]
22728	ENU06522	ANI61C6786: 22-45 1..361	22-45	314-340	LINAP		g2132273	99	59	0.000000			hypothetical protein YPR090w - yeast (Saccharomyces cerevisiae) ; (U51033) P9513.3 gene product [Saccharomyces cerevisiae]
22729	ENU06523	ANI61C7390: 31-50 313..1205	31-50	809-828	LINAP		g2388994	1466	235	2.00E-62	54	46	(Z98981) hypothetical grp-binding protein associated [Schizosaccharomyces pombe]
22730	ENU06524	ANI61C8005: 66-85 3207..1743	66-85	791-810	LINAP		g2465159	1080	231	6.00E-60	46	38	(Z99753) hypothetical protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22731	ENU06525	ANI61C378:4	22-46	550-569	LINAP		g2271503	90	57	0.000000	26	46	(AF009672) unknown [Acinetobacter sp. ADP1]
22732	ENU06526	ANI61C6790:567..5166			LINAP		g2688966	748	275	2.00E-73	51	46	(AF027979) carnitine acetyl transferase [Magnaporthe grisea]
22733	ENU06527	ANI61C7416:604..1555	38-57	805-829	LINAP		g728850	107	53	0.000003			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosylase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus] "
22734	ENU06528	ANI61C7393:4538..3586	22-46	785-804	LINAP		g547769	561	177	7.00E-44	44	54	KES1 protein ; KES1 protein - yeast (Saccharomyces cerevisiae) ; (U03913) Kes1p [Saccharomyces cerevisiae] ; (U43703) Kes1p [Saccharomyces cerevisiae] ; (Z73501) ORF YPL145c [Saccharomyces cerevisiae] ; (X96770) P2614 product [Saccharomyces cerevisiae]
22735	ENU06529	ANI61C9798:22-45		734-761	LINAP		g522302	1289	182	3.00E-45	40	23	(L35053) endonuclease [Magnaporthe grisea]
22736	ENU06530	ANI61C3204:22-42		679-706	LINAP		g1169871	1040	120	4.00E-65	65	29	GCN20 protein ; GCN20 protein - yeast (Saccharomyces cerevisiae) ; (U19971) Gen20p [Saccharomyces cerevisiae] ; (D50617) YFR009W [Saccharomyces cerevisiae]
22737	ENU06531	ANI61C6807:22-45		727-748	LINAP		g4499840	209	93	2.00E-18	33	7	(AJ011964) d-lysceryl-peptide-synthetase [Claviceps purpurea]
22738	ENU06532	ANI61C9792:22-45		762-781	LINAP		g3738149	190	36	0.27			(AL031852) conserved protein-PHD-finger family [Schizosaccharomyces pombe]

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22739	ENU06533	ANI61C6772: 54-73 703..1	54-73	627-647	LINAP		g3877858	68	51	0.000007			(Z34801) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans]; (Z66514) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans] (AB010810) phospholipase D [Candida albicans] (U89352) lysophospholipase I [Mus musculus]; (U97148) calcium-independent phospholipase A2 isoform 2 [Oryctolagus cuniculus] hypothetical 30.9 KD protein K07C11.7 in chromosome V; (U53336) coded for by C. elegans cDNA cm12g2; coded for by C. elegans cDNA yk56a6.5; coded for by C. elegans cDNA yk70a12.5; coded for by C. elegans cDNA cm11d9; coded for by C. elegans cDNA yk102d1.5; coded for by C. elegans cDNA yk102d1.3;...
22743	ENU06537	ANI61C8012: 48-67 3101..2742	48-67	456-479	LINAP		g3650394	77	52	0.000003	61		(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe]
22744	ENU06538	ANI61C7420: 22-49 1040..48	22-49	773-796	LINAP		g2408067	860	280	8.00E-75	50	44	(Z99165) protein kinase [Schizosaccharomyces pombe]
22745	ENU06539	ANI61C805:8 22-42 17..2051	22-42	803-829	LINAP		g2462679	138	66	4.00E-10	24	26	(Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]
22746	ENU06540	ANI61C7418: 105-124 1135..1594	105-124	363-381	LINAP		g746510	310	144	3.00E-34	48	48	(U23517) similar to ubiquitin conjugating enzyme [Caenorhabditis elegans]
22747	ENU06541	ANI61C3955: 27-46 1386..2039	27-46	519-538	LINAP		g4107287	320	85	5.00E-36	43	39	(AL035076) putative allantoinase [Schizosaccharomyces pombe]

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22748	ENU06542	ANI61C7422: 25-44 838..1366	25-44	486-508	LINAP		g731584	125	41	0.007			hypothetical 17.1 KD protein in PUR5 3'region ; hypothetical protein YHR217c - yeast (Saccharomyces cerevisiae) ; (U00029) Yhr217cp [Saccharomyces cerevisiae] (Z95397) unknown [Schizosaccharomyces pombe] (U95159) gelsolin-related protein GRP125 [Dictyostelium discoideum] (AF091042) putative cercosporin transporter [Cercospora kikuchii] (U74380) cholinesterase 1 [Branchiostoma floridae] (U78523) histidine secretory acid phosphatase [Leishmania donovani] (AB010810) phospholipase D [Candida albicans] probable sterigmatocystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62) ; (U34740) putative p450 monooxygenase [Emicella nidulans] sperm histone P2 precursor (protamine P2) ; protamine P2 - rhesus macaque ; (X71338) Protamine P2 [Macaca mulatta] (AF055904) acetylornithine deacetylase; ArgE [Myxococcus xanthus] amino-acid permease IND1 ; IND1 protein - fungus (Trichoderma harzianum) ; (Z22594) IND1 [Trichoderma harzianum] probable oxygenase - Streptomyces fradiae ; (X87093) putative oxygenase [Streptomyces fradiae]
22749	ENU06543	ANI61C3946: 24-51 1..2030	24-51	803-829	LINAP		g2104460	359	124	7.00E-28	34	25	
22750	ENU06544	ANI61C9800: 41-68 2754..2065	41-68	648-669	LINAP		g4100186	110	43	0.002			
22751	ENU06545	ANI61C3970: 34-61 853..1	34-61	722-744	LINAP		g3885836	333	156	2.00E-37	36	45	
22752	ENU06546	ANI61C3143: 35-54 7868..8751	35-54	810-829	LINAP		g3435078	362	154	8.00E-43	40	46	
22753	ENU06547	ANI61C3210: 22-46 894..1457	22-46	516-543	LINAP		g2058526	63	40	0.009			
22754	ENU06548	ANI61C8088: 108-127 1555..687	108-127	801-820	LINAP		g3413518	467	94	2.00E-35	38	14	
22755	ENU06549	ANI61C7429: 31-49 2809..3315	31-49	465-485	LINAP		g2493391	303	145	2.00E-34	43	38	
22756	ENU06550	ANI61C397:1 22-48 674..1	22-48	739-758	LINAP		g462350	324	33	2.3			
22757	ENU06551	ANI61C3228: 50-69 645..1352	50-69	492-512	LINAP		g3044087	217	94	1.00E-18			
22758	ENU06552	ANI61C9804: 41-60 3576..4030	41-60	417-438	LINAP		g462414	320	135	2.00E-31	52	23	
22759	ENU06553	ANI61C7396: 22-44 4450..3405	22-44	806-827	LINAP		g1076090	349	139	2.00E-32	33	54	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22760	ENU06554	ANI61C3230: 69-87 1731..1062		625-649	LINAP		g1730591	132	76	2.00E-13			hypothetical 41.1 KD protein ON CDC91-PAU4 intergenic region ; hypothetical protein YLR460c - yeast (Saccharomyces cerevisiae) ; (U22383) Ylr460cp [Saccharomyces cerevisiae]
22761	ENU06555	ANI61C9803: 22-49 2173..3113		806-829	LINAP		g586486	328	71	2.00E-26	32	38	hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912) ORF YBR043c [Saccharomyces cerevisiae]
22762	ENU06556	ANI61C3999: 122-141 1..310		264-289	LINAP		g3581887	70	48	0.00002			"(AL031540) internalin- related, Leucine rich repeat containing protein [Schizosaccharomyces pombe] "
22763	ENU06557	ANI61C3208: 22-47 2326..4042		794-813	LINAP		g3242458	382	111	2.00E-36	38	15	(AB010466) multidrug resistance-associated protein (MRP)-like protein-1 (MLP-1) [Rattus norvegicus] ; (U73038) multidrug resistance-associated protein 6 [Rattus norvegicus]
22764	ENU06558	ANI61C9820: 588..235			LINAP		g4481949	149	63	7.00E-11	44	33	(AL035637) glycoprotein endopeptidase-like protein. [Schizosaccharomyces pombe]
22765	ENU06559	ANI61C7446: 27-54 1..1120		650-669	LINAP		g3395584	843	229	2.00E-59	42	25	(AL031179) importin beta subunit [Schizosaccharomyces pombe]
22766	ENU06560	ANI61C318:5 23-50 44..1929		792-819	LINAP		g1706177	210	110	1.00E-23	26	28	cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]
22767	ENU06561	ANI61C9777: 22-46 5806..7241		810-829	LINAP		g2507070	253	51	0.000009			N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]

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22768	ENU06562	ANI61C7436: 458..1	125-152	437-464	LINAP		g2499507	211	46	0.000000	32	28	"6-phosphofructo-2-kinase / fructose-2,6-bisphosphatase liver isozyme (6PF-2-K/FRU-2,6-P2ASE) ; 6-phosphofructo-2-kinase (EC 2.7.1.105) / fructose-2, 6-bisphosphate 2-phosphatase (EC 3.1.3.46) - chicken ; (S54076) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase [chickens, liver, Peptide, 469 aa] [Gallus gallus] "
22769	ENU06563	ANI61C318:3 50-77 444..2978	50-77	454-479	LINAP		g2764632	651	233	8.00E-61	73	73	(AJ001520) 19.3kD iron-sulfur subunit of mitochondrial complex I [Neurospora crassa]
22770	ENU06564	ANI61C9796: 22-48 7361..6942	22-48	453-472	LINAP		g2149953	141	56	9.00E-18	39	10	(U97066) sulfonyleurea receptor 2B [Mus musculus]
22771	ENU06565	ANI61C3216: 28-47 1375..803	28-47	515-534	LINAP		g2894086	118	65	5.00E-10	38	36	(Y11395) seventransmembrane-domain protein [Homo sapiens]
22772	ENU06566	ANI61C4015: 64-83 1923..1370	64-83	494-513	LINAP		g2414599	74	52	0.000004	32	38	(Z99295) dihydrofolate reductase [Schizosaccharomyces pombe]
22773	ENU06567	ANI61C7419: 22-44 2705..1866	22-44	783-810	LINAP		g133323	68	63	0.000000			DNA-directed RNA polymerase II largest subunit (RPB1) ; DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - Chinese hamster (fragment) ; (M19538) RNA polymerase II largest subunit [Cricetulus griseus]
22774	ENU06568	ANI61C7451: 1913..2465			LINAP		g2347100	423	136	3.00E-33	40	50	(U76846) ubiquitin-specific protease [Arabidopsis thaliana] ; (AC007168) putative ubiquitin-specific protease [Arabidopsis thaliana]
22775	ENU06569	ANI61C3238: 81-100 942..1	81-100	715-737	LINAP		g1077530	263	96	4.00E-24	32	48	hypothetical protein YDR132c - yeast (Saccharomyces cerevisiae) ; (Z48179) unknown [Saccharomyces cerevisiae]
22776	ENU06570	ANI61C3257: 53-72 1104..339	53-72	715-734	LINAP		g3914096	214	116	2.00E-25	38	24	NA(+)/H(+) antiporter 2 ; (AB010106) Zsod22p [Zygosaccharomyces rouxii]

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22777	ENU06571	ANI61C7427: 41-60 5672..3569	41-60	769-788	LINAP		g549627	997	127	1.00E-28	39	37	hypothetical 83.6 KD protein in CCP1-MET1 intergenic region ; hypothetical protein YBL011w homolog YKR067w - yeast (Saccharomyces cerevisiae) ; (Z28292) ORF YKR067w [Saccharomyces cerevisiae] heat shock protein 70 homolog precursor ; (Z68136) unknown [Schizosaccharomyces pombe] "(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum]" trichodiene oxygenase (cytochrome P450 58) ; trichodiene oxygenase 4 - fungus (Fusarium sporotrichioides) ; (U22462) trichodiene oxygenase [Fusarium sporotrichioides] (AF008915) EVI-5 homolog [Homo sapiens] (AF053084) putative cinnamyl alcohol dehydrogenase [Malus domestica] hypothetical amino-acid permease in STE3-GIN10 intergenic region ; probable transport protein YKL174c - yeast (Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28174) ORF YKL174c [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae] (AL023288) hypothetical protein [Schizosaccharomyces pombe] (AL022305) putative transcription factor [Schizosaccharomyces pombe] salicylate 1-monoxygenase (EC 1.14.13.1) - Pseudomonas putida ; (X83926) salicylate 1-monoxygenase [Pseudomonas putida] (AF110766) transcription factor AFLR [Aspergillus parasiticus]
22778	ENU06572	ANI61C4052: 26-46 1755..251	26-46	802-829	LINAP		g1351681	479	141	5.00E-33	36	31	
22779	ENU06573	ANI61C8108: 102-127 3842..3264	102-127	532-558	LINAP		g2924313	226	124	5.00E-28	35	18	
22780	ENU06574	ANI61C4051: 37-63 326..1	37-63	453-475	LINAP		g3915154	70	47	0.00007			
22781	ENU06575	ANI61C3252: 32-51 2449..1630	32-51	765-792	LINAP		g3093476	306	157	7.00E-38	33	31	
22782	ENU06576	ANI61C7454: 22-48 2674..2011	22-48	617-642	LINAP		g2981475	108	74	1.00E-15	31	60	
22783	ENU06577	ANI61C7447: 22-46 1052..2869	22-46	809-829	LINAP		g549738	610	158	4.00E-38	33	45	
22784	ENU06578	ANI61C4067: 24-43 17..1066	24-43	803-829	LINAP		g3116134	379	141	6.00E-33	36	10	
22785	ENU06579	ANI61C3274: 35-55 1629..2588	35-55	801-820	LINAP		g3006175	524	196	2.00E-49	39	53	
22786	ENU06580	ANI61C4055: 66-85 308..670	66-85	454-473	LINAP		g1073049	70	69	1.00E-11	28	36	
22787	ENU06581	ANI61C3287: 22-48 865..1187	22-48	459-478	LINAP		g4581773	111	62	0.000000	32	24	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22788	ENU06582	ANI61C815:1 933..3247	22-49	776-802	LINAP		g2497523	820	260	1.00E-68	50	16	kinesin-like protein KIF1A (axonal transporter of synaptic vesicles) ; (X90840) axonal transporter of synaptic vesicles [Homo sapiens] (AB017641) polyketide synthase [Micromonospora griseorubida] (AL035161) putative secreted peptidase [Streptomyces coelicolor] probable phosphatidylinositol-4-phosphate 5-kinase FAB1 (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PTDINS(4)P-5-kinase) (diphosphoinositide kinase) ; (U01017) Fab1p [Saccharomyces cerevisiae]
22789	ENU06583	ANI61C4055: 25-48 2176..3551	25-48	724-747	LINAP		g4586928	757	263	9.00E-70	43	6	[Schizosaccharomyces pombe]
22790	ENU06584	ANI61C8073: 32-58 948..339	32-58	552-572	LINAP		g4154074	76	56	0.000000	36	27	[Caenorhabditis elegans]
22791	ENU06585	ANI61C3281: 40-59 1..1001	40-59	811-829	LINAP		g462047	759	225	4.00E-58	36	12	"(U93872) ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]" (M63836) beta-glucuronidase [Mus musculus]
22792	ENU06586	ANI61C7469: 102-127 2810..2349	102-127	415-441	LINAP		g3873550	95	41	0.004			(U89492) arylsulfatase [Neurospora crassa]
22793	ENU06587	ANI61C4090: 69-87 612..1175	69-87	500-519	LINAP		g1943773	94	47	0.00008	34	22	(AF033013) Notch homolog [Bombyx mori]
22794	ENU06588	ANI61C8141: 67-86 2209..1414	67-86	740-759	LINAP		g2246532	148	60	0.000000	20	24	(AF116463) unknown [Streptomyces lincolnensis]
22795	ENU06589	ANI61C329:1 596..408			LINAP		g193723	458	59	2.00E-21	33	41	(AF027979) carnitine acetyl transferase [Magnaporthe grisea]
22796	ENU06590	ANI61C7490: 27-54 1227..1	27-54	729-749	LINAP		g2873363	841	237	8.00E-62	47	39	(AL035075) putative transcription factor tffiib component [Schizosaccharomyces pombe]
22797	ENU06591	ANI61C817:1 22-45 052..594	22-45	459-478	LINAP		g2654086	167	57	0.000000			erythrocyte ankyrin [Homo sapiens]
22798	ENU06592	ANI61C409:4 117-135 619..4038	117-135	517-536	LINAP		g4455041	77	33	1.4			(AC006284) putative ankyrin [Arabidopsis thaliana]
22799	ENU06593	ANI61C8142: 22-41 1160..1665	22-41	463-485	LINAP		g2688966	449	130	8.00E-30	68	24	
22800	ENU06594	ANI61C7484: 116-135 5427..5005	116-135	379-402	LINAP		g4107317	222	104	4.00E-22	38	27	
22801	ENU06595	ANI61C814:1 ..347			LINAP		g226788	86	64	3.00E-10	41	5	
22802	ENU06596	ANI61C411:6 9..588			LINAP		g4335756	99	65	3.00E-10	30	66	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22803	ENU06597	ANI61C814:5 540..3606	23-50	796-823	LINAP	g2342601	805	3.00E-34	100	3.00E-34	33	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22804	ENU06598	ANI61C4133: 92-111 1..502	23-50	456-479	LINAP	g557084	78	0.000000	56	0.000000	32	10	(L35601) ankyrin [Drosophila melanogaster] ; ankyrin [Drosophila melanogaster]
22805	ENU06599	ANI61C7512: 48-74 1..828	23-50	770-789	LINAP	g3859678	398	3.00E-46	185	3.00E-46	36	30	(AL033503) conserved hypothetical protein [Candida albicans]
22806	ENU06600	ANI61C3310: 22-43 1328..712	22-43	541-560	LINAP	g2791489	156	1.00E-14	70	1.00E-14	38	36	(AL021246) hypothetical protein Rv2449c [Mycobacterium tuberculosis]
22807	ENU06601	ANI61C3306: 22-48 1895..310	22-48	806-829	LINAP	g1546072	714	2.00E-50	129	2.00E-50	45	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
22808	ENU06602	ANI61C4133: 2028..1713	22-48		LINAP	g730197	54	0.0005	43	0.0005	31	18	protein N-terminal amidase (NT-amidase) ; amino-terminal amidase NTA1 - yeast (Saccharomyces cerevisiae) ; (L35564) N-terminal amidase [Saccharomyces cerevisiae] ; (Z49562) ORF YJR062c [Saccharomyces cerevisiae] ; (L47993) ORF YJR062c [Saccharomyces cerevisiae]
22809	ENU06603	ANI61C8187: 29-48 409..1	29-48	460-479	LINAP	g2497685	51	0.000000	55	0.000000			platelet-activating factor acetylhydrolase precursor (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetyl-glycerophospho... ; (U34246) plasma PAF acetylhydrolase [Canis familiaris] ; platelet-activating factor acetylhydrolase [Canis familiaris]
22810	ENU06604	ANI61C413:1 49-68 205..1889	49-68	612-631	LINAP	g3153851	236	1.00E-27	94	1.00E-27	41	38	(AF064524) carboxylesterase [Anisopteromalus calandrae]
22811	ENU06605	ANI61C8185: 107-126 1..715	107-126	672-693	LINAP	g1352321	561	9.00E-32	137	9.00E-32	45	57	ubiquitin-like protein DSK2 ; (L40587) ubiquitin-like protein [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22812	ENU06606	ANI61C8180: 25-51 3057..1914	25-51	805-827	LINAP		g4522026	74	40	0.018			"(AC004886) C-terminus matches KIAA0559, N-terminus similar to Bassoon protein; match to PID:g3043642; similar to PID:g3413810 [Homo sapiens] "
22813	ENU06607	ANI61C7516: 24-51 563..1	24-51	427-447	LINAP		g4505121	160	78	1.00E-15	39	22	unknown ; (AF072250) methyl-CpG binding protein MBD4 [Homo sapiens] ; (AF114784) methyl-CpG binding endonuclease [Homo sapiens]
22814	ENU06608	ANI61C4132: 37-56 1828..2556	37-56	671-690	LINAP		g1084945	282	99	1.00E-28	35	19	probable membrane protein YPR022c - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
22815	ENU06609	ANI61C7536: 43-62 1972..2335	43-62	380-399	LINAP		g729786	170	89	2.00E-17	31	28	putative polyketide hydroxylase
22816	ENU06610	ANI61C8186: 22-47 719..1	22-47	589-614	LINAP		g3766365	454	212	3.00E-54	44	20	(AL031907) putative cysteine-rich transcriptional regulator [Schizosaccharomyces pombe]
22817	ENU06611	ANI61C7535: 44-62 1494..2105	44-62	566-591	LINAP		g4538674	132	70	2.00E-13	34	81	(AL035592) hypothetical protein [Schizosaccharomyces pombe]
22818	ENU06612	ANI61C4134: 51-70 4974..4135	51-70	790-815	LINAP		g731409	264	124	6.00E-28	39	36	hypothetical 78.3 KD protein in RIP1-URA3 intergenic region ; hypothetical protein YEL023c - yeast (Saccharomyces cerevisiae) ; (U18530) Yel023cp [Saccharomyces cerevisiae]
22819	ENU06613	ANI61C8218: 34-53 1330..1709	34-53	447-466	LINAP		g729862	120	64	3.00E-10	32	27	sexual differentiation process protein ISP7 ; isp7 protein - fission yeast (Schizosaccharomyces pombe) ; (D14064) ORF [Schizosaccharomyces pombe]
22820	ENU06614	ANI61C4168: 38-58 2042..1557	38-58	429-449	LINAP		g4506399	222	32	3.4			homolog of yeast Rae1 (Bharathi) mRNA-associated protein of 41 kDa (Kraemer) ; MRNA-associated protein MRNP41 (RAE1 protein homolog) ; (U84720) mRNA export protein [Homo sapiens]

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22821	ENU06615	ANI61C7519: 23-44 6109..4986	23-44	802-829	LINAP		g2132156	336	150	2.00E-35	36	45	hypothetical protein YPL030w - yeast (Saccharomyces cerevisiae) ; (U36624)
22822	ENU06616	ANI61C4155: 22-47 1674..2564	22-47	804-829	LINAP		g3850704	443	94	1.00E-40	44	59	Lpb1p [Saccharomyces cerevisiae] (AJ005273) Kin17 [Homo sapiens]
22823	ENU06617	ANI61C7554: 102-128 53..499	102-128	458-477	LINAP		g1208874	66	57	0.00000008	33	8	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans] ; (U39847) AO66 ankyrin [Caenorhabditis elegans]
22824	ENU06618	ANI61C8221: 33-53 291..644	33-53	426-445	LINAP		g3451460	72	48	0.000002	26	25	(AL031349) zinc-finger protein [Schizosaccharomyces pombe]
22825	ENU06619	ANI61C8238: 22-48 1..1254	22-48	809-829	LINAP		g4115619	254	32	5.3			(AB014768) chitinase [Aeromonas sp. 10S-24]
22826	ENU06620	ANI61C412:5 24-48 746..3420	24-48	808-828	LINAP		g586455	784	73	3.00E-12	37	15	hypothetical 83.0 KD protein in ATP1-ROX3 intergenic region ; hypothetical protein YBL097w - yeast (Saccharomyces cerevisiae) ; (X79489) C-728 protein [Saccharomyces cerevisiae] ; (Z35858) ORF YBL097w [Saccharomyces cerevisiae]
22827	ENU06621	ANI61C4161: 29-48 1..2181	29-48	799-823	LINAP		g4499840	1058	109	3.00E-23	35	8	(AJ011964) d-lysergyl-peptide-synthetase [Claviceps purpurea] (U41278) contains similarity to G beta repeats (PROSITE:PS00670) of the beta-transducin family [Caenorhabditis elegans]
22829	ENU06623	ANI61C4153: 24-51 1988..2361	24-51	441-460	LINAP		g3551484	107	38	0.046			(AB015708) photosynthetic reaction center M subunit [Erythrobacter sp.] (AL049498) hypothetical rho1 gdp-gtp exchange protein
22830	ENU06624	ANI61C4153: 56-75 3043..4469	56-75	765-784	LINAP		g4539278	117	82	5.00E-15	24	20	[Schizosaccharomyces pombe] "(AL031525) RNA binding protein, pumilio-family [Schizosaccharomyces pombe]"
22831	ENU06625	ANI61C825:1 22-47 714..2502	22-47	726-745	LINAP		g3560162	674	276	1.00E-73	54	34	probable chitin biosynthesis protein C6G9.12 (CHS5 homolog) ; (Z81317) yeast chs5 homolog [Schizosaccharomyces pombe]
22832	ENU06626	ANI61C8266: 59-78 10..898	59-78	795-814	LINAP		g2842702	544	228	4.00E-59	44	45	

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22833	ENU06627	ANI61C4186: 448..1	119-138	452-473	LINAP		g1175456	119	78	3.00E-14	34	29	hypothetical 60.5 KD protein C13G6.08 in chromosome I; hypothetical protein SPAC13G6.08 - fission yeast (Schizosaccharomyces pombe) ; (Z54308) putative cdc protein [Schizosaccharomyces pombe] "(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum] "
22834	ENU06628	ANI61C4107: 1..1585	25-46	796-817	LINAP		g2924313	956	107	1.00E-29	49	18	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22835	ENU06629	ANI61C8222: 3752..4677	22-46	805-829	LINAP		g1723918	178	62	1.00E-10	30	20	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22836	ENU06630	ANI61C8252: 1012..1	23-44	661-680	LINAP		g940303	309	111	5.00E-24	29	51	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22837	ENU06631	ANI61C4198: 1575..2050	50-71	457-476	LINAP		g3242253	218	106	8.00E-23	38	7	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22838	ENU06632	ANI61C8234: 1163..5989	23-48	794-813	LINAP		g2147662	2178	97	1.00E-19	25	11	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22839	ENU06633	ANI61C8283: 1208..897	68-87	231-250	LINAP		g3882183	89	66	1.00E-10	35	9	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22840	ENU06634	ANI61C4234: 1..351	122-147	308-330	LINAP		g1943844	201	101	3.00E-21	50	8	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22841	ENU06635	ANI61C4240: 2166..1839	72-91	423-441	LINAP		g3980387	59	57	0.000000			hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22842	ENU06636	ANI61C4216: 4493..5022	22-42	484-509	LINAP		g417806	107	66	2.00E-10	28	22	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]
22843	ENU06637	ANI61C8298: 941..481			LINAP		g2408014	288	68	3.00E-11	40	22	hypothetical 145.6 KD protein in SSM1B-CEG1 intergenic region ; probable membrane protein YGL133w - yeast (Saccharomyces cerevisiae) ; (Z72655) ORF YGL133w [Saccharomyces cerevisiae]

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22844	ENU06638	ANI61C4252: 26-53 1694..2273	26-53	416-443	LINAP		g3688380	379	147	5.00E-35	51	26	(AJ006267) ClpX-like protein [Homo sapiens]
22845	ENU06639	ANI61C8280: 26-45 2187..1518	26-45	603-622	LINAP		g3953466	201	73	3.00E-27	34	28	(AC002328) F20N2.11 [Arabidopsis thaliana]
22846	ENU06640	ANI61C4233: 47-66 2205..1278	47-66	803-829	LINAP		g3004489	351	100	1.00E-34	43	75	(AJ223304) geranylgeranyl transferase type I [Schizosaccharomyces pombe]
22847	ENU06641	ANI61C4220: 22-42 5089..6046	22-42	806-829	LINAP		g1351690	216	104	8.00E-22	24	47	hypothetical 63.5 KD protein C3H1.06C in chromosome I ; (Z68144) putative major facilitator superfamily transporter [Schizosaccharomyces pombe]
22848	ENU06642	ANI61C8282: 67-86 3721..358	67-86	772-795	LINAP		g3451312	1627	126	3.00E-42	45	17	(AL031324) membrane atpase [Schizosaccharomyces pombe]
22849	ENU06643	ANI61C8303: 41-60 1..461	41-60	414-438	LINAP		g3879389	147	78	3.00E-14	50	9	(Z83123) Similarity to S.pombe ATP-dependent DNA helicase (SW:Q09811); cDNA EST EMBL:D27628 comes from this gene; cDNA EST CEMSC83FB comes from this gene; cDNA EST EMBL:D35012 comes from this gene; cDNA EST yk398a1.3 comes from...
22850	ENU06644	ANI61C4272: 36-55 1..1707	36-55	796-813	LINAP		g4007734	256	44	0.001			(AL034447) putative transmembrane protein [Streptomyces coelicolor]
22851	ENU06645	ANI61C8296: 2006..2485			LINAP		g88462	162	37	0.00001	31	70	"proline-rich phosphoprotein (gene PRH1, Db allele) - human "
22852	ENU06646	ANI61C4276: 46-65 3055..2585	46-65	414-433	LINAP		g4505829	108	76	2.00E-13	32	21	gene from NF2/meningioma region of 22q12 ; gene anonymous protein - human ; (L18972) anonymous [Homo sapiens]
22853	ENU06647	ANI61C8291: 23-42 1038..686	23-42	457-479	LINAP		g116415	147	79	2.00E-14	37	8	Cubitus interruptus dominant protein ; DNA-binding protein ci (D) - fruit fly (Drosophila melanogaster) ; (X54360) ciD product [Drosophila melanogaster]
22854	ENU06648	ANI61C4283: 37-56 802..489	37-56	454-473	LINAP		g4507069	143	42	0.000000 05			"SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 ; SNF2alpha protein - human ; (D26155) hSNF2a [Homo sapiens] "

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22855	ENU06649	ANI61C8302: 24-43 2038..668	24-43	810-829	LINAP		g2342601	375	95	5.00E-19	27	5	(X89442) peptide synthetase [Metarhizium anisopliae]
22856	ENU06650	ANI61C8316: 23-44 932..1611	23-44	627-646	LINAP		g1730692	54	49	0.00003			putative transcriptional regulatory protein in BIO3-HXT17 intergenic region ; probable membrane protein YNR063w - yeast (Saccharomyces cerevisiae) ; (Z71678) ORF YNR063w [Saccharomyces cerevisiae]
22857	ENU06651	ANI61C4300: 42-69 1208..773	42-69	460-479	LINAP		g4008551	647	144	4.00E-40	52	28	(AL034490) pseudouridylate synthase [Schizosaccharomyces pombe]
22858	ENU06652	ANI61C8320: 24-51 2159..1676	24-51	422-449	LINAP		g729298	231	107	6.00E-23			RHO-type GTPase activating protein RGA1/DBM1 ; DBM1 protein - yeast (Saccharomyces cerevisiae) ; (U07421) Dbp1p [Saccharomyces cerevisiae] ; (X90518) ORF O3290 [Saccharomyces cerevisiae] ; (X94335) YOR3290w [Saccharomyces cerevisiae] ; (Z75035) ORF YOR127w [Saccharomyces cerevisiae] ; GTPase-activating protein [Saccharomyces cerevisiae]
22859	ENU06653	ANI61C8338: 22-43 335..752	22-43	404-428	LINAP		g1706094	122	76	9.00E-15	34	31	cytochrome P450 4F5 (CYP1VF5) ; cytochrome P450 4F5 protein - rat ; (U39207) cytochrome P450 4F5 [Rattus norvegicus]
22860	ENU06654	ANI61C8332: 22-48 2196..1878	22-48	271-290	LINAP		g1082604	106	42	0.002			mucin 5AC (clone JER58) - human (fragment) ; (Z34278) mucin [Homo sapiens]
22861	ENU06655	ANI61C8344: 48-70 1..905	48-70	787-814	LINAP		g135969	619	274	6.00E-73			TRNA nucleotidyltransferase precursor (TRNA adenyllyltransferase) (TRNA CCA-pyrophosphorylase) (CCA-adding enzyme) ; tRNA nucleotidyltransferase - yeast (Saccharomyces cerevisiae) ; (M59870) transfer RNA nucleotidyltransferase [Saccharomyces cerevisiae] ; (U18922) Cca1p: tRNA nucleotidyltransferase(tRNA CCA-pyrophosphorylase) [Saccharomyces cerevisiae]

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22862	ENU06656	ANI61C8337: 1..1325	22-46	807-826	LINAP		g3810845	686	243	1.00E-63	46	53	(AL032684) possible ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]
22863	ENU06657	ANI61C8362: 31-53	480-499		LINAP		g3746895	258	98	8.00E-20	36	30	(AF088906) clock-controlled gene-9 protein [Neurospora crassa]
22864	ENU06658	ANI61C8308: 22-48	452-479		LINAP		g729853	62	45	0.0003	29	50	protein-tyrosine-phosphatase precursor ; dual specificity phosphatase (EC 3.1.3.-) IphP - Nostoc commune ; (L11392) protein tyrosine/serine phosphatase [Nostoc commune]
22865	ENU06659	ANI61C8356: 50-69	785-804		LINAP		g728850	78	54	0.000001			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosylase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus] "
22866	ENU06660	ANI61C1000 22-48	803-822		LINAP		g2132941	157	57	3.00E-18	29	57	probable membrane protein YOR301w - yeast (Saccharomyces cerevisiae) ; (Z75209) ORF YOR301w [Saccharomyces cerevisiae]
22867	ENU06661	ANI61C1002 22-49	802-829		LINAP		g2497214	508	114	5.00E-45	44	27	hypothetical 107.7 KD protein in TSP3-IPP2 intergenic region ; probable membrane protein YMR266w - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae]
22868	ENU06662	ANI61C1000 24-43	792-811		LINAP		g2498597	699	206	1.00E-52	42	27	MRNA transport regulator MTR10 ; MTR10 protein - yeast (Saccharomyces cerevisiae) ; (U55020) Mtr10p [Saccharomyces cerevisiae] ; (Z75068) ORF YOR160w [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22869	ENU06663	ANI61C1004 7:3106..992	22-41	805-829	LINAP		g731872	777	99	3.00E-20	34	26	"putative 108.8 KD transcriptional regulatory protein in FKHI-STH1 intergenic region ; probable membrane protein YIL130w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 964, CAI: 0.15, possible regulatory protein [Saccharomyces cerevisiae] "
22870	ENU06664	ANI61C1006 2:1184..1	24-45	713-737	LINAP		g2924771	181	64	0.000000			(AC002334) putative dimethylaniline monooxygenase [Arabidopsis thaliana]
22871	ENU06665	ANI61C1005 5:379..755	39-58	449-476	LINAP		g1723454	219	55	0.000000	33	25	hypothetical 43.9 KD protein C13G7.10 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; [Z69729] hypothetical protein [Schizosaccharomyces pombe]
22872	ENU06666	ANI61C1008 4:878..441	208-229	388-411	LINAP		g435736	44	64	5.00E-10			(AC006248) putative copia polyprotein [Arabidopsis thaliana]
22873	ENU06667	ANI61C1009 9:1217..228	22-48	777-800	LINAP		g1723513	250	64	0.000000	31	49	hypothetical 63.9 KD protein C1F12.09 in chromosome I ; hypothetical protein - fission yeast (Schizosaccharomyces pombe) ; (Z69944) unknown [Schizosaccharomyces pombe]
22874	ENU06668	ANI61C1010 6:336..699	22-44	456-479	LINAP		g1652216	93	68	3.00E-11			(D90903) esterase [Synechocystis sp.]
22875	ENU06669	ANI61C1008 5:5678..6236	28-55	502-521	LINAP		g4335736	166	85	1.00E-18	32	14	(AC006248) putative copia polyprotein [Arabidopsis thaliana]
22876	ENU06670	ANI61C1012 6:445..1	102-121	449-476	LINAP		g630383	178	85	3.00E-16	40	25	proline transport protein - Emericella nidulans
22877	ENU06671	ANI61C1010 1:357..32	112-139	450-477	LINAP		g1352914	132	63	0.000000	37	40	"putative 40S ribosomal protein YJR113C ; probable ribosomal protein S7, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49613) ORF YJR113c [Saccharomyces cerevisiae] "
22878	ENU06672	ANI61C1015 1:1039..1346	22-42	279-299	LINAP		g3617954	105	65	4.00E-10			(AF079900) tetracycline efflux protein [Streptomyces rimosus]
22879	ENU06673	ANI61C1016 5:1056..686	54-77	328-350	LINAP		g3746666	91	57	0.000000	42	30	(AF076848) trihydroxytoluene oxygenase [Burkholderia cepacia]

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22880	ENU06674	ANI61C1011	26-53	457-477	LINAP		g4107286	50	59	0.000000			(AL035076) putative zinc-finger protein [Schizosaccharomyces pombe]
22881	ENU06675	0:3727..3264 ANI61C1017	66-85	456-478	LINAP		g1877327	162	96	1.00E-19			(Z92771) hypothetical protein Rv3272 [Mycobacterium tuberculosis]
22882	ENU06676	0:100..552 ANI61C1018	22-41	452-472	LINAP		g47149	90	62	0.000000			carboxyphosphoenolpyruvate mutase [Streptomyces hygroscopicus]
22883	ENU06677	5:1..359 ANI61C1020	42-61	311-332	LINAP		g1942321	69	59	0.000000	29	13	"Bacterial Chitinase Complexed With Chitinase (Dinag) ; Bacterial Chitinase, Glycosyl Hydrolase Family 20 "
22884	ENU06678	7:1..680 ANI61C1019	122-149	635-658	LINAP		g2498702	138	55	9.00E-14	35	35	sterigmatocystin 7-O-methyltransferase precursor ; (L25835) O-methyltransferase [Aspergillus flavus] ; (L25834) O-methyltransferase [Aspergillus parasiticus] ; (L22091) O-methyltransferase [Aspergillus parasiticus]
22885	ENU06679	6:1368..252 ANI61C1022	36-61	802-829	LINAP		g1709181	283	78	6.00E-14	28	46	"high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae] "
22886	ENU06680	7:787..276 ANI61C1023	64-83	461-480	LINAP		g2501427	152	66	9.00E-19	45	24	tyrosinase (monophenol monooxygenase) ; (U66807) tyrosinase [Podospira anserina] ; (U66808) tyrosinase [Podospira anserina]
22887	ENU06681	8:2789..2174 ANI61C1062	41-60	576-594	LINAP		g3850105	179	65	3.00E-15	38	17	(AL033388) leucine-rich repeat protein - weak similarity to adenylate cyclase [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22888	ENU06682	ANI61C1024 0:1709..2074	22-49	367-386	LINAP		g1172542	267	88	3.00E-27	60	14	dolichyl-phosphate-mannose--protein mannosyltransferase 4 ; dolichyl- phosphate-mannose--protein mannosyltransferase (EC 2.4.1.109) PMT4 - yeast (Saccharomyces cerevisiae) ; (X83798) PMT4 [Saccharomyces cerevisiae] ; (Z49643) ORF YJR143c [Saccharomyces cerevisiae]
22889	ENU06683	ANI61C1065 1:812..1496	41-62	619-639	LINAP		g4584202	123	42	0.000000	29	45	(AJ000394) chromate transport protein [Bacillus cereus]
22890	ENU06684	ANI61C1058 9:3081..1748	22-47	805-829	LINAP		g3150136	460	90	1.00E-18	33	38	(AL023594) protein complex assembly protein [Schizosaccharomyces pombe]
22891	ENU06685	ANI61C1058 9:9595..10143	22-44	503-528	LINAP		g94816	98	42	0.002			regulatory protein algR3 - Pseudomonas aeruginosa
22892	ENU06686	ANI61C1024 3:722..1	23-46	657-681	LINAP		g2673951	324	140	8.00E-33	36	17	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]
22893	ENU06687	ANI61C1058 9:10697..1163	100-119	713-732	LINAP		g3130045	203	89	3.00E-17	31	17	(AL023518) hypothetical protein [Schizosaccharomyces pombe]
22894	ENU06688	ANI61C4949: 640..2097	22-48	756-780	LINAP		g3080393	1399	118	1.00E-34	39	50	(AL022603) NADH dehydrogenase like protein [Arabidopsis thaliana]
22895	ENU06689	ANI61C4971: 681..319	22-46	421-442	LINAP		g3327019	80	63	0.000000			(Z99168) putative heat shock transcription factor
22896	ENU06690	ANI61C4972: 739..1406	22-49	614-633	LINAP		g3184059	536	96	4.00E-48	65	39	[Schizosaccharomyces pombe] (AL023776) prephenate dehydrogenase
22897	ENU06691	ANI61C4990: 809..255	119-144	486-505	LINAP		g1345955	106	46	3.00E-12	31	40	[Schizosaccharomyces pombe] glutathione-dependent formaldehyde dehydrogenase (FDH) (FALDH) ; (L33464) alcohol dehydrogenase 3 [Methylobacter marinus]
22898	ENU06692	ANI61C1067 2:1359..546	51-70	767-786	LINAP		g3282044	216	99	3.00E-20	35	17	(Y13967) alpha-aminoacidate reductase large subunit [Penicillium chrysogenum]

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22899	ENU06693	ANI61C4929: 52-71 2226..1582	585-603	585-603	LINAP	g125727		291	76	5.00E-29			killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase ; RF2 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1 ; (X07127) RF2 gene product (AA 1 - 1146) [Kluyveromyces lactis] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactis] ; (X01095) URFP2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactis]
22900	ENU06694	ANI61C4929: 25-44 5034..5547	469-493	469-493	LINAP	g584748		53	52	0.000004			autolysin (N-acetylmuramoyl-L-alanine amidase) ; autolysin - Enterococcus faecalis ; (M58002) bacterial cell wall hydrolase [Streptococcus faecalis]
22901	ENU06695	ANI61C1068 1:1252..1586	79-98	360-380	LINAP	g113517		95	72	3.00E-12			alpha-glucosidase precursor (maltase) ; alpha-glucosidase (EC 3.2.1.20) - yeast (Candida tsukubaensis) ; (X56024)
22902	ENU06696	ANI61C5004: 58-77 495..903	455-476	455-476	LINAP	g1077401		477	151	3.00E-36	49	18	alpha-glucosidase [Pseudozyma tsukubaensis] probable membrane protein YLR277c - yeast (Saccharomyces cerevisiae) ; (U17245) Ysh1p: subunit of polyadenylation factor I (PF I) [Saccharomyces cerevisiae]
22903	ENU06697	ANI61C1069 8:1..499	36-59	442-461	LINAP	g2507475		87	57	0.000000	27	9	paired amphipathic helix protein ; regulatory protein SIN3 - yeast (Saccharomyces cerevisiae) ; (Z74746) ORF YOL004w [Saccharomyces cerevisiae]
22904	ENU06698	ANI61C1068 7:2970..2166	22-48	758-784	LINAP	g2618766		327	153	7.00E-38	39	46	(U94362) glycogenin-2 alpha [Homo sapiens]
22905	ENU06699	ANI61C5009: 61-80 1519..964	61-80	515-534	LINAP	g1469400		50	34	0.6			(U44088) TDAG51 [Mus musculus]
22906	ENU06700	ANI61C1025 1:1382..3059	22-45	802-829	LINAP	g125935		418	118	6.00E-26	29	44	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis]

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22907	ENU06701	ANI61C1027 4:1..2053	22-48	804-824	LINAP		g3559970	656	66	8.00E-24	37	28	(AL031514) putative beta-mannosidase [Streptomyces coelicolor]
22908	ENU06702	ANI61C8537: 3561..4370	52-71	765-789	LINAP		g121087	162	56	3.00E-18			GCY protein ; GCY1 protein - yeast (Saccharomyces cerevisiae) ; (X13228)
													GCY protein (AA 1-312) [Saccharomyces cerevisiae] ; (X90518)
													ORF O31567 [Saccharomyces cerevisiae] ; (X94335) YOR3269w
													[Saccharomyces cerevisiae] ; (X96740)
													GCY protein [Saccharomyces cerevisiae] ; (Z75028) ORF YOR120w
22909	ENU06703	ANI61C5049: 1594..928	102-121	539-558	LINAP		g3367750	322	81	2.00E-28	46	34	[Saccharomyces cerevisiae] (AL031155) putative amidase
22910	ENU06704	ANI61C8646: 1427..393	22-48	807-829	LINAP		g1351677	241	88	9.00E-17	35	72	[Streptomyces coelicolor] hypothetical 36.9 KD protein C21E11.07 in chromosome I ; hypothetical protein SPAC21E11.07 - fission yeast (Schizosaccharomyces pombe) ; (Z67999) hypothetical protein [Schizosaccharomyces pombe]
22911	ENU06705	ANI61C5053: 244..639	48-68	448-467	LINAP		g2764520	117	61	0.000000	42	16	[Schizosaccharomyces pombe] (AJ000482) Hormone-sensitive lipase [Sus scrofa] ; (AJ000483) hormone-sensitive lipase [Sus scrofa]
22912	ENU06706	ANI61C1070 8:1752..1	25-44	726-753	LINAP		g2104438	429	138	2.00E-43	50	22	(Z95396) putative ubiquitin transferase [Schizosaccharomyces pombe]
22913	ENU06707	ANI61C1027 3:3030..3552	44-71	472-499	LINAP		g2494132	74	70	9.00E-12			(AC002376) Contains similarity to human dimethylalanine monooxygenase (gb M64082). [Arabidopsis thaliana]
22914	ENU06708	ANI61C8658: 1172..303	41-68	802-829	LINAP		g2239203	431	89	2.00E-36	39	92	(Z97209) aldolase reductase [Schizosaccharomyces pombe]
22915	ENU06709	ANI61C5032: 1..1205	22-49	809-828	LINAP		g2134102	564	198	6.00E-50	48	19	kinesin-like protein 1 - African clawed frog ; (X82012) kinesin-like protein 1 [Xenopus laevis]
22916	ENU06710	ANI61C1024 7:1405..1982	48-67	537-555	LINAP		g168849	114	77	6.00E-15	33	13	(M80368) pathway-specific regulatory protein [Neurospora crassa]
22917	ENU06711	ANI61C1024 7:4812..6215	22-43	803-825	LINAP		g2731377	988	175	3.00E-43	32	29	(U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]

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22918	ENU06712	ANI61C507:2 675..3025	89-116	453-479	LINAP		g3080535	391	177	4.00E-44	57	7	(AL022600) RNA helicase [Schizosaccharomyces pombe]
22919	ENU06713	ANI61C1024 7:7226..6876	22-42	453-479	LINAP		g2495215	184	94	8.00E-19	39	67	hypothetical 20.9 KD protein in ROX1- SPE3 intergenic region ; hypothetical protein YPR067w - yeast (Saccharomyces cerevisiae) ; (Z49219) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
22920	ENU06714	ANI61C1073 3:1577..2268	42-61	644-671	LINAP		g1351612	256	90	3.00E-29	39	64	hypothetical oxidoreductase C23D3.11 in chromosome I ; hypothetical protein SPAC23D3.11 - fission yeast (Schizosaccharomyces pombe)
22921	ENU06715	ANI61C507:3 990..3468	32-52	481-502	LINAP		g2135950	122	39	0.017			PQ-rich protein - human ; (Z50194) PQ-rich protein [Homo sapiens]
22922	ENU06716	ANI61C1028 3:766..1	23-46	678-700	LINAP		g1175484	276	110	2.00E-28	41	15	ATP-dependent DNA helicase HUS2 ; hypothetical protein SPAC2G11.12 - fission yeast (Schizosaccharomyces pombe) ; (Z54354) atp-dependent dna helicase hus2 [Schizosaccharomyces pombe] ; (Y09426) DNA-helicase [Schizosaccharomyces pombe]
22923	ENU06717	ANI61C5107: 503..913	22-46	455-479	LINAP		g1077552	286	135	2.00E-31	40	49	hypothetical protein YDR051c - yeast (Saccharomyces cerevisiae) ; (Z49209) unknown [Saccharomyces cerevisiae] ; (Z74347) ORF YDR051c [Saccharomyces cerevisiae]
22924	ENU06718	ANI61C505:1 606..564	34-53	810-828	LINAP		g2114323	106	41	0.011	21	32	(D88734) membrane glycoprotein [Equine herpesvirus 1]
22925	ENU06719	ANI61C1028 1:2699..3282	47-66	365-388	LINAP		g115918	128	63	1.00E-17			cell division control protein 2 cognate ; protein kinase (EC 2.7.1.37) cdc2 homolog C - fruit fly (Drosophila sp.) ; (X57486) p34-cdc2 homologue [Drosophila melanogaster]

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22926	ENU06720	ANI61C1074 7:1714..362	22-45	773-790	LINAP		g1351636	860	292	2.00E-78	49	22	hypothetical 143.3 KD TRP-ASP repeats containing protein C12G12.13C in chromosome I; hypothetical protein SPAC12G12.13c - fission yeast (Schizosaccharomyces pombe)
22927	ENU06721	ANI61C1028 8:1152..1	35-58	785-812	LINAP		g112713	184	63	0.000000 003			"1-aminocyclopropane-1-carboxylate synthase CMW33 (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase) ; 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14), wound-induced - winter squash ; (D01032) 1-aminocyclopropane-1-carboxylate synthase [Cucurbita maxima] ; aminocyclopropane carboxylate synthase [Cucurbita maxima] ; aminocyclopropane carboxylate synthase:ISOtype=wound-induced [Cucurbita maxima] "
22928	ENU06722	ANI61C1027 0:612..1042	31-50	419-438	LINAP		g586486	90	57	0.000000 06			hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912) ORF YBR043c [Saccharomyces cerevisiae]
22929	ENU06723	ANI61C8691: 1089..553	69-87	492-516	LINAP		g729562	442	160	2.00E-44	60	23	UDP-glucose 4-epimerase (galactowaldenase) / aldose 1-epimerase (mutarotase) ; UDPglucose 4-epimerase (EC 5.1.3.2) - yeast (Pachysolen tannophilus) ; (X68593) UDP-galactose- 4-epimerase [Pachysolen tannophilus]
22930	ENU06724	ANI61C8668: 600..1	22-45	520-539	LINAP		g2147899	275	77	2.00E-21	40	32	phosphate transporter - Glomus versiforme ; (U38650) phosphate transporter [Glomus versiforme] ; phosphate transporter [Glomus versiforme]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22931	ENU06725	ANI61C8674: 32-51 2419..1690	32-51	673-692	LINAP		g1730741	143	51	0.000000 002			hypothetical 65.3 KD protein in SUN4- MAS5 intergenic region ; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae) ; (U12141) membrane protein [Saccharomyces cerevisiae] ; (Z71341) ORF YNL065w [Saccharomyces cerevisiae] (U05211) Ttp1p [Saccharomyces cerevisiae]
22932	ENU06726	ANI61C5139: 211-230 980..303	211-230	628-647	LINAP		g500628	280	120	1.00E-26	37	37	hypothetical 57.6 KD protein C30D10.15 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe] (AL035216) probable involvement in ergosterol biosynthesis
22933	ENU06727	ANI61C1070 22-44 6:6562..5865	22-44	638-657	LINAP		g3219924	276	112	2.00E-24	36	43	[Schizosaccharomyces pombe]
22934	ENU06728	ANI61C8669: 46-65 627..1	46-65	542-561	LINAP		g4160344	171	88	6.00E-17	51	23	[Schizosaccharomyces pombe] (AF038585) pyruvate dehydrogenase kinase isoform 1; PDK1 [Zea mays] (X97119) pectate lyase [Erwinia chrysanthemi] cyclosporin synthetase - Tolypocladium inflatum ; (Z28383) cyclosporine synthetase [Tolypocladium inflatum] putative 89.3 KD transcriptional regulatory protein C1F7.11C ; hypothetical protein SPAC1F7.11c - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown [Schizosaccharomyces pombe] (AL021837) histone promoter control 2 protein [Schizosaccharomyces pombe] (X89442) peptide synthetase [Metarhizium anisopliae] (S58126) Unknown [Saccharomyces cerevisiae] (AL049497) hypothetical protein [Streptomyces coelicolor] "(AJ002397) beta-1,3 exoglucanase [Trichoderma harzianum]"
22935	ENU06729	ANI61C5129: 24-50 1253..1604	24-50	446-471	LINAP		g3746431	244	62	0.000000 002	44	24	
22936	ENU06730	ANI61C1027 22-41 8:4789..5584	22-41	748-775	LINAP		g1765918	190	61	0.000000 008	34	57	
22937	ENU06731	ANI61C1067 22-41 7:1299..1	22-41	719-743	LINAP		g1083855	388	131	9.00E-30	35	1	
22938	ENU06732	ANI61C5136: 22-44 1914..1594	22-44	457-476	LINAP		g1351672	63	38	0.061	21	20	
22939	ENU06733	ANI61C1030 22-44 5:277..769	22-44	458-479	LINAP		g2894295	162	90	6.00E-18	40	39	
22940	ENU06734	ANI61C1067 36-55 7:3220..1716	36-55	805-828	LINAP		g2342601	571	140	1.00E-32	32	5	
22941	ENU06735	ANI61C8697: 46-70 1460..1832	46-70	295-314	LINAP		g4261597	79	55	0.000000 2	30	11	
22942	ENU06736	ANI61C5133: 39-58 2148..974	39-58	807-829	LINAP		g4539214	817	177	1.00E-43	52	64	
22943	ENU06737	ANI61C1077 22-43 0:1696..2012	22-43	454-473	LINAP		g2924313	109	64	6.00E-10	27	15	

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22944	ENU06738	ANI61C8696: 2694..628	43-63	628-647	LINAP		g2499841	1691	315	3.00E-85	54	31	26S proteasome regulatory subunit MTS4 (19S regulatory CAP region of 26S protease subunit 2) ; (Y09819) 19S regulatory cap region of 26S protease subunit 2 [Schizosaccharomyces pombe]
22945	ENU06739	ANI61C506:1 121-140	307-326		LINAP		g3550985	194	63	8.00E-10	35	34	(AB010740) OsS5a [Oryza sativa]
22946	ENU06740	ANI61C8681: 1356..1			LINAP		g1293655	407	107	1.00E-22	35	35	(U51327) versicolorin B synthase [Aspergillus parasiticus] ; (U51328) versicolorin B synthase [Aspergillus parasiticus]
22947	ENU06741	ANI61C1079: 26-46	452-479		LINAP		g3550283	80	55	0.000000	31	40	(AJ007590) XRP2 protein [Homo sapiens]
22948	ENU06742	ANI61C5149: 109-129	571-590		LINAP		g133322	78	49	0.00003			DNA-directed RNA polymerase II largest subunit ; DNA-directed RNA polymerase (EC 2.7.7.6) II large chain - Caenorhabditis elegans ; (M29235) RNA polymerase II [Caenorhabditis elegans]
22949	ENU06743	ANI61C1032 3:115..1300			LINAP		g1805251	275	92	6.00E-18	30	51	(U58946) transposase [Aspergillus awamori]
22950	ENU06744	ANI61C1077 7:2749..3110	41-59	262-285	LINAP		g479395	77	51	0.000005	34	6	probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
22951	ENU06745	ANI61C1031 7:1497..1193	29-48	459-479	LINAP		g2224683	121	68	6.00E-11	28	10	(AB002369) KIAA0371 [Homo sapiens]
22952	ENU06746	ANI61C1078 7:109..687	25-46	536-558	LINAP		g4503247	126	55	0.000000	33	29	novel nuclear protein 1 ; NNP-1 protein (D21S2056E) ; (U79775) NNP-1 [Homo sapiens]
22953	ENU06747	ANI61C1032 1:1452..1008	34-53	459-479	LINAP		g2950464	185	75	4.00E-17	55	17	(AL022071) hypothetical protein [Schizosaccharomyces pombe]
22954	ENU06748	ANI61C1032 0:2635..2956	24-51	453-479	LINAP		g3136055	76	57	0.000000	24	27	(AL023592) betaine-aldehyde dehydrogenaseprecursor [Schizosaccharomyces pombe]
22955	ENU06749	ANI61C8702: 2218..1	32-51	710-730	LINAP		g1546072	925	108	7.00E-23	32	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]

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22956	ENU06750	ANI61C8694: 2043..3242	53-72	803-821	LINAP		g481230	566	104	4.00E-30	41	63	L-idoitol 2-dehydrogenase (EC 1.1.1.14) precursor - rat ; (X74593) L-idoitol 2-dehydrogenase [Rattus norvegicus] (X75561) GTPase activating protein [Saccharomyces cerevisiae] (AF080119) similar to Schizosaccharomyces pombe isp4 protein (GB:D14061) [Arabidopsis thaliana] probable membrane protein YOL119c - yeast (Saccharomyces cerevisiae) ; (Z74861) ORF YOL119c [Saccharomyces cerevisiae] ; (X95258) unknown protein [Saccharomyces cerevisiae]
22957	ENU06751	ANI61C5154: 22-49 3762..2248	22-49	782-802	LINAP		g414689	329	146	1.00E-34	30	30	
22958	ENU06752	ANI61C1078 27-46 6:2776..3568	27-46	653-674	LINAP		g3600039	103	59	1.00E-10	25	31	
22959	ENU06753	ANI61C8703: 27-46 1195..649	27-46	459-478	LINAP		g2132846	139	73	2.00E-12			
22960	ENU06754	ANI61C1079 22-43 6:3310..2263	22-43	804-829	LINAP		g2414601	414	149	3.00E-35	39	43	[Z99295] phosphatidyl synthase [Schizosaccharomyces pombe] putative transporter C1B3.16C ; (Z98598) putative transporter [Schizosaccharomyces pombe] (AL023634) hypothetical protein [Schizosaccharomyces pombe] "hypothetical 32.9 KD protein in NFO-FRUA intergenic region ; (U00007) yeiN [Escherichia coli] ; (AE000306) orf, hypothetical protein [Escherichia coli] ; yeiN gene [Escherichia coli] " exocyst complex component SEC3 (PSL1 protein) ; PSL1 protein - yeast (Saccharomyces cerevisiae) ; (L22204) Psl1p [Saccharomyces cerevisiae] ; (U18778) Sec3p [Saccharomyces cerevisiae]
22961	ENU06755	ANI61C8703: 66-93 3367..2756	66-93	572-591	LINAP		g3183364	178	100	1.00E-20	33	30	
22962	ENU06756	ANI61C1033 116-143 8:176..494	116-143	450-473	LINAP		g3150252	62	50	0.00001	38	6	
22963	ENU06757	ANI61C1145 34-54 9:2028..411	34-54	754-780	LINAP		g465602	389	70	2.00E-11			
22964	ENU06758	ANI61C5147: 22-42 2509..3155	22-42	598-625	LINAP		g464482	235	100	1.00E-20	42	11	
22965	ENU06759	ANI61C1081 22-47 7:1303..337	22-47	804-823	LINAP		g3334796	373	154	1.00E-45	41	55	putative secreted glucosidase [Streptomyces coelicolor]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
22966	ENU06760	ANI61C1147 9:685..1078	22-44	452-479	LINAP		g127992	117	31	6			"beta-(1->2)glucan export ATP-binding protein NDVA ; beta-1,2-glucan export protein ndvA - Rhizobium meliloti ; (M20726) ndvA peptide (put.); putative [Rhizobium meliloti] "
22967	ENU06761	ANI61C8695: 663..1023	22-44	460-479	LINAP		g1799532	77	59	0.000000 02	33	38	(AB000564) salicylate hydroxylase [Spingomonas sp.]
22968	ENU06762	ANI61C5176: 827..1444	40-59	572-591	LINAP		g2193933	66	46	0.0002			(Z96800) hypothetical protein Rv0312 [Mycobacterium tuberculosis]
22969	ENU06763	ANI61C1079 7:258..1799	27-46	767-786	LINAP		g1020413	464	143	2.00E-33	34	50	(D63703) isobutene-forming enzyme and benzoate 4-hydroxylase [Rhodotorula minuta]
22970	ENU06764	ANI61C1032 9:5912..4715	22-49	807-829	LINAP		g3023956	787	256	2.00E-67	51	20	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserina]
22971	ENU06765	ANI61C8710: 2634..2074			LINAP		g3367797	472	208	2.00E-53	55	22	(AL031154) hypothetical protein [Schizosaccharomyces pombe]
22972	ENU06766	ANI61C5177: 357..1	108-127	454-477	LINAP		g4191793	71	40	0.000000 4			(AC005917) putative zinc finger protein [Arabidopsis thaliana]
22973	ENU06767	ANI61C1079 7:4799..5578	22-43	732-751	LINAP		g4453664	347	166	2.00E-40	37	13	(AL035480) putative polyketide synthase [Mycobacterium leprae]
22974	ENU06768	ANI61C1032 4:7594..8132	40-59	490-508	LINAP		g2582351	370	164	4.00E-40	43	40	(AF018639) unknown [Dictyostelium discoideum]
22975	ENU06769	ANI61C5177: 1806..1464	22-49	456-479	LINAP		g1703534	68	67	7.00E-11	43	29	(U80030) short region of weak similarity to rat dihydroxypolyprenylbenzoate methyltransferase (GI:457372) [Caenorhabditis elegans]
22976	ENU06770	ANI61C1082 0:1054..1	36-55	648-669	LINAP		g3023956	801	243	6.00E-69	51	20	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospira anserina]
22977	ENU06771	ANI61C1034 3:1453..323	25-44	802-829	LINAP		g1352911	983	112	2.00E-35	41	38	hypothetical 80.2 KD protein in CPA2-NNF1 intergenic region ; hypothetical protein YJR110w - yeast (Saccharomyces cerevisiae) ; (Z49610) ORF YJR110w [Saccharomyces cerevisiae]

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22978	ENU06772	ANI61C1147 6:3430..2272	22-47	809-829	LINAP		g1708195	190	66	5.00E-11	34	18	HFM1 protein ; (U22156) Hfm1p [Saccharomyces cerevisiae]
22979	ENU06773	ANI61C1081 9:2123..721	22-47	805-829	LINAP		g538067	461	141	6.00E-33	34	18	(M77661) putative pol polyprotein [Magnaporthe grisea]
22980	ENU06774	ANI61C1035 1:652..2179	22-46	805-824	LINAP		g1723769	247	55	0.000000	5		putative transporter YGR260W ; probable membrane protein YGR260w - yeast (Saccharomyces cerevisiae) ; (Z73044) ORF YGR260w [Saccharomyces cerevisiae] ; (Y07777) YGR260w ORF [Saccharomyces cerevisiae]
22981	ENU06775	ANI61C1081 5:2112..1574	22-41	495-518	LINAP		g127060	184	77	4.00E-24	40	92	zinc finger protein MFG-1 (zinc finger protein 58) ; finger protein mfg1 - mouse (fragment) ; (M28513) zinc finger protein mfg1 mRNA (put.) ; putative [Mus musculus]
22982	ENU06776	ANI61C1034 8:2197..1015	22-46	779-806	LINAP		g1706591	412	175	3.00E-43	48	23	elongation factor 3B (EF-3B) ; probable membrane protein YNL014w - yeast (Saccharomyces cerevisiae) ; (Z71290) ORF YNL014w [Saccharomyces cerevisiae]
22983	ENU06777	ANI61C1030 2:13086..1179 8	43-62	807-826	LINAP		g1169645	227	32	5.3			"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) alpha chain - yeast (Candida albicans) ; (L29063) fatty acid synthase alpha subunit [Candida albicans] "
22984	ENU06778	ANI61C5932: 9680..11615	22-41	771-791	LINAP		g3724089	212	58	4.00E-16	35	8	(AJ011849) fengycin synthetase [Bacillus subtilis]
22985	ENU06779	ANI61C5994: 2179..3833	22-46	798-825	LINAP		g2547314	466	192	3.00E-48	40	12	(AF000149) ATP-binding cassette transporter [Mus musculus]
22986	ENU06780	ANI61C5187: 1264..779	22-44	454-477	LINAP		g3850080	120	58	3.00E-14			(AL033389) putative antioxidant protein [Schizosaccharomyces pombe]
22987	ENU06781	ANI61C1148 5:319..1797	25-46	737-755	LINAP		g1078634	2239	323	e-127	97	35	sepB protein - Emericella nidulans ; sepB protein - Emericella nidulans ; (X86399) sepB [Emericella nidulans]

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22988	ENU06782	ANI61C6060: 1366..2025	58-83	482-501	LINAP		g549628	413	171	4.00E-43	57	90	hypothetical 22.1 KD protein in CCP1-MET1 intergenic region ; hypothetical protein YKR068c - yeast (Saccharomyces cerevisiae) ; (Z28293) ORF YKR068c [Saccharomyces cerevisiae]
22989	ENU06783	ANI61C1080 7:3996..5261	53-72	807-829	LINAP		g125727	533	90	8.00E-35			killer toxin alpha and beta subunits precursor (RF2 protein) (endochitinase ; RF2 protein - yeast (Kluyveromyces marxianus var. lactis) plasmid k1 ; (X07127) RF2 gene product (AA 1 - 1146) [Kluyveromyces lactis] ; (X00762) ORF2 (put. killer toxin large subunit) [Kluyveromyces lactis] ; (X01095) URFP2 (put. 97 kd glycoprotein 31 kd subunit precursor of the killer toxin ; aa 1-1146) [Kluyveromyces lactis]
22990	ENU06784	ANI61C6076: 359..1325	27-46	802-829	LINAP		g3560253	470	139	7.00E-37	50	39	(AL031532) sap2 family putative cell cycle dependent phosphatase associated protein [Schizosaccharomyces pombe] (AJ224865) IgE-binding protein [Aspergillus fumigatus]
22991	ENU06785	ANI61C1148 4:3284..3668	22-47	423-448	LINAP		g2980819	135	88	5.00E-17			alpha-glucosidase precursor (maltase) ; (D45356) alpha-glucosidase [Aspergillus niger]
22992	ENU06786	ANI61C8728: 29-51 1012..2089	29-51	805-827	LINAP		g3023267	950	209	8.00E-58	45	26	[Yersinia enterocolitica]
22993	ENU06787	ANI61C6090: 1..364	63-80	308-327	LINAP		g2765195	79	58	0.000000			(Y12527) HMWP1 protein [Yersinia enterocolitica]
22994	ENU06788	ANI61C1163: 1..518	72-92	469-488	LINAP		g2642224	61	57	0.000000	26	16	telomere-associated recQ-like helicase [Ustilago maydis]
22995	ENU06789	ANI61C1084 6:668..1854	49-67	766-785	LINAP		g1708325	638	137	9.00E-32	45	46	HST1 protein (homologous TO SIR2 protein 1) ; HST1 protein - yeast (Saccharomyces cerevisiae) ; (L47120) homolog of SIR2; transcribed ORF flanked by NUF2 (X72225) and RTG1 (M97690) [Saccharomyces cerevisiae] ; (U39041) Hst1p [Saccharomyces cerevisiae] ; (Z74810) ORF YOL068c [Saccharomyces cerevisiae]

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22996	ENU06790	ANI61C8729: 5126..5536			LINAP		g1731071	66	72	2.00E-12	30	35	hypothetical 47.0 KD protein in GLNQ-ANSR intergenic region ; (D84432) YqjH [Bacillus subtilis] ; (Z99116) similar to DNA-damage repair protein [Bacillus subtilis] (AF024496) contains similarity to Plasmodium falciparum glycoprotein-binding protein homolog 2 (GB:X69769) [Caenorhabditis elegans] (AB002377) KIAA0379 [Homo sapiens] (M74066) Major body wall myosin [Onchocerca volvulus] (AP000003) 348aa long hypothetical dehydrogenase [Pyrococcus horikoshii] regulatory protein CYS-3 ; regulatory protein cys-3 - Neurospora crassa ; (M26008) cys-3 [Neurospora crassa] (AL034563) putative yeast CFIb (RNA3' Cleavage factor I) homolog; ribonucleoprotein [Schizosaccharomyces pombe] cell cycle protein kinase CDC5/MSD2 ; protein kinase CDC5 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (M84220) PKX2 protein kinase [Saccharomyces cerevisiae] ; (Z48613) Cdc5p [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea] (AL049559) protein kinase cekl [Schizosaccharomyces pombe] "(AL031540) internalin- related, Leucine rich repeat containing protein [Schizosaccharomyces pombe] " (AE001017) conserved hypothetical protein [Archaeoglobus fulgidus] UV-endonuclease - Neurospora crassa
22997	ENU06791	ANI61C5223: 2348..825	23-44	805-827	LINAP		g2394451	212	59	0.000000	31	18	
22998	ENU06792	ANI61C1086 1:302..1	97-117	432-451	LINAP		g2224699	117	80	1.00E-14	31	18	
22999	ENU06793	ANI61C1036 5:1658..1991	30-49	364-385	LINAP		g159893	80	52	0.000004			
23000	ENU06794	ANI61C5213: 1108..1539			LINAP		g3257063	123	45	1.00E-10			
23001	ENU06795	ANI61C1085 6:2845..2191	22-48	593-620	LINAP		g118126	226	71	9.00E-12	33	91	
23002	ENU06796	ANI61C1034 9:3166..4194	44-64	797-816	LINAP		g4049514	642	153	2.00E-45	49	53	
23003	ENU06797	ANI61C1178: 1625..2522	22-49	772-799	LINAP		g416768	438	203	1.00E-51	41	36	
23004	ENU06798	ANI61C8746: 619..1315	39-58	639-658	LINAP		g4499843	203	74	9.00E-13	37	40	
23005	ENU06799	ANI61C5230: 2738..464	25-52	806-829	LINAP		g4581521	696	240	7.00E-63	68	12	
23006	ENU06800	ANI61C1085 8:3973..4384	22-45	263-289	LINAP		g3581887	234	92	2.00E-18	34	15	
23007	ENU06801	ANI61C1086 0:2530..2876	22-45	437-458	LINAP		g2649315	98	63	0.000000	29	65	
23008	ENU06802	ANI61C1037 8:900..1809	22-48	803-827	LINAP		g1362529	1047	391	e-108	69	40	

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23009	ENU06803	ANI61C1037 6:2137..433	22-49	805-824	LINAP		g2655202	1286	206	3.00E-70	56	32	(AF026402) U5 snRNP 100 kD protein [Homo sapiens]
23010	ENU06804	ANI61C9209: 8281..7674	22-44	522-541	LINAP		g3914934	129	99	2.00E-20			probable RNA 3'-terminal phosphate cyclase (RNA-3'-phosphate cyclase) (RNA cyclase); (AP000006) 369aa long hypothetical phosphate cyclase [Pyrococcus horikoshii]
23011	ENU06805	ANI61C9263: 1380..883	22-43	441-460	LINAP		g2414601	235	106	8.00E-23	43	28	(Z99295) phosphatidyl synthase [Schizosaccharomyces pombe]
23012	ENU06806	ANI61C5998: 10102..10727	135-158	484-503	LINAP		g3123165	372	167	7.00E-41	42	57	zinc finger protein 183; (X98253) ZNF183 [Homo sapiens]; (AC002477) zinc-finger protein [Homo sapiens]
23013	ENU06807	ANI61C9250: 3162..4281	37-56	798-825	LINAP		g2257514	480	182	2.00E-45	39	49	(AB004535) ATP-dependent RNA helicase MSS116 precursor [Schizosaccharomyces pombe]
23014	ENU06808	ANI61C8731: 4890..3869	59-78	807-829	LINAP		g1169823	219	109	2.00E-23	28	28	regulatory protein GAL4; regulatory protein GAL4 - yeast (Saccharomyces cerevisiae); (K01486) GAL4 protein [Saccharomyces cerevisiae]; (Z67751) GAL4 [Saccharomyces cerevisiae]; (Z773604) ORF YPL248c [Saccharomyces cerevisiae]
23015	ENU06809	ANI61C5930: 388..933	175-195	499-518	LINAP		g125935	56	45	0.0004	24	24	lactose permease; lactose permease - yeast (Kluyveromyces marxianus var. lactis); (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis]
23016	ENU06810	ANI61C120:1 015..1	30-57	797-824	LINAP		g1711577	697	222	2.00E-68	53	61	"succinyl-CoA ligase (GDP-forming), beta-chain precursor (succinyl-CoA synthetase, beta chain) (SCS-beta); beta-succinyl CoA synthetase - rumen fungus (Neocallimastix frontalis); (X84222) beta-succinyl CoA synthetase [Neocallimastix frontalis]" (U58946) transposase [Aspergillus awamori]
23017	ENU06811	ANI61C5930: 3180..1803	24-43	803-822	LINAP		g1805251	1122	289	1.00E-77	50	50	(AL031764) putative FAD synthetase [Schizosaccharomyces pombe]
23018	ENU06812	ANI61C5245: 452..1	104-127	451-477	LINAP		g3668151	111	59	0.000000	32	52	[Schizosaccharomyces pombe]
23019	ENU06813	ANI61C9251: 295..851	23-47	513-536	LINAP		g3873550	105	50	0.00002	28	34	(AL033534) serine-rich protein [Schizosaccharomyces pombe]

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23020	ENU06814	ANI61C8754: 1291..2226	23-48	783-810	LINAP		g138350	121	57	0.000000 1			glycoprotein X precursor ; glycoprotein X precursor - equine herpesvirus 1 (strain Ab4p) ; (M86664) membrane glycoprotein [Equine herpesvirus 1] "(AJ223012) rifamycin polyketide synthase, type 1 [Amocolatopsis mediterranei] ; (AF040570) polyketide synthase [Amocolatopsis mediterranei] "
23021	ENU06815	ANI61C6099: 1..625	22-46	575-602	LINAP		g2764761	51	34	0.0006			hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti] putative amidase CY50.19C ; (Z77137) amiE2 [Mycobacterium tuberculosis] (Z70310) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST
23022	ENU06816	ANI61C1086 0:4578..3752	22-46	780-806	LINAP		g1353088	176	89	4.00E-17	32	69	EMBL:D32723 comes from this gene; cDNA EST E... ; (Z70686) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST
23023	ENU06817	ANI61C1159: 11409..12069	27-46	616-640	LINAP		g1703266	249	109	2.00E-23	41	43	EMBL:D32723 comes from this gene; cDNA EST E... ; (Z70686) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST
23024	ENU06818	ANI61C6067: 2562..1697			LINAP		g3879121	265	128	4.00E-29			EMBL:D32723 comes from this gene; cDNA EST E... ; (Z70686) predicted using Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST
23025	ENU06819	ANI61C5243: 1..423	109-132	364-391	LINAP		g1711534	261	112	1.00E-24	47	37	succinate semialdehyde dehydrogenase (NAD(+)-dependent succinic semialdehyde dehydrogenase) ; succinate-semialdehyde dehydrogenase (EC 1.2.1.24) - human (fragment) ; (L34820) succinate semialdehyde dehydrogenase [Homo sapiens]

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23026	ENU06820	ANI61C1160: 22-45 1711..1001	22-45	663-690	LINAP		g119164	271	134	5.00E-31	40	48	elongation factor 1-gamma (EF-1-gamma) ; translation elongation factor eEF-1 gamma chain - brine shrimp ; (M28020) elongation factor 1-gamma [Artemia sp.]
23027	ENU06821	ANI61C9253: 4863..4221			LINAP		g2494878	828	319	1.00E-89	90	55	guanine nucleotide-binding protein alpha subunit ; (U49917) FadA [Emicella nidulans]
23028	ENU06822	ANI61C8748: 22-45 1477..713	22-45	654-679	LINAP		g1172741	337	111	1.00E-37	40	36	peptide transporter PTR2 ; (U09781) peptide transporter [Candida albicans]
23029	ENU06823	ANI61C9281: 48-67 12..891	48-67	769-789	LINAP		g4164426	403	159	2.00E-38	42	29	(AL035247) putative spindle pole body-associating protein [Schizosaccharomyces pombe]
23030	ENU06824	ANI61C8743: 23-50 2013..1378	23-50	570-589	LINAP		g1729825	101	47	6.00E-10	31	57	transaldolase ; transaldolase (EC 2.2.1.2) - yeast (Saccharomyces cerevisiae) ; (U19102) Tal1p: Transaldolase [Saccharomyces cerevisiae]
23031	ENU06825	ANI61C5255: 22-46 1577..1250	22-46	451-478	LINAP		g1176486	114	80	1.00E-14	34	25	hypothetical 63.9 KD protein in IME2-MEF2 intergenic region ; protein YKR029c homolog YJL105w - yeast (Saccharomyces cerevisiae) ; (X85021) YKR029c homologue [Saccharomyces cerevisiae] ; (Z49380) ORF YJL105w [Saccharomyces cerevisiae]
23032	ENU06826	ANI61C1084 22-45 7:693..1	22-45	572-592	LINAP		g2493399	74	77	1.00E-13			putative cytochrome P450 T10B9.5 in chromosome II ; (Z48717) similar to cytochrome P450 [Caenorhabditis elegans]
23033	ENU06827	ANI61C9282: 22-43 533..1	22-43	449-468	LINAP		g731628	436	167	2.00E-44	59	44	putative mitochondrial carrier YHR002W ; hypothetical protein YHR002w - yeast (Saccharomyces cerevisiae) ; (U10555) Yhr002wp [Saccharomyces cerevisiae]

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23034	ENU06828	ANI61C8744: 39-58 1843..3172	803-822	LINAP		g1175977	738	185	3.00E-58	47	48	hypothetical 61.8 KD peptidase in MPR1-GCN20 intergenic region ; probable membrane protein YFR006w - yeast (Saccharomyces cerevisiae) ; (D50617) YFR006W [Saccharomyces cerevisiae]
23035	ENU06829	ANI61C6078: 23-43 1..494	446-473	LINAP		g284667	100	36	0.13			neurofilament triplet H1 protein - rabbit (fragment) ; (M94315) neurofilament-H [Oryctolagus cuniculus]
23036	ENU06830	ANI61C5244: 26-46 1829..2440	562-584	LINAP		g586937	171	34	0.66			zinc-finger protein 2 (zinc-finger homeodomain protein 2) ; homeotic protein zfh-2 - fruit fly (Drosophila melanogaster) ; (M63450) zinc-finger homeodomain protein 2 [Drosophila melanogaster]
23037	ENU06831	ANI61C1088 22-47 2:1437..737	656-675	LINAP		g2492758	123	38	2.00E-10	34	66	probable short-chain type dehydrogenase/reductase VDLC
23038	ENU06832	ANI61C8753: 52-71 2335..1445	807-829	LINAP		g114967	244	71	2.00E-17	35	30	beta-glucosidase (gentiobiase) (cellobiase) (beta-D-glucoside glucohydrolase) ; beta-glucosidase (EC 3.2.1.21) - Agrobacterium tumefaciens ; (M59852) beta-D-glucosidase [Agrobacterium tumefaciens] (AB025420) Family 19 chitinase (pRYA1 ORF) [Aeromonas sp. 10S-24]
23039	ENU06833	ANI61C527:1 25-44 ..389	306-325	LINAP		g4587324	142	39	0.011			(D90908) hypothetical protein [Synecocystis sp.]
23040	ENU06834	ANI61C1187: 54-73 1685..1184	459-478	LINAP		g1652749	201	117	4.00E-26	45	65	(AL035076) putative carboxylesterase-lipase family member
23041	ENU06835	ANI61C1089 38-59 5:1458..3116	781-800	LINAP		g4107289	654	94	2.00E-18	32	47	[Schizosaccharomyces pombe] (D88802) ydhJ [Bacillus subtilis] ; (Z99107) similar to hypothetical proteins [Bacillus subtilis]
23042	ENU06836	ANI61C1090 22-47 3:1026..1529	464-483	LINAP		g1945094	145	48	0.00004	31	51	high-affinity glucoSE transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
23043	ENU06837	ANI61C6147: 45-64 1..1043	801-820	LINAP		g1346290	423	137	1.00E-31	33	45	

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23044	ENU06838	ANI61C9285: 1551..941	58-77	568-590	LINAP		g1082283	125	34	0.78			protein kinase (EC 2.7.1.37) cdc2-related PITSLE alpha 2-1 - human (X91243) XrpFibeta1 [Xenopus laevis]
23045	ENU06839	ANI61C8762: 2587..2010	25-52	530-557	LINAP		g992626	64	49	0.00003	29	35	(AF026032) ATRX protein [Mus musculus]
23046	ENU06840	ANI61C6148: 536..1492			LINAP		g3002558	72	57	0.0000002	26	9	hypothetical 73.8 KD protein in SPC98-TOM70 intergenic region ; probable membrane protein YNL125c - yeast (Saccharomyces cerevisiae) ; (Z46843) orf23 [Saccharomyces cerevisiae] ; (Z69382) Identical to putative protein ESBP6 [Saccharomyces cerevisiae] ; (Z71401) ORF YNL125c [Saccharomyces cerevisiae]
23047	ENU06841	ANI61C1210: 4317..3508	47-73	740-759	LINAP		g1730773	211	103	2.00E-21			(D89164) unnamed protein product [Schizosaccharomyces pombe] "epoxide hydrolase (microsomal epoxide hydrolase) (epoxide hydratase) ; epoxide hydrolase (EC 3.3.2.3), microsomal - rabbit ; (M21496) microsomal epoxide hydrolase (EC 3.3.2.3) [Oryctolagus cuniculus] " (AC002294) Similar to transcription factor gb[Z46606]1658307 and others [Arabidopsis thaliana] "(Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia] " (AF052435) odd-paired-like [Danio rerio]
23048	ENU06842	ANI61C9292: 2016..1490	23-50	480-506	LINAP		g1749536	235	103	8.00E-22	45	44	(M77661) putative pol polypeptide [Magnaporthe grisea] (U58946) transposase [Aspergillus awamori]
23049	ENU06843	ANI61C8740: 2899..2451	64-83	459-478	LINAP		g123927	84	54	1.00E-12			
23050	ENU06844	ANI61C6153: 1472..1033			LINAP		g2443887	166	61	0.000000005	29	11	
23051	ENU06845	ANI61C5274: 1181..611	53-74	528-549	LINAP		g3850821	247	33	1.8	45	26	
23052	ENU06846	ANI61C1214: 3821..4206	22-44	364-391	LINAP		g3283028	182	53	8.00E-17	40	30	
23053	ENU06847	ANI61C9286: 2977..4449	22-45	775-795	LINAP		g538067	718	270	7.00E-72	47	20	
23054	ENU06848	ANI61C876: 037..324			LINAP		g1805251	475	190	8.00E-48	42	42	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23055	ENU06849	ANI61C526:1 484..775	25-45	662-689	LINAP		g3219917	167	89	3.00E-17	31	85	hypothetical 27.4 KD protein C30D10.14 in chromosome II ; (Z97992) conserved hypothetical protein [Schizosaccharomyces pombe]
23056	ENU06850	ANI61C1092 0:1147..1			LINAP		g493955	223	71	1.00E-11	35	38	Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase) ; Lipase (E.C.3.1.1.3) (Triacylglycerol Hydrolase)
23057	ENU06851	ANI61C9299: 105-124 1..642		597-616	LINAP		g2224699	133	49	2.00E-13	32	23	(AB002377) KIAA0379 [Homo sapiens]
23058	ENU06852	ANI61C122:3 278..2954	22-49	278-304	LINAP		g731739	188	92	1.00E-18	50	19	hypothetical 55.5 KD GTP-binding protein in CDC23-DBP8 intergenic region ; probable purine nucleotide-binding protein YHR168w - yeast (Saccharomyces cerevisiae) ; (U00027)
23059	ENU06853	ANI61C8758: 22-47 2220..998	22-47	807-827	LINAP		g3367789	530	109	2.00E-23	48	50	Yhr168wp [Saccharomyces cerevisiae] (AL031154) hypothetical protein [Schizosaccharomyces pombe]
23060	ENU06854	ANI61C6155: 22-41 917..201	22-41	629-647	LINAP		g532113	77	41	0.01			(U13646) homeotic region most like HMPB_DROME: homeotic proboscipedia protein [Caenorhabditis elegans]
23061	ENU06855	ANI61C5259: 33-54 3275..2159	33-54	809-828	LINAP		g2133035	226	82	8.00E-30	36	51	probable membrane protein YPR157w - yeast (Saccharomyces cerevisiae) ; (U28371) P9584.4 gene product [Saccharomyces cerevisiae]
23062	ENU06856	ANI61C9288: 27-53 2693..896	27-53	801-828	LINAP		g2342601	408	101	9.00E-21	29	5	(X89442) peptide synthetase [Metarhizium anisopliae]
23063	ENU06857	ANI61C8774: 22-48 3868..3465	22-48	272-291	LINAP		g1729996	69	54	0.000000	29	51	TOXD protein ; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]
23064	ENU06858	ANI61C6159: 54-73 2762..3303	54-73	477-494	LINAP		g2808720	152	55	0.000000	32	27	(AL021428) hypothetical protein Rv0063 [Mycobacterium tuberculosis]
23065	ENU06859	ANI61C5247: 30-50 1364..936	30-50	454-476	LINAP		g1353088	151	75	3.00E-13	34	37	hypothetical 36.4 KD protein in MOCC-MOCA intergenic region (ORF334) ; hypothetical protein 334 - Rhizobium meliloti ; (X78503) ORF334 [Sinorhizobium meliloti]

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23066	ENU06860	ANI61C1092 9:1120..1693	22-42	529-552	LINAP		g3023677	67	50	0.00001			probable translation initiation factor EIF-2B gamma subunit (EIF-2B GDP-GTP exchange factor) ; (Z98602)
													translation initiation factor eif-2b gamma subunit [Schizosaccharomyces pombe]
23067	ENU06861	ANI61C8761: 4912..402			LINAP		g3080535	4244	395	e-109	67	14	(AL022600) RNA helicase [Schizosaccharomyces pombe]
23068	ENU06862	ANI61C6176: 800..1	45-63	753-779	LINAP		g3122874	354	105	2.00E-35	37	50	D-3-phosphoglycerate dehydrogenase (PGDH) ; phosphoglycerate dehydrogenase (EC 1.1.1.95) - Methanococcus jannaschii ; (U67544) phosphoglycerate dehydrogenase (serA) [Methanococcus jannaschii]

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23069	ENU06863	ANI61C1091 5:3250..2860	22-47	419-439	LINAP		g2780921	29	41	0.004			"Chain A, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non-Selective Inhibitor, Flurbiprofen ; Chain B, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non- Selective Inhibitor, Flurbiprofen ; Chain C, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non-Selective Inhibitor, Flurbiprofen ; Chain D, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non- Selective Inhibitor, Flurbiprofen ; Chain A, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non-Selective Inhibitor, Indomethacin ; Chain B, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non- Selective Inhibitor, Indomethacin ; Chain C, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non-Selective Inhibitor, Indomethacin ; Chain D, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non- Selective Inhibitor, Indomethacin ; Chain C, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non-Selective Inhibitor, Indomethacin ; Chain D, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non- Selective Inhibitor, Indomethacin ; Chain C, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non-Selective Inhibitor, Indomethacin ; Chain D, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Non- Selective Inhibitor, Indomethacin ; Chain A, Uninhibited Mouse Cyclooxygenase-2 (Prostaglandin Synthase-2) ; Chain B, Uninhibited Mouse Cyclooxygenase-2 (Prostaglandin Synthase-2) ; Chain C, Uninhibited Mouse Cyclooxygenase-2 (Prostaglandin Synthase-2) ; Chain D, Uninhibited Mouse Cyclooxygenase-2 (Prostaglandin Synthase-2) ; Chain A, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Selective Inhibitor, Sc-558 In I222 Space Group ; Chain B, Cyclooxygenase-2 (Prostaglandin Synthase-2) Complexed With A Selective Inhibitor, Sc-558 In I222 Space Group ; Chain A,

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23070	ENU06864	ANI61C9267: 22-47 7363..7704	22-47	416-435	LINAP		g1706177	147	48	0.00004	38	15	cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]
23071	ENU06865	ANI61C8784: 28-53 2558..1722	28-53	762-781	LINAP		g2781417	162	109	3.00E-23	25	15	(AF081920) polyketide synthase type I; PktC [Pseudomonas fluorescens]
23072	ENU06866	ANI61C6188: 93-113 1002..282	93-113	678-700	LINAP		g4102999	440	168	3.00E-41	46	64	(AF019630) pathogenicity protein [Magnaporthe grisea]
23073	ENU06867	ANI61C5275: 40-59 1687..3309	40-59	756-783	LINAP		g1176583	924	162	3.00E-61	49	28	hypothetical 102.5 KD protein in KRE1-HXT14 intergenic region ; probable membrane protein YNL321w - yeast (Saccharomyces cerevisiae) ; (Z46259) NO339 [Saccharomyces cerevisiae] ; (Z71597) ORF YNL321w [Saccharomyces cerevisiae]
23074	ENU06868	ANI61C1191: 45-68 11557..10509	45-68	784-808	LINAP		g2832742	576	199	3.00E-50	42	59	(Z99163) similar to nitrogen permease regulator. [Schizosaccharomyces pombe]
23075	ENU06869	ANI61C8791: 22-48 1038..702	22-48	331-352	LINAP		g4455009	91	60	0.000000			(AF1111179) G-septin alpha [Rattus norvegicus]
23076	ENU06870	ANI61C6183: 45-72 1..1296	45-72	742-767	LINAP		g3288709	997	139	2.00E-62	50	18	(AB010442) PMR1 [Penicillium digitatum]
23077	ENU06871	ANI61C1191: 22-48 11790..13388	22-48	730-749	LINAP		g586394	369	100	9.00E-23			hypothetical 98.1 KD TRP-ASP repeats containing protein in PAF1-MRPL27 intergenic region ; hypothetical protein YBR281c - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2018-ORF [Saccharomyces cerevisiae] ; (Z36150) ORF YBR281c [Saccharomyces cerevisiae] ; ORF YBR2018 [Saccharomyces cerevisiae]
23078	ENU06872	ANI61C8759: 52-71 5302..4296	52-71	779-798	LINAP		g1173638	301	144	7.00E-34	30	75	(U35779) 1-aminocyclopropane-1- carboxylate synthase [Triticum aestivum]

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23079	ENU06873	ANI61C5284: 1696..245	82-101	712-732	LINAP		g1168817	847	136	1.00E-48	52	20	cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe) ; (X78799) cdc7 [Schizosaccharomyces pombe] ; (AL035537) cell division control protein 7 [Schizosaccharomyces pombe] (U61955) Similar to kinesin-like protein; coded for by C. elegans cDNA yk184h5.3; coded for by C. elegans cDNA yk13d7.3; coded for by C. elegans cDNA yk13d7.5; coded for by C. elegans cDNA yk31e1.5; co... ; (AF057567) kinesin-like protein ZEN-4a [Caenorhabditis elegans] proline utilization trans-activator ; transcription activator PUT3 - yeast (Saccharomyces cerevisiae) ; (X55384) proline utilization trans-activator [Saccharomyces cerevisiae] ; (X74152) orf5; homologous to S.cerevisiae PUT3 gene [Saccharomyces cerevisiae] ; (Z28015) ORF YKL015w [Saccharomyces cerevisiae] PTM1 protein ; pim1 hypothetical protein - fission yeast (Schizosaccharomyces pombe) (AF041382) microtubule binding protein D-CLIP-190 [Drosophila melanogaster] (AL049608) putative protein [Arabidopsis thaliana] cell-cycle nuclear autoantigen SG2NA (S/G2 nuclear antigen) ; nuclear autoantigen - human ; (U17989) GS2NA [Homo sapiens]
23080	ENU06874	ANI61C1093: 1275..602	61-87	587-614	LINAP		g1397341	85	44	7.00E-10	35	23	
23081	ENU06875	ANI61C1212: 11259..10711	22-48	503-528	LINAP		g131653	62	45	0.000008			
23082	ENU06876	ANI61C5251: 5260..4784	49-68	433-452	LINAP		g132172	108	63	0.000000	26	28	
23083	ENU06877	ANI61C1095: 6:243..861	22-47	565-584	LINAP		g2773363	85	52	0.000002	26	11	
23084	ENU06878	ANI61C6137: 937..280	22-45	599-618	LINAP		g4584545	125	84	7.00E-16	35	55	
23085	ENU06879	ANI61C2185: 438..805	71-90	455-476	LINAP		g3122872	177	65	3.00E-11	31	20	

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23086	ENU06880	ANI61C1239: 98-118 578..1	98-118	456-474	LINAP		g547902	89	35	0.37			putative mucin core protein precursor 24 (multi-glycosylated core protein 24) (MUC-24) (MUC-24) (CD164 antigen) ; core protein MGC-24 - human ; (D14043) MGC-24 precursor [Homo sapiens]
23087	ENU06881	ANI61C2134: 24-51 3035..2486	24-51	506-529	LINAP		g559044	160	68	4.00E-11	26	27	(L29296) alpha-adducin [Homo sapiens]
23088	ENU06882	ANI61C8786: 22-48 624..1273	22-48	609-629	LINAP		g559964	145	52	4.00E-15	40	68	(J05282) insect-type dehydrogenase [Pseudomonas cepacia]
23089	ENU06883	ANI61C6181: 22-49 2291..1059	22-49	803-828	LINAP		g2842510	423	96	2.00E-19	26	30	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
23090	ENU06884	ANI61C5251: 24-45 5998..5213	24-45	741-765	LINAP		g1076802	106	64	0.000000	34	11	extensin-like protein - maize ; (Z34465) extensin-like protein [Zea mays] ; extensin-like domain [Zea mays]
23091	ENU06885	ANI61C1216: 22-48 637..4272	22-48	806-829	LINAP		g538067	2006	169	2.00E-41	38	19	(M77661) putative pol polypeptide [Magnaporthe grisea]
23092	ENU06886	ANI61C8786: 22-49 3439..4250	22-49	675-693	LINAP		g1709181	249	42	0.000000	36	40	"high affinity methionine permease ; methionine transport protein, high affinity - yeast (Saccharomyces cerevisiae) ; (U40316) high affinity methionine permease [Saccharomyces cerevisiae] ; (Z72840) ORF YGR055w [Saccharomyces cerevisiae] "
23093	ENU06887	ANI61C1216: 28-47 7517..5870	28-47	804-829	LINAP		g2132868	160	34	1.4			probable membrane protein YOR053w - yeast (Saccharomyces cerevisiae) ; (Z74961) ORF YOR053w [Saccharomyces cerevisiae] ; (Z70678) YOR29-04 [Saccharomyces cerevisiae] (AF074951) cellobiose dehydrogenase [Thielavia heterothallica]
23094	ENU06888	ANI61C1096 22-47 9:515..1175	22-47	586-605	LINAP		g3319315	340	150	1.00E-35	38	26	cytochrome P450 3A2 (CYP3A2) (P450-PCN2) ; cytochrome P450 3A2 - rat ; (M13646) cytochrome P450 [Rattus norvegicus]
23095	ENU06889	ANI61C2160: 102-126 308..1	102-126	447-474	LINAP		g117154	113	66	1.00E-10	34	23	cytochrome P450 3A2 (CYP3A2) (P450-PCN2) ; cytochrome P450 3A2 - rat ; (M13646) cytochrome P450 [Rattus norvegicus]
23096	ENU06890	ANI61C9256: 23-42 7147..5656	23-42	805-829	LINAP		g1083855	340	96	2.00E-19	25	1	cyclosporin synthetase - Tolypocladium inflatum ; (Z28383) cyclosporine synthetase [Tolypocladium inflatum]

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23097	ENU06891	ANI61C8777: 22-48 2603..1599	22-48	804-829	LINAP		g1491795	672	248	4.00E-65	47	28	"(U39812) beta-1,4-mannanase [Caldicellulosiruptor saccharolyticus] "
23098	ENU06892	ANI61C6218: 37-57 1141..230	37-57	809-828	LINAP		g4522004	160	94	9.00E-19	31	38	"(AC007069) putative histidine kinase, sensory transduction [Arabidopsis thaliana] "
23099	ENU06893	ANI61C5291: 22-44 1929..1250	22-44	615-638	LINAP		g3850084	85	83	1.00E-15	37	62	(AL033389) alcohol dehydrogenase [Schizosaccharomyces pombe]
23100	ENU06894	ANI61C9272: 83-102 728..1	83-102	603-625	LINAP		g2773203	545	224	8.00E-61	51	43	(AF039713) Similar to phosphoglycerate mutase; coded for by C. elegans cDNA yk357d11.5; coded for by C. elegans cDNA yk387c10.5; coded for by C. elegans cDNA yk384f12.5; coded for by C. elegans cDNA cm10f9; coded for by C. elegans cDNA cm18g...
23101	ENU06895	ANI61C8802: 22-46 512..2226	22-46	793-812	LINAP		g3395351	350	79	3.00E-14	29	25	(AB012696) DNA polymerase V [Schizosaccharomyces pombe] ; (AL022305) DNA polymerase V [Schizosaccharomyces pombe]
23102	ENU06896	ANI61C5300: 22-41 1457..1984	22-41	453-473	LINAP		g2120949	87	77	9.00E-14	37	28	[Schizosaccharomyces pombe] lipase-like enzyme - Alcaligenes eutrophus ; (L36817) lipase-like enzyme [Alcaligenes eutrophus] ; ORF 8 [Ralstonia eutropha]
23103	ENU06897	ANI61C1095 72-95 0:1..423	72-95	376-400	LINAP		g1181493	97	61	0.000000	33	21	"(U42580) 4 ankyrin repeats; similar to Drosophila melanogaster ankyrin, encoded by GenBank Accession Number L35601 [Paramecium bursaria Chlorella virus 1] "
23104	ENU06898	ANI61C219:1 22-48 677..2320	22-48	595-615	LINAP		g3757521	302	121	4.00E-27	40	17	(AC005167) unknown protein [Arabidopsis thaliana]
23105	ENU06899	ANI61C9301: 23-46 3610..3956	23-46	414-432	LINAP		g2673951	172	50	4.00E-14	31	11	(U62933) multidrug resistance protein 1 [Aspergillus fumigatus] ; (U62934) multidrug resistance protein 1 [Aspergillus fumigatus]
23106	ENU06900	ANI61C8766: 34-53 590..2566	34-53	802-821	LINAP		g2494692	999	118	6.00E-26	36	22	[Aspergillus fumigatus] White collar 1 protein (WC1) ; (X94300) wc-1 [Neurospora crassa]
23107	ENU06901	ANI61C219:3 22-47 639..4561	22-47	781-800	LINAP		g4539260	123	53	0.000003			(AL049495) hypothetical protein [Schizosaccharomyces pombe]

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23108	ENU06902	ANI61C8806: 29-50 1480..1947	29-50	444-463	LINAP		g1723291	489	150	6.00E-36	47	69	hypothetical 26.3 KD protein C13D6.03C in chromosome I; (Z69725) unknown [Schizosaccharomyces pombe]
23109	ENU06903	ANI61C625:6 39-58 70..1414	39-58	626-643	LINAP		g464347	135	82	3.00E-15	29	17	peroxisome biosynthesis protein PAS5 (peroxin-6) ; (Z22556) PAS5 [Pichia pastoris]
23110	ENU06904	ANI61C5296: 53-80 1627..3637	53-80	724-746	LINAP		g2094857	599	108	5.00E-23	42	32	[Schizosaccharomyces pombe]
23111	ENU06905	ANI61C1098: 22-44 2023..2692	22-44	627-649	LINAP		g3980042	135	85	6.00E-16			(AL033514) similar to ABC transporters ; ABC transporter transmembrane region. [Caenorhabditis elegans]
23112	ENU06906	ANI61C8822: 31-50 2014..319	31-50	778-804	LINAP		g4262148	772	190	1.00E-47	40	35	(AC005275) predicted protein of unknown function [Arabidopsis thaliana]
23113	ENU06907	ANI61C6255: 143-170 642..1	143-170	592-612	LINAP		g2388993	392	98	1.00E-35	49	10	(Z98981) putative sodium channel [Schizosaccharomyces pombe]
23114	ENU06908	ANI61C5309: 52-71 1418..1978	52-71	489-510	LINAP		g2498971	131	64	0.000000	37	26	putative sterigmatocystin biosynthesis monooxygenase STCW ; (U34740) putative FAD-containing monooxygenase [Emicella nidulans]
23115	ENU06909	ANI61C8764: 23-48 920..4304	23-48	809-828	LINAP		g1175466	1302	215	2.00E-55	43	23	hypothetical 126.9 KD protein C22G7.04 in chromosome I; hypothetical protein SPAC22G7.04 - fission yeast (Schizosaccharomyces pombe) ; (Z54328) putative poly(a)-specific ribonuclease subunit [Schizosaccharomyces pombe]
23116	ENU06910	ANI61C6247: 65-84 1889..2799	65-84	803-829	LINAP		g119857	1026	309	2.00E-83	72	80	fibrillarin (nucleolar protein 1) ; nucleolar protein NOP1 - yeast (Saccharomyces cerevisiae) ; (J05230) fibrillarin [Saccharomyces cerevisiae] ; (Z48432) nucleolar protein NOP1 (J05230) [Saccharomyces cerevisiae] ; (Z74062) ORF YDL014w [Saccharomyces cerevisiae]
23117	ENU06911	ANI61C5311: 797..89			LINAP		g1772352	181	106	1.00E-22	34	52	(D85895) diacylglycerol lipase [Aspergillus oryzae]

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23118	ENU06912	ANI61C1099 5:1443..1117	107-132	254-273	LINAP		g3122326	90	59	0.000000	43	17	LEC14B protein ; (D83074) LEC14B protein [Lithospermum erythrorhizon]
23119	ENU06913	ANI61C8817: 41-60	454-473		LINAP			85			29		hypothetical 180.2 KD protein C31A2.05C in chromosome I ;
23120	ENU06914	ANI61C1099: 34-53 1268..1617 2673..422	731-755		LINAP		g1175399	288	89	4.00E-17			hypothetical protein SPAC31A2.05c - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe] ;
23121	ENU06915	ANI61C930:1 29-51 033..2253	796-815		LINAP		g4154078	472	98	9.00E-30	37	29	[Schizosaccharomyces pombe] (AB016866) Mis4 [Schizosaccharomyces pombe] (AL035161) putative efflux protein [Streptomyces coelicolor]
23122	ENU06916	ANI61C6811: 122-142 812..364	427-446		LINAP		g1171755	279	82	3.00E-23	54	36	"neutral protease II precursor (deuterolysin) (NPII) ; neutral proteinase II - Aspergillus oryzae ; (S53810) neutral protease II, NPII [Aspergillus oryzae, Peptide, 352 aa] [Aspergillus oryzae] ; neutral protease II [Aspergillus oryzae] "
23123	ENU06917	ANI61C2244: 22-41 684..1034	460-479		LINAP		g549706	183	68	4.00E-11	38	35	KTI12 protein ; KTI12 protein - yeast (Saccharomyces cerevisiae) ; (Z28110) ORF YKL110c [Saccharomyces cerevisiae] ; (X77511) KTI12 [Saccharomyces cerevisiae]
23124	ENU06918	ANI61C6808: 22-45 1232..232	613-633		LINAP		g3559998	312	116	2.00E-27	37	62	(AL031515) hypothetical protein SC5C7.08 [Streptomyces coelicolor]
23125	ENU06919	ANI61C8823: 43-63 1..1336	808-829		LINAP		g2558839	204	118	5.00E-26	34	14	(AF016585) polyketide synthase module 3 [Streptomyces caelestis]
23126	ENU06920	ANI61C6788: 108-127 1..861	749-766		LINAP		g1175438	223	100	2.00E-20	27	34	hypothetical 84.5 KD protein C24H6.09 in chromosome I ;
													hypothetical protein SPAC24H6.09 - fission yeast (Schizosaccharomyces pombe) ; (Z54142) putative guanine nucleotide exchange factor [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23127	ENU06921	ANI61C6265: 50-69 909..1657	50-69	693-712	LINAP		g2275336	263	44	0.001			(AF001978) differentially expressed in relation to the extent of cell elongation [Candida albicans]
23128	ENU06922	ANI61C931:1 ..598	102-125	552-573	LINAP		g4490644	155	66	2.00E-10	36	18	"(Z98762) SPAC4A8.06c, unknown, len:578aa, some similarity eg. to BAH_STRHY, Q01109, acetylhydrolase, (299aa), fasta sco res, opt:259, E0:8.2e-17, (35.6% identity in 118 aa overl ap) [Schizosaccharomyces pombe]"
23129	ENU06923	ANI61C8833: 22-42 1833..609	22-42	810-829	LINAP		g4096660	376	104	1.00E-27			(U34807) extracellular lipase [Candida albicans]
23130	ENU06924	ANI61C6788: 22-49 3962..4460	22-49	451-478	LINAP		g2257504	171	90	1.00E-17	37	39	(AB004535) similar to S.pombe unknown protein : DDBJ ACC#
23131	ENU06925	ANI61C6269: 35-54 1..1100	35-54	810-829	LINAP		g2627268	71	36	0.35	28	57	D89156 [Schizosaccharomyces pombe] (U72998) ErpM [Borrelia burgdorferi]
23132	ENU06926	ANI61C1209: 23-47 7140..6797	23-47	428-455	LINAP		g3367791	149	65	4.00E-10	31	26	(AL031154) hypothetical protein [Schizosaccharomyces pombe]
23133	ENU06927	ANI61C9291: 48-67 1094..432	48-67	608-627	LINAP		g3334663	59	38	0.000003	31	21	(Y10491) putative cytochrome P450 [Glycine max]
23134	ENU06928	ANI61C6814: 67-86 1..341	67-86	299-320	LINAP		g3924609	91	34	0.38			(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
23135	ENU06929	ANI61C6274: 22-44 607..1048	22-44	420-439	LINAP		g2315475	59	52	0.000002			(AF016449) Similar to cytochrome P450 [Caenorhabditis elegans]
23136	ENU06930	ANI61C1259: 967..385			LINAP		g2133082	128	79	3.00E-14	38	29	regulatory protein MSR1 - yeast (Saccharomyces cerevisiae) ; (Z68329) unknown [Saccharomyces cerevisiae] ; (Z70202) unknown [Saccharomyces cerevisiae]
23137	ENU06931	ANI61C1098 22-49 1:5200..5803	22-49	559-580	LINAP		g2271503	156	45	0.0006	26	51	(AF009672) unknown [Acinetobacter sp. ADP1]
23138	ENU06932	ANI61C9265: 122-144 11512..10812	122-144	657-680	LINAP		g3650376	283	122	3.00E-27	37	24	(AL031740) dna ligase protein [Schizosaccharomyces pombe]
23139	ENU06933	ANI61C8847: 22-47 740..1109	22-47	452-479	LINAP		g1825739	123	39	0.016	24	59	(U88309) T23B3.5 gene product [Caenorhabditis elegans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23140	ENU06934	ANI61C5355: 105-124 1074..1826	105-124	648-666	LINAP		g2257531	155	68	4.00E-19	34	15	(AB004537) WEB1 protein [Schizosaccharomyces pombe] ; (AL022072) web1 homolog; protein transport protein; WD-repeat protein [Schizosaccharomyces pombe]
23141	ENU06935	ANI61C1208: 25-43 1785..2107	25-43	452-472	LINAP		g3123302	150	81	6.00E-15	31	24	hypothetical 75.1 KD protein C22E12.19 in chromosome I
23142	ENU06936	ANI61C6833: 22-48 3809..4322	22-48	433-452	LINAP		g1351664	310	78	9.00E-24	43	28	hypothetical 59.0 KD protein C30D11.14 in chromosome I; hypothetical protein SPAC30D11.14 - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe]
23143	ENU06937	ANI61C6224: 22-48 4438..6280	22-48	802-829	LINAP		g1168457	782	130	1.00E-29	29	15	Ankyrin ; ankyrin - mouse ; (M84756) ankyrin [Mus musculus]
23144	ENU06938	ANI61C2250: 315..754			LINAP		g1172906	165	60	7.00E-11	31	24	cell division cycle related-protein RES2/PCT1 ; cell cycle regulator res2 - fission yeast (Schizosaccharomyces pombe) ; RES2 protein - fission yeast (Schizosaccharomyces pombe) ; (D17761) cell cycle regulator Res2 [Schizosaccharomyces pombe] ; (Z54285) Res2 [Schizosaccharomyces pombe]
23145	ENU06939	ANI61C932:8 44-63 09..1	44-63	682-701	LINAP		g731024	711	259	2.00E-68	62	59	"branched-chain amino acid aminotransferase, mitochondrial precursor (BCAT) (TWT1 protein) ; TWT1 protein - yeast (Saccharomyces cerevisiae) ; (U00029) Bat1p: Branched-Chain Amino Acid Transaminase [Saccharomyces cerevisiae] ; (X78961) TWT1 [Saccharomyces cerevisiae] "
23146	ENU06940	ANI61C628:3 106-128 84..1	106-128	444-471	LINAP		g2117302	710	173	7.00E-43	49	48	(Z95620) putative ribose-phosphate pyrophosphokinase [Schizosaccharomyces pombe]
23147	ENU06941	ANI61C5335: 22-46 905..2028	22-46	799-818	LINAP		g1749560	134	41	0.00003			(D89176) unnamed protein product [Schizosaccharomyces pombe]

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23148	ENU06942	ANI61C1273: 1086..712	69-88	260-282	LINAP		g547991	62	57	0.000000	25	35	NA(+)/H(+) antiporter ; Na+/H+-exchanging protein - fission yeast (Schizosaccharomyces pombe) ; (Z11736) putative sodium/proton antiporter [Schizosaccharomyces pombe]
23149	ENU06943	ANI61C1100: 22-48	22-48	481-500	LINAP		g2497628	114	65	4.00E-10	38	62	microsomal SIGNAL peptidase 21.3 KD subunit ; probable membrane protein YLR066w - yeast (Saccharomyces cerevisiae) ; (X94607) L2186 [Saccharomyces cerevisiae] ; (Z73238) ORF YLR066w [Saccharomyces cerevisiae] ; (U92975) signal peptidase subunit [Saccharomyces cerevisiae] (Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]
23150	ENU06944	ANI61C2231: 637..1	22-40	502-521	LINAP		g2462679	56	58	0.000000	25	22	SCY1 protein ; SCY1 protein - yeast (Saccharomyces cerevisiae) ; (X97305) suppressor of GTPase mutant [Saccharomyces cerevisiae] ; (Z72605) ORF YGL083w [Saccharomyces cerevisiae]
23151	ENU06945	ANI61C932:1 682..3727	33-52	762-783	LINAP		g1711351	585	83	2.00E-15			hypothetical 147.4 KD protein C12C2.02C in chromosome II ; (Z54140) conserved hypothetical protein [Schizosaccharomyces pombe] ; (AJ223984) Ste20 protein [Schizosaccharomyces pombe]
23152	ENU06946	ANI61C6847: 1662..4157	23-42	767-793	LINAP		g1175418	1174	229	2.00E-59	43	21	50S ribosomal protein L1 ; (M94319) ribosomal protein L1 [Citrus greening disease-associated bacterium-like organism] ; ribosomal protein L1 [Citrus greening disease-associated bacterium]
23153	ENU06947	ANI61C6256: 4907..4259	28-47	590-609	LINAP		g548757	202	106	2.00E-22	33	83	vanillin dehydrogenase [Pseudomonas sp.]
23154	ENU06948	ANI61C1100 7:1209..2066	22-45	773-800	LINAP		g1946288	442	200	9.00E-51	46	55	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23155	ENU06949	ANI61C2241: 33-51 1732..719		808-827	LINAP		g131777	746	247	2.00E-77	53	25	DNA repair protein RAD13 ; excision repair protein - fission yeast (Schizosaccharomyces pombe) ; (X66795) excision repair protein [Schizosaccharomyces pombe] cytochrome C oxidase polypeptide IV precursor ; cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - yeast (Saccharomyces cerevisiae) ; (X01418) cytochrome c oxidase subunit IV precursor [Saccharomyces cerevisiae] ; (X91489) cytochrome C oxidase chain IV precursor [Saccharomyces cerevisiae] ; (Z72709) ORF YGL187c [Saccharomyces cerevisiae] exocyst complex component SEC8 ; SEC8 protein - yeast (Saccharomyces cerevisiae) ; (X64693) SEC8 [Saccharomyces cerevisiae] ; (Z49219) Sec8p [Saccharomyces cerevisiae] ; (Z71255) Sec8p [Saccharomyces cerevisiae]
23156	ENU06950	ANI61C9340: 30-57 1050..1515		446-473	LINAP		g117090	259	80	9.00E-25			
23157	ENU06951	ANI61C8861: 22-45 2192..2787		548-575	LINAP		g417762	227	114	5.00E-25	30	18	
23158	ENU06952	ANI61C1098 56-75 2:1..1262		780-799	LINAP		g4107287	474	83	6.00E-24			putative allantoate permease [Schizosaccharomyces pombe]
23159	ENU06953	ANI61C2241: 40-59 1676..2069		429-448	LINAP		g2606019	84	38	0.061			(AF030027) 71 [Equine herpesvirus 4]
23160	ENU06954	ANI61C1098 44-63 2:2486..3656		771-790	LINAP		g128340	262	120	1.00E-26	30	29	nitrogen assimilation transcription factor NIRA ; nitrate assimilation regulatory protein nirA - Emericella nidulans ; (M68900) NIRA protein [Emericella nidulans]
23161	ENU06955	ANI61C8867: 22-41 2737..2018		675-694	LINAP		g448109	160	82	6.00E-15	33	34	6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]
23162	ENU06956	ANI61C1230: 32-51 7214..8025		636-655	LINAP		g2132661	378	180	1.00E-44	42	45	probable membrane protein YLR020c - yeast (Saccharomyces cerevisiae) ; (Z73192) ORF YLR020c [Saccharomyces cerevisiae]

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23163	ENU06957	ANI61C6860: 31-50 1404..1	31-50	720-746	LINAP		g464912	1190	256	1.00E-68	47	19	helicase SGS1 (helicase TPS1) ; DNA helicase TPS1 - yeast (Saccharomyces cerevisiae) ; (L07870) bps. 390..881 = homology to E.coli recQ; bps. 414..430 = ATP binding site [Saccharomyces cerevisiae] ; (Z47815) Tps1p [Saccharomyces cerevisiae] ; (U22341) Sgs1p [Saccharomyces cerevisiae] (AF042799) suppressor of white apricot homolog 2 [Mus musculus] (AL031013) putative secreted protein [Streptomyces coelicolor] hypothetical 37.6 KD protein in GNTR-HTPG intergenic region ; (AB005554) see SWISS_PROT ACC#: P42106 [Bacillus subtilis] ; (Z99124) yxaG [Bacillus subtilis] (Z99113) polyketide synthase [Bacillus subtilis] cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisi] interleukin enhancer-binding factor 1 (cellular transcription factor ILF-1) ; (U58196) interleukin enhancer binding factor 1 [Homo sapiens] hypothetical 44.8 KD protein C57A10.01 in chromosome I
23164	ENU06958	ANI61C9827: 41-60 2990..4148	41-60	810-829	LINAP		g3941324	65	38	0.092			GAM1 gene [Saccharomyces cerevisiae]
23165	ENU06959	ANI61C9347: 33-54 1517..838	33-54	633-659	LINAP		g3288616	100	53	0.000001			probable membrane protein YDR109c - yeast (Saccharomyces cerevisiae) ; (Z48758) unknown [Saccharomyces cerevisiae]
23166	ENU06960	ANI61C6815: 22-48 3666..3211	22-48	448-475	LINAP		g1176967	105	42	0.000000	30	43	yeast (Saccharomyces cerevisiae) ; (D64006) Ap-4-A phosphorylase II [Synecocystis sp.]
23167	ENU06961	ANI61C9346: 1850..1301			LINAP		g2634103	157	80	1.00E-14	29	4	
23168	ENU06962	ANI61C2233: 22-46 2373..3739	22-46	767-790	LINAP		g1706177	322	109	3.00E-23	32	27	
23169	ENU06963	ANI61C8870: 22-42 2181..2534	22-42	455-479	LINAP		g3183529	60	64	6.00E-10			
23170	ENU06964	ANI61C6839: 22-43 6118..6445	22-43	378-398	LINAP		g3287948	152	82	2.00E-15	34	32	
23171	ENU06965	ANI61C6278: 41-60 4317..1706	41-60	781-800	LINAP		g228213	2404	265	4.00E-70	56	16	
23172	ENU06966	ANI61C2238: 29-54 1..1351	29-54	767-786	LINAP		g1077569	996	255	2.00E-67	47	39	
23173	ENU06967	ANI61C9335: 24-47 2550..2129	24-47	437-456	LINAP		g1001338	62	63	0.000000			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23174	ENU06968	ANI61C6798: 23-42 2622...3935	23-42	802-829	LINAP		g1708909	356	62	1.00E-19	27	56	malic acid transport protein (malate permease) ; C4-dicarboxylate transport protein mae1 - fission yeast (Schizosaccharomyces pombe) ; (U21002) malic acid transport protein [Schizosaccharomyces pombe] "hypothetical protein YCL010c - yeast (Saccharomyces cerevisiae) ; (X59720) YCL010c, len:146 [Saccharomyces cerevisiae]" (X89442) peptide synthetase [Metarhizium anisopliae] (Z64354) unknown [Schizosaccharomyces pombe] (Y15278) cytochrome P450 monooxygenase [Gibberella fujikuroi] alpha-amylase (EC 3.2.1.1) precursor - yeast (Lipomyces kononenkoae) (AL031179) hypothetical protein [Schizosaccharomyces pombe] (AL031825) rna binding protein - putative pre mna splicing factor [Schizosaccharomyces pombe] "ATP-dependent DNA helicase II, 86 KD subunit (lupus KU autoantigen protein P86) (86 KD subunit of KU antigen) (thyroid-lupus autoantigen) (TLAA) (CTC BOX binding factor 85 KD subunit) (CTCBF) (CTC85) (nuclear factor IV) (... ; Ku antigen 80K chain - human ; (J04977) Ku antigen [Homo sapiens] ; (M30938) Ku (p70/p80) subunit [Homo sapiens] " TRNA-splicing endonuclease positive effector ; SEN1 protein - yeast (Saccharomyces cerevisiae) ; (U20939) Sen1p [Saccharomyces cerevisiae] (AB023145) KIAA0928 protein [Homo sapiens]
23175	ENU06969	ANI61C1229: 50-69 9252..8767	50-69	460-479	LINAP		g2146829	173	91	5.00E-18	43	54	
23176	ENU06970	ANI61C9328: 28-47 3897..405	28-47	776-794	LINAP		g2342601	1390	166	1.00E-40	35	5	
23177	ENU06971	ANI61C6798: 22-44 9347..9688	22-44	453-479	LINAP		g4160354	125	69	1.00E-11	47	28	
23178	ENU06972	ANI61C2212: 5316..5983			LINAP		g3549891	170	75	7.00E-17	33	34	
23179	ENU06973	ANI61C9349: 24-51 1842..294	24-51	787-809	LINAP		g2144467	1068	159	1.00E-54	44	42	
23180	ENU06974	ANI61C6835: 158-179 7388..6866	158-179	476-499	LINAP		g3395590	193	90	1.00E-17	37	56	
23181	ENU06975	ANI61C6308: 48-67 570..1	48-67	527-549	LINAP		g3702642	398	98	7.00E-42	56	41	
23182	ENU06976	ANI61C1322: 22-42 407..1279	22-42	777-797	LINAP		g125731	162	75	1.00E-16	30	32	
23183	ENU06977	ANI61C2259: 36-55 1529..1856	36-55	442-467	LINAP		g3123282	98	56	0.000000	20	7	
23184	ENU06978	ANI61C9795: 22-49 9306..10624	22-49	804-829	LINAP		g4589488	54	75	9.00E-13	24	11	

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23185	ENU06979	ANI61C8832: 22-46 356..2018	22-46	795-822	LINAP		g3122656	1264	161	2.00E-61	57	50	amidophosphoribosyltransferase (glutamine phosphoribosylpyrophosphate amidotransferase) (ATASE) ; (U32992)
23186	ENU06980	ANI61C5401: 22-48 518..1	22-48	380-398	LINAP		g1438949	60	53	0.000001			glutamine phosphoribosylpyrophosphate amidotransferase [Saccharomyces kluyveri]
23187	ENU06981	ANI61C227:1 22-48 482..521	22-48	806-825	LINAP		g2764761	171	104	6.00E-22	30	5	(U61841) cutinase G-box binding protein [Fusarium solani f. sp. pisi] "(AJ223012) rifamycin polyketide synthase, type 1 [Amycolatopsis mediterranei] ; (AF040570) polyketide synthase [Amycolatopsis mediterranei] "
23188	ENU06982	ANI61C8882: 22-43 1005..224	22-43	736-761	LINAP		g2497111	304	123	2.00E-27	30	35	hypothetical 84.6 KD protein in GLO1-YPT7 intergenic region ; probable membrane protein YML002w - yeast (Saccharomyces cerevisiae)
23189	ENU06983	ANI61C5382: 22-45 3101..3714	22-45	476-495	LINAP		g2494239	241	100	3.00E-24	37	52	probable peroxisomal enoyl-CoA hydratase ; peroxisomal enoyl hydratase-like protein - rat ; (U08976)
23190	ENU06984	ANI61C2257: 22-43 1281..1736	22-43	434-453	LINAP		g4581525	170	75	4.00E-13	34	27	peroxisomal enoyl hydratase-like protein [Rattus norvegicus] (AL049559) putative short-chain dehydrogenase [Schizosaccharomyces pombe]
23191	ENU06985	ANI61C8894: 22-44 419..1567	22-44	794-817	LINAP		g1168817	418	143	6.00E-35	37	24	cell division control protein 7 ; protein kinase cdc7 - fission yeast (Schizosaccharomyces pombe) ; (X78799) cdc7 [Schizosaccharomyces pombe] ; (AL035537) cell division control protein 7
23192	ENU06986	ANI61C6882: 36-60 901..271	36-60	587-610	LINAP		g4507075	250	122	2.00E-27	40	17	[Schizosaccharomyces pombe] "SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 ; (AB010882) hSNF2H [Homo sapiens] "

Seq num	Seq id	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23193	ENU06987	ANI61C5397: 22-46	414-434	LINAP		g2499778	176	41	0.007			cell binding factor 2 precursor (antigen PEB4A) ; cell binding factor 2 - Campylobacter jejuni ; (X84703) cell binding factor 2 [Campylobacter jejuni]
23194	ENU06988	ANI61C1337: 24-43	566-585	LINAP		g3122986	160	110	1.00E-23	33	42	beta-TRCP (beta-transducin repeat-containing protein) (BTRCP) ; beta-transducin repeat-containing protein - African clawed frog ; (M98268) beta-TRCP [Xenopus laevis]
23195	ENU06989	ANI61C5418: 24-45	443-466	LINAP		g1788578	90	63	0.000000			"(AE000314) orf, hypothetical protein [Escherichia coli] "
23196	ENU06990	ANI61C1329: 34-53	810-829	LINAP		g2499839	331	94	2.00E-18			thyroid receptor interacting protein 12 (TRIP12) (K1AA0045) ; (D28476)
23197	ENU06991	ANI61C2215: 31-50	777-796	LINAP		g3183326	351	151	5.00E-36	31	31	K1AA0045 [Homo sapiens]
		2977..4211										hypothetical 93.2 KD TRP-ASP repeats containing protein C4F8.11 in chromosome I ; (Z98530) beta-transducin [Schizosaccharomyces pombe]
23198	ENU06992	ANI61C1330: 22-45	782-801	LINAP		g2656001	294	109	2.00E-23	35	31	(Z98977) hypothetical protein [Schizosaccharomyces pombe]
23199	ENU06993	ANI61C8878: 25-45	559-586	LINAP		g2132218	263	139	2.00E-32	42	32	hypothetical protein YPL169c - yeast (Saccharomyces cerevisiae) ; (Z73525) ORF YPL169c [Saccharomyces cerevisiae] ; (X96770) P2520 protein [Saccharomyces cerevisiae]
23200	ENU06994	ANI61C539:2 64-83	542-567	LINAP		g3915438	151	89	2.00E-17	31	62	hypothetical protein C10D6.08 in chromosome I ; (Z98951) hypothetical protein [Schizosaccharomyces pombe]
23201	ENU06995	ANI61C1360: 66-93	776-795	LINAP		g2244866	215	80	6.00E-23	35	13	(Z97337) hypothetical protein [Arabidopsis thaliana]
23202	ENU06996	ANI61C538:8 22-45	758-781	LINAP		g1354473	2931	180	2.00E-90	67	21	(U53189) Os-1p [Neurospora crassa]
23203	ENU06997	ANI61C9831: 24-43	446-465	LINAP		g2132165	413	60	3.00E-17	54	51	hypothetical protein YPL051w - yeast (Saccharomyces cerevisiae) ; (U39205) Lpe21p [Saccharomyces cerevisiae] ; (AF017142) ADP-ribosylation factor-like protein 1 [Saccharomyces cerevisiae]

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23204	ENU06998	ANI61C9831: 24-43 7260..8033	22-47	646-673	LINAP	g3687829	182	52	104	6.00E-22	33	48	(AF069291) hT41 [Homo sapiens] ; (AF061326) T41p [Homo sapiens] (AB010636) SADH [Candida parapsilosis] (AL049474) hypothetical protein [Schizosaccharomyces pombe] (AJ011923) cell cycle checkpoint protein [Mus musculus] hypothetical 15.0 KD protein in SCY1-DBP3 intergenic region ; hypothetical protein YGL080w - yeast (Saccharomyces cerevisiae) ; (Z72602) ORF YGL080w [Saccharomyces cerevisiae] (AL009204) FAD-dependent oxidoreductase [Streptomyces coelicolor] (AL035536) phosphate-phosphoenolpyruvate translocator precu rsor. [Schizosaccharomyces pombe]
23205	ENU06999	ANI61C9321: 22-47 1925..2483	22-47	512-538	LINAP	g2815409	70	52	104	0.000003	35	40	
23206	ENU07000	ANI61C2281: 46-65 998..677	46-65	457-477	LINAP	g4538665	116	76	104	2.00E-13	35	27	
23207	ENU07001	ANI61C9878: 23-45 3322..4720	23-45	806-829	LINAP	g3758878	184	75	104	9.00E-13			
23208	ENU07002	ANI61C229:1 22-45 392..1801	22-45	455-479	LINAP	g1723875	233	96	104	2.00E-19	49	89	
23209	ENU07003	ANI61C9305: 54-75 8088..8641	54-75	510-533	LINAP	g2661710	129	48	104	0.000009	27	41	
23210	ENU07004	ANI61C6867: 22-48 2887..1896	22-48	791-815	LINAP	g4455784	612	249	104	3.00E-65	50	60	
23211	ENU07005	ANI61C6291: 25-52 3547..4908	25-52	810-829	LINAP	g3879422	220	84	104	1.00E-15	37	32	(Z78200) predicted using Genefinder; Weak similarity to elongation factors; cDNA EST EMBL:D32732 comes from this gene; cDNA EST EMBL:D32745 comes from this gene; cDNA EST EMBL:D33685 comes from this gene; cDNA EST EMBL:D34113 c...
23212	ENU07006	ANI61C9885: 22-45 763..226	22-45	488-514	LINAP	g1175364	111	55	104	0.000000	34	57	hypothetical 28.0 KD protein C13C5.04 in chromosome I ; hypothetical protein SPAC13C5.04 - fission yeast (Schizosaccharomyces pombe) ; (Z50112) hypothetical protein [Schizosaccharomyces pombe] (AL049559) protein kinase cck1 [Schizosaccharomyces pombe]
23213	ENU07007	ANI61C9366: 141-165 694..1	141-165	474-496	LINAP	g4581521	385	114	104	6.00E-25	43	16	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23214	ENU07008	ANI61C6898: 25-45 269..1113	25-45	738-757	LINAP		g136230	283	138	4.00E-32	38	18	"potassium transport protein, high-affinity ; potassium transport protein TRK1, high-affinity - yeast (Saccharomyces cerevisiae) (strain Saccharomyces uvarum) ; (M57508) high-affinity K+ transporter [Saccharomyces uvarum] " (AB014569) KIAA0669 protein [Homo sapiens] (D89340) dipeptidyl peptidase III [Rattus norvegicus] hypothetical 54.1 KD protein in TPS3-IPP2 intergenic region ; hypothetical protein YMR265c - yeast (Saccharomyces cerevisiae) ; (Z49260) unknown [Saccharomyces cerevisiae] (AF052606) chitin synthase 2 [Exophiala dermatitidis] hypothetical 65.9 KD protein C31A2.12 in chromosome I ; hypothetical protein SPAC31A2.12 - fission yeast (Schizosaccharomyces pombe) ; (Z50113) unknown [Schizosaccharomyces pombe] (U78318) chitinase [Entamoeba dispar] (AE000888) malate dehydrogenase [Methanobacterium thermoautotrophicum] (AL022598) hypothetical protein [Schizosaccharomyces pombe] (AF009921) I100 [Rattus norvegicus] enoyl-[acyl-carrier-protein] reductase (NADH) (NADH-dependent enoyl-ACP reductase) (AJ011965) oxidoreductase [Claviceps purpurea]
23215	ENU07009	ANI61C9885: 108-134 1609..1943	108-134	458-479	LINAP		g3327152	79	32	2.7			
23216	ENU07010	ANI61C89:88 7..1411	55-74	481-504	LINAP		g2832906	78	68	5.00E-11	35	18	
23217	ENU07011	ANI61C137:2 484..2939	22-46	450-477	LINAP		g2497213	70	54	0.000000	32	27	
23218	ENU07012	ANI61C9887: 27-46 4536..4956	27-46	375-398	LINAP		g3548904	270	129	1.00E-29	40	17	
23219	ENU07013	ANI61C9344: 25-44 1183..3128	25-44	761-780	LINAP		g1175406	479	45	0.0007			
23220	ENU07014	ANI61C6320: 53-72 2654..1308	53-72	792-811	LINAP		g1685360	221	48	6.00E-22			
23221	ENU07015	ANI61C1396: 23-42 1125..1834	23-42	578-597	LINAP		g2622314	390	169	2.00E-41	38	69	
23222	ENU07016	ANI61C2287: 22-49 5829..4008	22-49	805-829	LINAP		g3080513	254	75	9.00E-13	26	25	
23223	ENU07017	ANI61C1403: 92-111 1512..1	92-111	723-749	LINAP		g2653779	572	172	2.00E-42	37	37	
23224	ENU07018	ANI61C8897: 36-63 1180..874	36-63	454-479	LINAP		g1169593	77	59	0.000000			
23225	ENU07019	ANI61C9319: 52-71 7975..8612	52-71	582-601	LINAP		g4499843	134	54	0.000001	37	24	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23226	ENU07020	ANI61C1431: 55-75 1307..1908	55-75	446-465	LINAP		g2879805	87	46	0.0002			(AL021813) hypothetical protein [Schizosaccharomyces pombe]
23227	ENU07021	ANI61C8917: 22-43 830..1371	22-43	497-521	LINAP		g2330876	275	123	6.00E-28	38	33	(Z98603) hypothetical protein [Schizosaccharomyces pombe]
23228	ENU07022	ANI61C9370: 27-49 2680..3096	27-49	411-430	LINAP		g1352686	42	51	0.000006			"protein phosphatase 2C (PP2C) ; phosphoprotein phosphatase (EC 3.1.3.16) 2c, membrane-bound - Paramecium tetraurelia (SGC5) ; (Z36985) PP2C [Paramecium tetraurelia]"
23229	ENU07023	ANI61C2346: 65-84 1..1323	65-84	805-829	LINAP		g3885836	508	82	5.00E-20	28	42	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
23230	ENU07024	ANI61C1412: 22-42 2665..1680	22-42	789-807	LINAP		g117135	584	137	4.00E-60	47	57	cytochrome C oxidase assembly protein COX10 precursor ; COX10 protein precursor - yeast (Saccharomyces cerevisiae) ; (M55566) COX10 [Saccharomyces cerevisiae] ; (Z73528) ORF YPL172c [Saccharomyces cerevisiae]
23231	ENU07025	ANI61C6288: 35-54 2142..1088	35-54	783-802	LINAP		g2257512	577	46	0.0002			(AB004535) hypothetical protein YPR112c [Schizosaccharomyces pombe]
23232	ENU07026	ANI61C6888: 29-49 1..2334	29-49	810-829	LINAP		g1546072	735	126	2.00E-28	29	11	(U68040) polyketide synthase [Cochliobolus heterostrophus]
23233	ENU07027	ANI61C8905: 28-48 1938..1	28-48	765-784	LINAP		g128340	158	46	0.0003			nitrogen assimilation transcription factor NIRA ; nitrate assimilation regulatory protein nirA - Emericella nidulans ; (M68900) NIRA protein [Emericella nidulans]
23234	ENU07028	ANI61C1412: 22-49 3441..3876	22-49	405-425	LINAP		g3165391	151	78	4.00E-14	34	58	(AB014471) compared with Cricetulus griseus SL15 mRNA; GenBank Accession Number U55387 [Mus musculus]
23235	ENU07029	ANI61C8909: 22-42 530..1462	22-42	802-829	LINAP		g539247	840	121	5.00E-38	43	12	SPO14 protein - yeast (Saccharomyces cerevisiae) ; (Z28256) ORF YKR031c [Saccharomyces cerevisiae]
23236	ENU07030	ANI61C6288: 23-42 6978..4884	23-42	805-829	LINAP		g388367	1750	220	7.00E-57	40	38	[Saccharomyces cerevisiae] (L19875) Dur3 [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23237	ENU07031	ANI61C8926: 1015..1	22-47	772-792	LINAP		g122798	85	65	7.00E-10			hemocyanin D chain ; hemocyanin chain d - American tarantula (Eurypelma californica)
23238	ENU07032	ANI61C1439: 650..1414	26-53	716-735	LINAP		g118571	164	118	6.00E-26			granaticin polyketide synthase putative ketoacyl reductase 1 (ORF5) ; granaticin-producing polyketide synthase chain 5 - Streptomyces violaceoruber ; (X16144) ketoacyl reductase (AA 1-273) [Streptomyces violaceoruber] ; (X16300) ORF 5 (AA 1-272) [Streptomyces violaceoruber] ; (AJ011500) polyketide ketoreductase [Streptomyces violaceoruber]
23239	ENU07033	ANI61C8916: 282..845	24-43	520-539	LINAP		g266545	98	31	5.3			modifier 3 protein (M33) ; modifier-3 protein - mouse ; (X62537) modifier 3 (M33) [Mus musculus]
23240	ENU07034	ANI61C3321: 316..1	102-124	459-478	LINAP		g4530066	73	37	0.08	29	30	(AF060544) androgen receptor associated protein 54 [Homo sapiens]
23241	ENU07035	ANI61C9931: 1378..1	24-48	723-749	LINAP		g3560189	372	135	3.00E-31	37	35	(AL031518) putative phospholipase [Schizosaccharomyces pombe]
23242	ENU07036	ANI61C322: 92..1337			LINAP		g626598	199	75	4.00E-19	40	42	hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) ; (U10400) Ysc84p [Saccharomyces cerevisiae]
23243	ENU07037	ANI61C6894: 1533..2570	22-48	789-815	LINAP		g3738165	310	85	5.00E-23	34	34	(AL031856) hypothetical protein [Schizosaccharomyces pombe]
23244	ENU07038	ANI61C2329: 5487..5174			LINAP		g2498477	219	74	4.00E-13	49	7	IKI3 protein ; probable membrane protein YLR384c - yeast (Saccharomyces cerevisiae) ; (U19104) Iki3p [Saccharomyces cerevisiae] ; (D87841) Iki3p [Saccharomyces cerevisiae]
23245	ENU07039	ANI61C6906: 1..797	111-131	744-764	LINAP		g3334399	119	50	0.00002	27	28	ubiquitin carboxyl-terminal hydrolase 16 (ubiquitin thiolesterase 16) (ubiquitin-specific processing protease 16) (deubiquitinating enzyme 16) ; probable membrane protein YPL072w - yeast (Saccharomyces cerevisiae) ; (U41849) Lpf12p [Saccharomyces cerevisiae]

Seq num	Seq id	Primer	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23246	ENU07040	Contig source ANI61C9403: 22-41 1344..1768	5 pos 22-41	455-479 LINAP		g418404	335	159	1.00E-38	55	29	guanosine-diphosphatase (GDPASE) ; guanosine-diphosphatase (EC 3.6.1.42) - yeast (Saccharomyces cerevisiae) ; [Saccharomyces cerevisiae] (L19560) guanosine diphosphatase [Saccharomyces cerevisiae] ; (U18779) Gdalp: guanosine-diphosphatase of Golgi membrane [Saccharomyces cerevisiae]
23247	ENU07041	ANI61C3333: 22-47 3433..4136	576-595	LINAP		g1685364	233	130	1.00E-29	30	45	(U78320) chitinase [Entamoeba invadens]
23248	ENU07042	ANI61C2366: 29-48 1150..1	725-749	LINAP		g3282044	1664	510	e-144	86	19	(Y13967) alpha-aminoadipate reductase large subunit [Penicillium chrysogenum]
23249	ENU07043	ANI61C691:8 53-71 84..564	410-430	LINAP		g544446	43	47	0.00007			membrane transporter D1 ; membrane transport protein (clone D1.SH) - Leishmania donovani ; (M85072) D1 transporter [Leishmania donovani] ; myo-inositol/TH symporter [Leishmania donovani]
23250	ENU07044	ANI61C9381: 3456..3877		LINAP		g2706465	157	92	3.00E-18	34	19	(AL021046) positive regulator of camp dependent protein kin ase [Schizosaccharomyces pombe]
23251	ENU07045	ANI61C2373: 38-59 815..203	567-586	LINAP		g4263825	350	98	3.00E-35	42	16	(AC006067) hypothetical protein [Arabidopsis thaliana]
23252	ENU07046	ANI61C1454: 23-42 668..1	566-588	LINAP		g2415403	232	109	1.00E-23	32	50	(AF015775) acetylornitine deacetylase [Bacillus subtilis] ; (Z99114) acetylornitine deacetylase [Bacillus subtilis]
23253	ENU07047	ANI61C6226: 69-88 2377..306	805-823	LINAP		g1084543	546	230	1.00E-59	39	12	FAB1 protein - yeast (Saccharomyces cerevisiae) ; (D50617) FAB1 protein [Saccharomyces cerevisiae]
23254	ENU07048	ANI61C992:7 27-54 69..1308	488-507	LINAP		g1582765	126	67	8.00E-11	32	29	YFW1 gene [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23255	ENU07049	ANI61C2379: 835..1525			LINAP		g417780	145	50	3.00E-11	35	29	meiosis induction protein kinase IME2/SME1 ; probable protein kinase SME1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (X53262) protein kinase homologue [Saccharomyces cerevisiae] ; (X85021) SME1 [Saccharomyces cerevisiae] ; (Z49381) ORF YJL106w [Saccharomyces cerevisiae] (AL023592) rna binding protein [Schizosaccharomyces pombe] (Y12709) tea1p [Schizosaccharomyces pombe] ; (AL031579) cell polarity protein [Schizosaccharomyces pombe] hypothetical 98.4 KD protein C19G10.07 in chromosome I ; (Z69909) multiple BRCT domain containing protein [Schizosaccharomyces pombe] hypothetical 130.0 KD protein in SNF6-SPO11 intergenic region ; hypothetical protein YHL023c - yeast (Saccharomyces cerevisiae) ; (U11582) No definition line found [Saccharomyces cerevisiae] hypothetical protein YOR049c - yeast (Saccharomyces cerevisiae) ; (Z74957) ORF YOR049c [Saccharomyces cerevisiae] histone H1.1 ; histone H1.1 - Arabidopsis thaliana ; (X62458) Histone H1 [Arabidopsis thaliana] transaldolase ; (L47327) transaldolase [Anabaena variabilis] (Z99531) ubiquitin system protein [Schizosaccharomyces pombe]
23256	ENU07050	ANI61C6348: 23-43 1090..1		784-803	LINAP		g3136059	282	113	2.00E-24	26	21	
23257	ENU07051	ANI61C6908: 28-55 1934..721		803-829	LINAP		g2065436	609	192	3.00E-48	38	21	
23258	ENU07052	ANI61C9404: 22-42 1286..1		717-741	LINAP		g1723501	322	122	4.00E-27	28	29	
23259	ENU07053	ANI61C9946: 121-140 1..1277		804-824	LINAP		g731604	169	71	3.00E-17			
23260	ENU07054	ANI61C1405: 22-41 5270..6129		805-826	LINAP		g2132036	215	78	5.00E-17	33	68	
23261	ENU07055	ANI61C6251: 102-124 358..1		452-479	LINAP		g121902	86	33	1.2			
23262	ENU07056	ANI61C6955: 22-41 540..1014		374-392	LINAP		g1729831	114	64	5.00E-10	33	45	
23263	ENU07057	ANI61C9408: 72-91 2559..1452		806-829	LINAP		g2440180	412	126	2.00E-28	31	8	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23264	ENU07058	ANI61C3372: 107-127 1..343	107-127	299-321	LINAP		g730745	181	99	1.00E-20	43	9	"osomolarity two-component system protein SLN1 ; SLN1 protein - yeast (Saccharomyces cerevisiae) ; (U01835) Sln1p [Saccharomyces cerevisiae] ; (Z38059) sln1, len: 1220, CAl: 0.13, similar to two component regulatory proteins [Saccharomyces cerevisiae] " hypothetical 37.9 KD protein in STE12-NAM8 intergenic region ; hypothetical protein YHR085w - yeast (Saccharomyces cerevisiae) ; (U10556) Yhr085wp [Saccharomyces cerevisiae] STB2 protein ; SIN3 protein-binding protein STB2 - yeast (Saccharomyces cerevisiae) ; (Z49703) unknown [Saccharomyces cerevisiae] ; (U33438) Stb2p [Saccharomyces cerevisiae] (AL035521) hypothetical protein [Arabidopsis thaliana] (AL034352) hypothetical protein [Schizosaccharomyces pombe] (Z98849) putative dna repair helicase [Schizosaccharomyces pombe] hypothetical 71.9 KD protein in PM140-PAC2 intergenic region ; hypothetical protein YER005w - yeast (Saccharomyces cerevisiae) ; (U18778) Yer005wp [Saccharomyces cerevisiae] (Z98849) putative centromere protein [Schizosaccharomyces pombe] (AB004539) hypothetical 229.9KD protein in NUC1-PRP21 intergenic region [Schizosaccharomyces pombe] (AL034353) probable metabolite transport protein [Schizosaccharomyces pombe]
23265	ENU07059	ANI61C2389: 104-130 436..1	104-130	391-417	LINAP		g731682	143	56	0.000000	26	49	
23266	ENU07060	ANI61C1400: 58-77 7790..8761	58-77	786-805	LINAP		g1711559	258	125	5.00E-28	30	33	
23267	ENU07061	ANI61C3370: 22-49 472..1840	22-49	806-828	LINAP		g4455171	478	160	1.00E-38	36	26	
23268	ENU07062	ANI61C1472: 69-87 2044..1716	69-87	416-435	LINAP		g3925763	229	48	0.000000	36	51	
23269	ENU07063	ANI61C6341: 39-66 1805..2935	39-66	801-821	LINAP		g2370478	1370	354	e-106	74	34	
23270	ENU07064	ANI61C6930: 134-157 4924..4444	134-157	416-435	LINAP		g731435	216	74	3.00E-21	36	22	
23271	ENU07065	ANI61C9421: 65-86 390..1	65-86	457-479	LINAP		g2370479	227	111	2.00E-24	35	25	
23272	ENU07066	ANI61C1483: 33-52 850..202	33-52	579-606	LINAP		g2257560	173	93	1.00E-18	30	11	
23273	ENU07067	ANI61C6334: 22-44 883..2416	22-44	805-824	LINAP		g3925778	835	78	2.00E-29	43	46	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23274	ENU07068	ANI61C6965: 22-46 508..1471	803-829	803-829	LINAP		g1730664	698	152	1.00E-44	40	72	SMM1 protein ; hypothetical protein YNR015w - yeast (Saccharomyces cerevisiae) ; (Z71630) ORF YNR015w [Saccharomyces cerevisiae] ; (X91816) SMM1 protein [Saccharomyces cerevisiae]
23275	ENU07069	ANI61C9916: 22-44 324..1953	802-829	802-829	LINAP		g1706177	1207	183	1.00E-45	43	27	cutinase transcription factor 1 beta ; (U51672) cutinase transcription factor 1 [Fusarium solani f. sp. pisi]
23276	ENU07070	ANI61C1467: 102-124 1..392	349-368	349-368	LINAP		g3970880	193	101	2.00E-21	45	33	(AB015724) nuclear receptor binding factor-1 [Rattus norvegicus]
23277	ENU07071	ANI61C6366: 41-63 43..918	790-811	790-811	LINAP		g2330868	656	231	5.00E-60	58	88	(Z98603) putative proteosome component [Schizosaccharomyces pombe]
23278	ENU07072	ANI61C6991: 34-53 1151..781	312-330	312-330	LINAP		g4499843	204	45	0.0002	42	25	(AJ011965) oxidoreductase [Claviceps purpurea]
23279	ENU07073	ANI61C9395: 28-47 4754..5371	573-597	573-597	LINAP		g2780359	467	202	2.00E-51	52	34	(AB010110) ascorbate oxidase [Acremonium sp.]
23280	ENU07074	ANI61C237:1 54-78 822..2409	525-544	525-544	LINAP		g2634103	208	99	2.00E-20	31	4	(Z99113) polyketide synthase [Bacillus subtilis]
23281	ENU07075	ANI61C9452: 106-133 1..566	522-541	522-541	LINAP		g4502497	158	106	1.00E-22	33	61	chromosome 22 open reading frame 1 ; (U84894) 239AB [Homo sapiens]
23282	ENU07076	ANI61C6338: 22-44 2420..1309	800-819	800-819	LINAP		g2648929	102	38	0.000000			(AE000990) aspartate aminotransferase (aspB-3) [Archaeoglobus fulgidus]
23283	ENU07077	ANI61C146:2 36-55 232..745	805-829	805-829	LINAP		g3650387	570	121	7.00E-27	32	16	(AL031743) conserved hypothetical protein [Schizosaccharomyces pombe]
23284	ENU07078	ANI61C3374: 22-46 1098..2512	772-791	772-791	LINAP		g1703456	758	188	4.00E-47	48	24	Cation-transporting ATPase PAT1 ; PAT1 protein - slime mold (Dictyostelium discoideum) ; (X89369) PAT1 protein [Dictyostelium discoideum]
23285	ENU07079	ANI61C7547: 22-44 1306..1	761-780	761-780	LINAP		g3337389	1305	380	e-105	67	23	(AC004682) pre-mRNA splicing factor (PRP16)(KIAA0224) [Homo sapiens]
23286	ENU07080	ANI61C9916: 22-41 4011..5218	808-829	808-829	LINAP		g461830	575	104	8.00E-22	39	33	"carboxypeptidase S1 ; carboxypeptidase S1 - Penicillium janthinellum ; carboxypeptidase S1, CPD-S1 [Penicillium janthinellum, Peptide, 423 aa] ; carboxypeptidase S1 [Penicillium janthinellum] "

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23287	ENU07081	ANI61C3345: 1879..983	22-44	808-827	LINAP		g3319757	99	45	0.0007	24	27	(AL031035) putative ATP /GTP-binding protein [Streptomyces coelicolor]
23288	ENU07082	ANI61C6996: 22-46	456-483		LINAP		g3978134	312	64	7.00E-30	55	13	(U65409) Sla2p [Yarrowia lipolytica]
23289	ENU07083	ANI61C3379: 22-44	372-399		LINAP		g3925755	225	106	1.00E-22	40	30	(AL034352) putative phosphodiesterase-nucleotide pyrophosphatase precursor [Schizosaccharomyces pombe]
23290	ENU07084	ANI61C239:1..917			LINAP		g3219911	762	250	7.00E-66	54	32	putative kinesin-like protein C2F12.13 ; (Z97211) kinesin-like protein [Schizosaccharomyces pombe]
23291	ENU07085	ANI61C6990: 44-63	554-579		LINAP		g1352938	294	127	9.00E-29	37	60	hypothetical 39.7 KD protein in HOM6-PMT4 intergenic region ; hypothetical protein YJR142w - yeast (Saccharomyces cerevisiae) ; (Z49642) ORF YJR142w [Saccharomyces cerevisiae]
23292	ENU07086	ANI61C7552: 23-48	693-715		LINAP		g2648302	334	171	4.00E-42	50	83	"(AE000952) 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (hpcE-2) [Archaeoglobus fulgidus] "
23293	ENU07087	ANI61C9970: 22-48	465-492		LINAP		g1077378	114	44	0.0007			probable membrane protein YLR222c - yeast (Saccharomyces cerevisiae) ; (U19027) Ylr222cp [Saccharomyces cerevisiae]
23294	ENU07088	ANI61C3355: 1..522			LINAP		g2131504	282	106	1.00E-22	40	27	hypothetical protein YDR456w - yeast (Saccharomyces cerevisiae) ; (U33007) Ydr456wp; CAI: 0.16 [Saccharomyces cerevisiae]
23295	ENU07089	ANI61C2400: 53-72	803-822		LINAP		g2911284	478	90	3.00E-33	47	56	(U97681) putative splicing factor [Schizosaccharomyces pombe] ; (AL035675) putative splicing factor. [Schizosaccharomyces pombe]
23296	ENU07090	ANI61C6338: 40-60	796-815		LINAP		g2330697	240	88	4.00E-23			(Z98529) mating and morphogenesis protein Scd1p. [Schizosaccharomyces pombe]

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23297	ENU07091	ANI61C1504: 27-45 508..1	27-45	382-404	LINAP		g1174862	210	67	3.00E-21	35	33	putative ubiquitin carboxyl-terminal hydrolase C13A11.04C (ubiquitin thiolesterase) (ubiquitin-specific processing protease) (deubiquitinating enzyme) ; (Z54096) unknown [Schizosaccharomyces pombe]
23298	ENU07092	ANI61C6368: 22-49 3857..3370	22-49	287-306	LINAP		g2245021	125	82	3.00E-15	30	57	(Z97341) heat shock protein 110 homolog [Arabidopsis thaliana]
23299	ENU07093	ANI61C3343: 22-49 3736..2779	22-49	807-829	LINAP		g2147899	609	132	2.00E-30	40	47	phosphate transporter - Glomus versiforme ; (U38650) phosphate transporter [Glomus versiforme] ; phosphate transporter [Glomus versiforme]
23300	ENU07094	ANI61C6335: 66-85 3430..4017	66-85	519-538	LINAP		g725498	72	36	0.29			(U14651) protein V1 precursor [Human adenovirus type 40]
23301	ENU07095	ANI61C7006: 59-78 594..1277	59-78	556-575	LINAP		g3258637	82	71	1.00E-11			(AF041050) 4-coumarate:CoA ligase [Populus tremuloides]
23302	ENU07096	ANI61C6335: 163-182 7599..8160	163-182	384-403	LINAP		g2132853	93	48	0.00006	40	52	probable membrane protein YOL146w - yeast (Saccharomyces cerevisiae) ; (Z48239) orf6 [Saccharomyces cerevisiae] ; (Z74888) ORF YOL146w [Saccharomyces cerevisiae]
23303	ENU07097	ANI61C7575: 66-86 419..1	66-86	434-453	LINAP		g3114719	131	46	2.00E-12	34	9	(Z68906) ATP-binding multidrug cassette transporter [Botryotinia fuckeliana]
23304	ENU07098	ANI61C9442: 22-49 4191..3548	22-49	602-623	LINAP		g2827571	149	63	4.00E-10	30	54	(AL021646) hypothetical protein Rv3161c [Mycobacterium tuberculosis]
23305	ENU07099	ANI61C3385: 1126..1478			LINAP		g2135769	61	44	0.000000	30	10	"multidrug resistance protein, canalicular - human ; (X96395) [Homo sapiens] "
23306	ENU07100	ANI61C2418: 1..3138			LINAP		g3136094	5014	415	e-135	96	23	(AF032987) spindle assembly checkpoint protein SLDA [Emmericella nidulans]

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23307	ENU07101	ANI61C1519: 1..384	102-127	339-363	LINAP		g3874095	126	57	0.000000			(Z49908) cDNA EST EMBL:D67930 comes from this gene; cDNA EST EMBL:D27476 comes from this gene; cDNA EST EMBL:D27475 comes from this gene; cDNA EST yk317d5.5 comes from this gene; cDNA EST yk443d4.5 comes from this gene; cDNA ES...; (Z81573) cDNA EST EMBL:D67930 comes from this gene; cDNA EST EMBL:D27476 comes from this gene; cDNA EST EMBL:D27475 comes from this gene; cDNA EST yk317d5.5 comes from this gene; cDNA EST yk443d4.5 comes from this gene; cDNA ES...; (Z99268) cDNA EST EMBL:D67930 comes from this gene; cDNA EST EMBL:D27476 comes from this gene; cDNA EST EMBL:D27475 comes from this gene; cDNA EST yk317d5.5 comes from this gene; cDNA EST yk443d4.5 comes from this gene; cDNA EST yk443d4.5 comes from this gene; cDNA ES... cDNA ES... probable membrane protein YPR157w - yeast (Saccharomyces cerevisiae); (U28371) P9584.4 gene product [Saccharomyces cerevisiae] neutrophil cytosolic factor 2; p67phox; 67K neutrophil oxidase factor - human; (M32011) neutrophil oxidase factor [Homo sapiens] elongation factor 1-gamma (EF-1-gamma); translation elongation factor eEF-1 gamma chain - brine shrimp; (M28020) elongation factor 1-gamma [Artemia sp.] (Z99568) putative regulatory protein; zinc finger [Schizosaccharomyces pombe]
23308	ENU07102	ANI61C6992: 45-72 412..1	45-72	457-479	LINAP		g2133035	345	113	3.00E-29	48	30	
23309	ENU07103	ANI61C7532: 68-94 1..595	68-94	550-572	LINAP		g4557787	172	74	3.00E-19	31	35	
23310	ENU07104	ANI61C9963: 22-48 920..596	22-48	457-479	LINAP		g119164	149	54	0.000000	44	17	
23311	ENU07105	ANI61C3351: 22-42 6114..7195	22-42	785-809	LINAP		g2462679	110	75	9.00E-13	24	29	

Seq num	Seq id	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23312	ENU07106	ANI61C2433: 22-43	332-359	LINAP		g396376	247	119	1.00E-26	38	18	(U00006) glycerol-3-phosphate acyltransferase [Escherichia coli]
23313	ENU07107	ANI61C1524: 22-49	807-827	LINAP		g3218397	466	111	6.00E-24	38	34	(AL023860) hypothetical protein [Schizosaccharomyces pombe]
23314	ENU07108	ANI61C7026: 65..750		LINAP		g2660670	174	90	1.00E-17	30	23	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
23315	ENU07109	ANI61C7532: 38-57	453-479	LINAP		g1717966	88	46	0.0001	23	40	UFE1 protein ; UFE1 protein - yeast (Saccharomyces cerevisiae) ; (L15081)
23316	ENU07110	ANI61C9485: 42-60	487-511	LINAP		g2500938	314	74	2.00E-26	44	28	UFE1 gene product [Saccharomyces cerevisiae] ; (U53416) Ufe1p [Saccharomyces cerevisiae] ; (Z74983) ORF YOR075w [Saccharomyces cerevisiae] ; (Z70678) YOR29-26 [Saccharomyces cerevisiae]
23317	ENU07111	ANI61C339:1 22-43	607-629	LINAP		g3153821	20	41	0.006			myo-inositol transporter 1 ; (X98622) myo-inositol transporter [Schizosaccharomyces pombe]
23318	ENU07112	ANI61C2444: 22-48	430-457	LINAP		g1805251	152	85	3.00E-16	32	28	(AF062655) plenty-of-prolines-101; POP101; SH3-philo-protein [Mus musculus]
23319	ENU07113	ANI61C6363: 29-56	747-774	LINAP		g2388995	350	61	0.000000			(U58946) transposase [Aspergillus awamori]
23320	ENU07114	ANI61C9995: 39-58	717-741	LINAP		g4104400	130	38	0.11			(Z98981) hypothetical protein [Schizosaccharomyces pombe]
23321	ENU07115	ANI61C244:2 55-79	587-606	LINAP		g4200325	160	76	3.00E-13			(AF035401) exocellobiohydrolase precursor [Piromyces rhizinflata]
23322	ENU07116	ANI61C1494: 4073..4386		LINAP		g562121	106	62	0.000000	39	16	(Z98885) dJ52217.2 (Peregrin (BR140) like protein) [Homo sapiens]
23323	ENU07117	ANI61C6387: 71-90	457-476	LINAP		g3288594	198	74	3.00E-18	44	11	(U16137) Mvp1p [Saccharomyces cerevisiae]
23324	ENU07118	ANI61C1547: 22-47	447-466	LINAP		g1175451	131	80	1.00E-14	36	8	(AJ006340) 26S proteasome subunit p112 [Rattus norvegicus]
												hypothetical protein C22F3.14C in chromosome I ; hypothetical protein SPAC22F3.14c - fission yeast (Schizosaccharomyces pombe) ; (Z54285) unknown [Schizosaccharomyces pombe]

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23325	ENU07119	ANI61C7576: 1737..2047			LINAP		g1078614	212	96	3.00E-20	47	21	stearoyl-CoA desaturase (EC 1.14.99.5) - <i>Ajellomyces capsulata</i> ; (X85962) delta-9 fatty acid desaturase [<i>Ajellomyces capsulatus</i>] (AB010438) organic-cation transporter like 3 [<i>Homo sapiens</i>] putative tartrate transporter ; (U32375) membrane protein [<i>Agrobacterium vitis</i>] (AL023592) acetamidase [<i>Schizosaccharomyces pombe</i>] (AL023776) hypothetical protein [<i>Schizosaccharomyces pombe</i>] (AF017646) TFIIF subunit p47 [<i>Schizosaccharomyces pombe</i>] ; (AL031525) tflh subunit p47. [<i>Schizosaccharomyces pombe</i>] suppressor protein SEF1 ; (U92898) suppressor protein [<i>Kluyveromyces lactis</i>] (AF027868) YocH [<i>Bacillus subtilis</i>] ; (Z99114) similar to cell wall-binding protein [<i>Bacillus subtilis</i>] melanin biosynthetic polyketide synthase PKS1 - <i>Colletotrichum lagenarium</i> ; (D83643) polyketide synthase [<i>Colletotrichum lagenarium</i>] (Z99532) putative integral membrane protein [<i>Schizosaccharomyces pombe</i>] (AL023589) membrane transporter [<i>Schizosaccharomyces pombe</i>] (M36482) SNF5 protein [<i>Saccharomyces cerevisiae</i>]
23326	ENU07120	ANI61C339:2 41-59 465..2107		456-479	LINAP		g4586315	104	57	0.000000	28	29	
23327	ENU07121	ANI61C9972: 22-43 1208..2292		790-809	LINAP		g4033481	224	110	1.00E-23	33	53	
23328	ENU07122	ANI61C7593: 27-46 972..357		379-397	LINAP		g3136052	235	62	0.000000	40	34	
23329	ENU07123	ANI61C9992: 32-54 1870..1		779-803	LINAP		g3184062	240	59	7.00E-19	31	16	
23330	ENU07124	ANI61C2437: 1456..399			LINAP		g3406059	603	124	8.00E-55	52	61	
23331	ENU07125	ANI61C7578: 30-49 1121..2101		782-801	LINAP		g3024604	169	46	0.0004	26	23	
23332	ENU07126	ANI61S1068: 104-130 373-395 439..1			LINAP		g2619050	97	56	0.000000	27	55	
23333	ENU07127	ANI61C3399: 97-119 2562..1		708-731	LINAP		g2147662	793	103	1.00E-21	27	12	
23334	ENU07128	ANI61C2439: 62-82 318..1		456-476	LINAP		g2440206	307	136	8.00E-32	39	21	
23335	ENU07129	ANI61C6408: 40-59 2484..889		809-829	LINAP		g3135990	1070	171	4.00E-42	49	46	
23336	ENU07130	ANI61C7586: 46-65 1171..1		613-630	LINAP		g172638	430	153	1.00E-36	42	21	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23337	ENU07131	ANI61C9493: 3165..373	35-62	715-739	LINAP		g548817	2756	333	1.00E-90	59	15	DNA-directed RNA polymerase II largest subunit (RNA polymerase II subunit 1) ; DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain - fission yeast (Schizosaccharomyces pombe) ; (X56564) RNA polymerase II large subunit [Schizosaccharomyces pombe]
23338	ENU07132	ANI61C3414: 1630..2327	38-60	567-586	LINAP		g4107287	184	80	1.00E-23	41	32	(AL035076) putative allantoin permease [Schizosaccharomyces pombe]
23339	ENU07133	ANI61C243:2 14..1076	51-70	809-828	LINAP		g4200122	462	119	4.00E-35	48	100	(AJ009555) hypothetical protein [Arabidopsis thaliana]
23340	ENU07134	ANI61C9478: 44-63 721..1	44-63	644-663	LINAP		g3451474	753	300	9.00E-81	62	38	(AL031349) conserved hypothetical protein [Schizosaccharomyces pombe]
23341	ENU07135	ANI61C2443: 452..1	118-140	460-479	LINAP		g3875727	50	58	0.000000			(Z70751) similar to 4-coumarate-CoA ligase; cDNA EST EMBL:C07240 comes from this gene; cDNA EST EMBL:C08540 comes from this gene [Caenorhabditis elegans]
23342	ENU07136	ANI61C7019: 2157..358	22-42	785-812	LINAP		g731610	336	74	1.00E-12			hypothetical 210.4 KD protein in GUT1-RIM1 intergenic region ; hypothetical protein YHL030w - yeast (Saccharomyces cerevisiae) ; (U11583) YHL030w gene product [Saccharomyces cerevisiae]
23343	ENU07137	ANI61C3440: 402..795	42-69	362-381	LINAP		g3661614	604	228	3.00E-59	84	17	(AF093142) aconitase [Aspergillus terreus]
23344	ENU07138	ANI61C2443: 3603..2148	24-46	798-821	LINAP		g417782	773	212	5.00E-74	56	30	SMP2 protein ; SMP2 protein - yeast (Saccharomyces cerevisiae) ; (D01095) Smp2 protein [Saccharomyces cerevisiae] ; (Z49705) Smp2p [Saccharomyces cerevisiae] ; SMP2 gene [Saccharomyces cerevisiae]
23345	ENU07139	ANI61C9482: 3304..3985	24-46	635-659	LINAP		g710551	182	84	1.00E-15			(L40632) ankyrin 3 [Mus musculus]
23346	ENU07140	ANI61S138:9 67..501			LINAP			76				29	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23347	ENU07141	ANI61C342:2 543..874	22-44	809-829	LINAP	g4309732	141	33	2.3				(AC006439) hypothetical protein [Arabidopsis thaliana]
23348	ENU07142	ANI61C6406: 71-90 1516..4364	71-90	762-780	LINAP	g3298562	1004	61	0.000000	008			(U91543) zinc-finger helicase [Homo sapiens]
23349	ENU07143	ANI61C7015: 22-47 4595..3707	22-47	781-800	LINAP	g3133109	463	141	8.00E-33	33	38		(AL023554) fork head protein type transcription factor [Schizosaccharomyces pombe]
23350	ENU07144	ANI61S1513: 168-187 1..553	168-187	331-350	LINAP	g1351702	67	67	1.00E-10				hypothetical 61.1 KD protein C11D3.05 in chromosome I; (Z68166) unknown [Schizosaccharomyces pombe]
23351	ENU07145	ANI61C3439: 36-55 888..1	36-55	800-825	LINAP	g4107480	332	69	9.00E-27	47	39		(AL035085) putative mitochondrial carrier protein [Schizosaccharomyces pombe]
23352	ENU07146	ANI61C6426: 311..1385			LINAP	g2073105	546	185	4.00E-46	42	38		(AB0033310) chitin synthase regulatory factor [Candida albicans]
23353	ENU07147	ANI61C7062: 27-54 574..267	27-54	263-287	LINAP	g4557813	65	52	0.000001	30	11		"phosphatidylinositol polyphosphate 5-phosphatase, isoform a; (U57627) ocr1 [Homo sapiens] "
23354	ENU07148	ANI61C7611: 155-179 2352..1355	155-179	681-700	LINAP	g4049510	170	86	3.00E-16	29	49		(AL034563) putative polyA-binding protein. [Schizosaccharomyces pombe]
23355	ENU07149	ANI61S187:3 02..898			LINAP	g2493724	199	79	2.00E-14	44	32		"citrate synthase, mitochondrial precursor; (AB001565) citrate synthase [Candida tropicalis] "
23356	ENU07150	ANI61C2463: 146-165 425..1	146-165	455-479	LINAP	g2842469	360	157	6.00E-38	46	21		(AL021747) hypothetical protein [Schizosaccharomyces pombe]
23357	ENU07151	ANI61C6416: 38-57 4247..4853	38-57	558-585	LINAP	g1857082	62	39	0.023				(U59915) Noc1p [Schizosaccharomyces pombe]; (Z99568) noc1p. [Schizosaccharomyces pombe]
23358	ENU07152	ANI61C7029: 71-90 4146..2624	71-90	806-825	LINAP	g1169238	935	133	4.00E-63	56	51		"glutamate decarboxylase (GAD) ; glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia ; (L16797) glutamate decarboxylase [Petunia hybrida] ; (L16977) glutamate decarboxylase [Petunia hybrida] "
23359	ENU07153	ANI61S2140: 234..722			LINAP	g4539416	82	67	1.00E-10	37	20		(AL049171) 1-aminocyclopropane-1-carboxylate synthase-like protein [Arabidopsis thaliana]

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23360	ENU07154	ANI61C2464: 102-120 434..1	102-120	415-434	LINAP	ANI61C2464	g479416	189	87	1.00E-16	30	24	kinesin light chain isoform 3 - sea urchin (Strongylocentrotus purpuratus)
23361	ENU07155	ANI61C6433: 197-219 3153..2606	197-219	498-516	LINAP	ANI61C6433	g4033486	200	101	3.00E-21			putative tartrate transporter ; (U25634) putative tartrate transporter; inducible by tartrate; Method: conceptual translation supplied by author. [Agrobacterium vitis] ; tuB gene [Agrobacterium vitis]
23362	ENU07156	ANI61C955:9 21..1	44-68	722-749	LINAP	ANI61C955	g4481951	734	148	3.00E-74	59	10	(AL035637) putative alpha-glucan synthase [Schizosaccharomyces pombe]
23363	ENU07157	ANI61C2468: 22-48 1656..2169	22-48	470-493	LINAP	ANI61C2468	g2132222	117	48	0.00004	30	29	hypothetical protein YPL181w - yeast (Saccharomyces cerevisiae) ; (Z73538) ORF YPL181w [Saccharomyces cerevisiae]
23364	ENU07158	ANI61C6422: 22-49 4382..4079	22-49	443-462	LINAP	ANI61C6422	g4263745	38	47	0.00009			"(AC004912) similar to CR16, SH3 domain binding protein; similar to 2205340A (PID:g1587070) [Homo sapiens]"
23365	ENU07159	ANI61C3420: 22-45 4161..4662	22-45	373-392	LINAP	ANI61C3420	g539323	323	143	1.00E-33	42	21	mitochondrial intermediate peptidase (EC 3.4.24.-) precursor - yeast (Saccharomyces cerevisiae) ; (Z28134) ORF YKL134c [Saccharomyces cerevisiae]
23366	ENU07160	ANI61S2566: 28-49 144..575	28-49	274-300	LINAP	ANI61S2566	g417049	110	79	2.00E-14	36	20	Gephyrin (putative glycine receptor-tubulin linker protein) ; gephyrin - rat ; (X66366) Gephyrin [Rattus norvegicus]
23367	ENU07161	ANI61C7048: 24-46 2867..3715	24-46	715-739	LINAP	ANI61C7048	g1351661	128	82	4.00E-15	29	37	hypothetical 60.7 KD protein C30D11.08C in chromosome I ; hypothetical protein SPAC30D11.08c - fission yeast (Schizosaccharomyces pombe) ; (Z67961) PHD finger protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23368	ENU07162	ANI61C7624: 29-56 423..1	29-56	453-479	LINAP		g549758	67	50	0.00001			"FERRIC reductase transmembrane component 2 precursor; ferric reductase FRE2 precursor - yeast (Saccharomyces cerevisiae); (X75950) ORF5, F711 [Saccharomyces cerevisiae]; (Z28220) ORF YKL220c [Saccharomyces cerevisiae]; ORF 5 [Saccharomyces cerevisiae]"
23369	ENU07163	ANI61S269:1. 122-141 706	122-141	584-601	LINAP		g1679757	362	152	9.00E-40	39	30	(U77605) two-component histidine kinase CHK-1 [Glomerella cingulata]; (U77606) two-component histidine kinase CHK-1 [Glomerella cingulata] (Z37980) hypothetical 4-hydroxyphenylacetate permease [Escherichia coli]
23370	ENU07164	ANI61C3451: 36-63 2042..1199	36-63	792-819	LINAP		g757832	235	55	2.00E-15			(M18209) transcription factor S-II [Mus musculus] (L77234) glycine rich protein [Neurospora crassa] (M80368) pathway-specific regulatory protein [Neurospora crassa] chromosome scaffold protein sudA - Emericella nidulans; (U40146) chromosome scaffold protein [Emericella nidulans]
23371	ENU07165	ANI61C2468: 22-48 2660..3004	22-48	454-479	LINAP		g201937	81	74	6.00E-13	33	58	maltose permease MAL3T (maltose transport protein MAL3T); maltose transport protein MAL3T - yeast (Saccharomyces cerevisiae); (Z36167) ORF YBR298c [Saccharomyces cerevisiae]
23372	ENU07166	ANI61C7056: 22-45 2961..992	22-45	807-826	LINAP		g1261823	944	122	4.00E-27	36	28	(X89442) peptide synthetase [Metarhizium anisopliae] (AL035523) putative protein [Arabidopsis thaliana]
23373	ENU07167	ANI61C9538: 26-53 2083..1066	26-53	801-820	LINAP		g168849	144	56	5.00E-11	29	22	
23374	ENU07168	ANI61S298:1. 149-168 458	149-168	291-318	LINAP		g2133266	311	97	8.00E-20	68	11	
23375	ENU07169	ANI61C248:1 25-45 359..1	25-45	757-780	LINAP		g585446	310	88	7.00E-17	23	45	
23376	ENU07170	ANI61C7021: 22-43 1..5469	22-43	801-828	LINAP		g2342601	2446	157	3.00E-44	38	5	
23377	ENU07171	ANI61S3228: 136-161 569..243	136-161	276-294	LINAP		g4455254	181	94	4.00E-19	74	16	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23378	ENU07172	ANI61C9548: 2731..2342	72-91	301-320	LINAP		g586300	275	125	1.00E-28	44	34	hypothetical 44.4 KD protein in CDC28-ARL1 intergenic region ; SUR1 protein homolog YBR161w - yeast (Saccharomyces cerevisiae) ; (X80224) YBR1212 [Saccharomyces cerevisiae] ; (Z36030) ORF YBR161w [Saccharomyces cerevisiae] (U78597) kinesin light chain [Plectonema boryanum] (AJ010981) putative transposase [Talaromyces stipitatus] conidial green pigment synthase ; probable polyketide synthase - Emericella nidulans ; (X65866) putative polyketide or fatty acid synthase [Emericella nidulans] ; wA gene [Emericella nidulans] SIS2 protein (halotolerance protein HAL3) ; hal3 protein - yeast (Candida tropicalis) ; (X88900) hal3 [Candida tropicalis]
23379	ENU07173	ANI61S3294: 1..457	134-153	290-312	LINAP		g2645229	217	89	2.00E-17	36	31	lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (Z99163) hypothetical protein [Schizosaccharomyces pombe] (Z68119) cDNA EST EMBL:Z14951 comes from this gene; cDNA EST EMBL:T00215 comes from this gene; cDNA EST EMBL:D71583 comes from this gene; cDNA EST EMBL:D74238 comes from this gene; cDNA EST yk376f7.3 comes from this gene; cDNA ...
23380	ENU07174	ANI61C2501: 1..479	143-169	414-441	LINAP		g3646479	198	94	7.00E-19	32	94	
23381	ENU07175	ANI61C7017: 1088..1	26-45	722-749	LINAP		g549443	569	214	7.00E-55	39	14	
23382	ENU07176	ANI61S3549: 615..290			LINAP		g2498915	89	56	0.000000	33	19	
23383	ENU07177	ANI61C3502: 278..991	47-66	669-692	LINAP		g125935	248	112	2.00E-24	31	40	
23384	ENU07178	ANI61C252:1 513..953	22-48	519-538	LINAP		g2408040	116	46	0.000000	29	70	
23385	ENU07179	ANI61C7653: 750..401	22-46	433-452	LINAP		g3879884	138	33	1.4	5		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23386	ENU07180	ANI61C9555: 1733..899	72-91	793-814	LINAP		g548976	101	49	0.00004	21	54	suppressor protein SRP40 ; SRP40 protein - yeast (Saccharomyces cerevisiae) ; (X73541) ORF YKR412 [Saccharomyces cerevisiae] ; (Z28317) ORF YKR092c [Saccharomyces cerevisiae]
23387	ENU07181	ANI61S3624: 1..392	47-66	301-323	LINAP		g2687633	61	43	0.00006	44	18	(AF035756) 2-dehydro-3-deoxyphosphoheptonate aldolase; phospho-2-dehydro-3-deoxyheptonate aldolase [Streptomyces sp.] (U28943) similar to ribitol dehydrogenase [Caenorhabditis elegans]
23388	ENU07182	ANI61C2550: 1249..1549	51-70	459-478	LINAP		g861340	69	46	0.0002			
23389	ENU07183	ANI61C7020: 1296..2568	22-48	804-829	LINAP		g4581524	695	260	8.00E-69	47	48	(AL049559) conserved hypothetical protein [Schizosaccharomyces pombe]
23390	ENU07184	ANI61C7660: 1990..1287	114-131	661-682	LINAP		g4063766	102	41	0.008			(D87895) chitinase [Emericella nidulans]
23391	ENU07185	ANI61S3795: 343..1	122-149	259-280	LINAP		g2327061	181	90	9.00E-18	44	12	(AF001304) protease 1 [Pneumocystis carinii f. sp. carinii]
23392	ENU07186	ANI61C7664: 1..735	30-49	692-714	LINAP		g4033486	225	108	6.00E-23			putative tartarate transporter ; (U25634) putative tartarate transporter; inducible by tartarate; Method: conceptual translation supplied by author. [Agrobacterium vitis] ; tuB gene [Agrobacterium vitis]
23393	ENU07187	ANI61S4106: 416..1	138-158	299-318	LINAP		g2970667	157	81	6.00E-15	28	48	(AF052586) beta-ketoacyl reductase [Pseudomonas aeruginosa]
23394	ENU07188	ANI61C9570: 3084..1369	22-47	798-817	LINAP		g2496987	140	96	4.00E-19	35	8	hypothetical 216.3 KD protein R06F6.8 in chromosome II ; (Z46794) cDNA EST EMBL:T01654 comes from this gene; cDNA EST EMBL:D32326 comes from this gene; cDNA EST EMBL:D32810 comes from this gene; cDNA EST EMBL:D34680 comes from this gene; cDNA EST EMBL:D35556 comes from this gene; cDN...

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23395	ENU07189	ANI61S4269: 1..380	87-106	229-248	LINAP		g730742	159	83	6.00E-16	32	10	SIP3 protein ; SIP3 protein - yeast (Saccharomyces cerevisiae) ; (U03376)
23396	ENU07190	ANI61C2478: 72-91 2192..1830	72-91	452-471	LINAP		g2501705	125	87	1.00E-16			Sip3p [Saccharomyces cerevisiae] ; (X96722) ORF N0844 [Saccharomyces cerevisiae] ; (Z71533) ORF YNL257c [Saccharomyces cerevisiae] zinc finger protein GLI4 (neural specific DNA binding protein XGLI4) (XGLI-4) ; (U42462) neural specific DNA binding protein [Xenopus laevis] A-agglutinin attachment subunit precursor ; a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae) ; (M60590) a-agglutinin core subunit [Saccharomyces cerevisiae] ; (Z71659) ORF YNR044w [Saccharomyces cerevisiae] (Z99165) hypothetical protein [Schizosaccharomyces pombe] (U59303) glucoamylase precursor [Aspergillus awamori] (U75445) alpha-amylase [Bacillus sp. MK 716] HC-toxin synthetase (HTS) ; (M98024) HC-toxin synthetase [Cochliobolus carbonum] (Z98741) oxidoreductase [Mycobacterium leprae] hypothetical 73.1 KD protein C3H1.09C in chromosome I ; (Z68144) major facilitator superfamily protein [Schizosaccharomyces pombe] (Z50144) kynurenine/alpha-aminoadipate aminotransferase [Rattus norvegicus] "(U66480) xylan beta-1,4-xylosidase [Bacillus subtilis] ; (Z99113) xylan beta-1,4-xylosidase [Bacillus subtilis] "
23397	ENU07191	ANI61C7092: 24-43 925..89	24-43	796-816	LINAP		g416592	84	46	0.0002			
23398	ENU07192	ANI61C9586: 46-65 1358..1838	46-65	410-431	LINAP		g2408062	189	87	1.00E-16	45	20	
23399	ENU07193	ANI61C2555: 22-45 2559..2969	22-45	428-447	LINAP		g1389841	380	122	2.00E-27	50	26	
23400	ENU07194	ANI61S4557: 32-51 221..599	32-51	328-347	LINAP		g1667474	69	61	0.000000			
23401	ENU07195	ANI61S4598: 61-85 480..1	61-85	443-469	LINAP		g462367	212	106	1.00E-22	33	3	
23402	ENU07196	ANI61C347:3 118-137 443-462 07..1	118-137	443-462	LINAP		g2342610	88	43	0.000000	32	21	
23403	ENU07197	ANI61S4611: 33-53 1..391	33-53	334-353	LINAP		g1351692	194	92	2.00E-18	37	19	
23404	ENU07198	ANI61C2593: 56-75 1288..568	56-75	667-689	LINAP		g1050752	110	60	6.00E-12			
23405	ENU07199	ANI61C3538: 48-75 1607..354	48-75	810-829	LINAP		g1750122	303	57	1.00E-11			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23406	ENU07200	ANI61C7098:1349..2123			LINAP		g416820	447	205	3.00E-52	48	57	para-hydroxybenzoate—polyprenyltransferase precursor (PHB:polyprenyltransferase) ; para-hydroxybenzoate--polyprenyltransferase - yeast (Saccharomyces cerevisiae) ; (M81698) p-hydroxybenzoate:polyprenyl transferase [Saccharomyces cerevisiae] ; (Z71656) ORF YNR041c [Saccharomyces cerevisiae] "(AF008220) SHCHC synthase [Bacillus subtilis] ; (Z99119) 2-oxoglutarate decarboxylase and 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacillus subtilis] "
23407	ENU07201	ANI61S53:1..551			LINAP		g2293146	370	165	2.00E-40	49	31	Ammonium transporter MEP2 ; ammonium transport protein MEP2 - yeast (Saccharomyces cerevisiae) ; (X83608) ammonium transporter [Saccharomyces cerevisiae] ; (Z46843) NH3 permease [Saccharomyces cerevisiae] ; (Z71418) ORF YNL142w [Saccharomyces cerevisiae] [Saccharomyces cerevisiae] (AL031004) RNA lariat debranching enzyme - like protein [Arabidopsis thaliana]
23408	ENU07202	ANI61C2584: 60-79 1..1175		790-809	LINAP		g1170922	725	169	8.00E-60	44	53	Bud site selection protein BUD6 (actin interacting protein 3) ; actin-interacting protein AIP3 - yeast (Saccharomyces cerevisiae) ; (U20618) Bud6p: actin interacting protein [Saccharomyces cerevisiae] ; (U35668) Aip3p [Saccharomyces cerevisiae] (Z99107) similar to pet112-like protein [Bacillus subtilis]
23409	ENU07203	ANI61C7071: 24-43 2672..1828		791-810	LINAP		g3281851	707	251	4.00E-66	54	60	beta-glucuronidase - Escherichia coli ; (Z32701) beta-glucuronidase [synthetic construct]
23410	ENU07204	ANI61C7679: 22-41 361..1632		802-829	LINAP		g1168699	432	159	2.00E-38	37	34	
23411	ENU07205	ANI61S559:549..1			LINAP		g2632983	462	139	3.00E-50	59	43	
23412	ENU07206	ANI61C2598: 66-89 1..460		375-394	LINAP		g541048	457	196	6.00E-50	62	25	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23413	ENU07207	ANI61C355:3 085..1963	22-45	807-828	LINAP	g2136300	g1799570	492	34	1	39	19	transcription factor NFATx - human ; (U14510) NFATx [Homo sapiens] (D87671) TIP120 [Rattus norvegicus]
23414	ENU07208	ANI61C7071: 3980..6963			LINAP			680	105	2.00E-27	29	27	(Z97193) hypothetical protein Rv1894c [Mycobacterium tuberculosis]
23415	ENU07209	ANI61S577:1.. 62-81	62-81	249-272	LINAP	g2225966	g126643	112	53	0.000000	29	27	Aminoacidate-semialdehyde dehydrogenase large subunit (alpha-aminoacidate reductase) (alpha-AR) ; L-aminoacidate-semialdehyde dehydrogenase (EC 1.2.1.31) - yeast (Saccharomyces cerevisiae) ; (M36287)
23416	ENU07210	ANI61C7706: 30-51 1007..584	30-51	454-476	LINAP	g126643		63	55	0.000000		4	alpha-aminoacidate reductase (LYS2; EC 1.2.1.31) [Saccharomyces cerevisiae] ; (X78993) alpha-aminoacidate reductase [Saccharomyces cerevisiae] ; (Z35984) ORF YBR115c [Saccharomyces cerevisiae] ; (AD001531) alpha-aminoacidate reductase [Cloning vector pGR8]
23417	ENU07211	ANI61C3550: 22-44 3384..4143	22-44	691-710	LINAP	g3876027		147	92	5.00E-18	34	16	(Z78062) cDNA EST EMBL:D34090 comes from this gene; cDNA EST EMBL:D37114 comes from this gene; cDNA EST EMBL:D64639 comes from this gene; cDNA EST EMBL:D67728 comes from this gene; cDNA EST EMBL:C12617 comes from this gene; cDN...
23418	ENU07212	ANI61S77:33 8..1			LINAP	g2492657		336	149	1.00E-35	62	8	putative sterigmatocystin biosynthesis fatty acid synthase alpha subunit ; (U34740) putative fatty acid synthase alpha [Emericella nidulans]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23419	ENU07213	ANI61C7674: 29-52 3380..2309	5 pos	802-829	LINAP		g1730824	363	60	5.00E-10	40	42	hypothetical 56.6 KD protein in URE2-SSU72 intergenic region ; hypothetical protein YNL223w - yeast (Saccharomyces cerevisiae) ; (Z69381) N1274 [Saccharomyces cerevisiae] ; (Z71499) ORF YNL223w [Saccharomyces cerevisiae]
23420	ENU07214	ANI61S79:1..595			LINAP		g127736	183	94	1.00E-18	30	12	myoSIN-2 isoform ; myosin myo2 - yeast (Saccharomyces cerevisiae) ; (M35532) myosin 1 isoform (myo2) [Saccharomyces cerevisiae] ; (Z75234) ORF YOR326w [Saccharomyces cerevisiae]
23421	ENU07215	ANI61C7677: 49-68 4030..3702	49-68	457-479	LINAP		g607855	120	61	0.000000			(U11098) hydroxyindole-O-methyltransferase [Homo sapiens]
23422	ENU07216	ANI61S816:1..318			LINAP		g728913	135	74	4.00E-13	33	11	"MG(2+) transport ATPase, P-type 1 ; (AE000495) Mg2+ transport ATPase, P-type 1 [Escherichia coli] "
23423	ENU07217	ANI61C2621: 34-61 1731..3003	34-61	794-813	LINAP		g2132651	473	155	3.00E-37	33	47	probable membrane protein YLL028w - yeast (Saccharomyces cerevisiae) ; (Z73133) ORF YLL028w [Saccharomyces cerevisiae]
23424	ENU07218	ANI61C3547: 52-71 3428..1912	52-71	766-785	LINAP		g140201	1005	206	8.00E-67	55	28	protein kinase YAK1 ; protein kinase YAK1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) ; (X16056) Yak1 kinase (AA 1 - 807) [Saccharomyces cerevisiae] ; (X87371) protein kinase [Saccharomyces cerevisiae] ; (Z49417) ORF YJL141c [Saccharomyces cerevisiae]
23425	ENU07219	ANI61C7112: 114-133 1..425	114-133	360-380	LINAP		g4539606	195	73	8.00E-13	39	65	(AL049522) hypothetical DNAJ domain protein [Schizosaccharomyces pombe]
23426	ENU07220	ANI61C2637: 106-126 1..497	106-126	452-476	LINAP		g2924449	42	37	0.1			(AL022022) PE_PGRS [Mycobacterium tuberculosis]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23427	ENU07221	ANI61C7691: 22-47 2634..5362		647-666	LINAP		g3915963	1425	228	3.00E-59	47	16	ATP-dependent bile acid permease ; probable membrane protein YLL048c - yeast (<i>Saccharomyces cerevisiae</i>) ; (Z73153) ORF YLL048c [<i>Saccharomyces cerevisiae</i>] 3-isopropylmalate dehydratase (EC 4.2.1.33) - <i>Phycomyces blakesleeanus</i> ; (X53090) alpha-isopropylmalate isomerase (AA 1-689) [<i>Phycomyces blakesleeanus</i>] "serine-type carboxypeptidase - Penicillium janthinellum ; carboxypeptidase S3, penicillopeptidase S3, CPD-S3 [<i>Penicillium janthinellum</i> , IBT 3991, Peptide, 481 aa] "
23428	ENU07222	ANI61C8374: 29-48 36..1769		771-796	LINAP		g283065	1718	351	3.00E-96	64	40	
23429	ENU07223	ANI61S846:1. 68-89 .365		206-225	LINAP		g1363903	233	115	1.00E-25	51	24	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23430	ENU07224	ANI61C8374: 28-48 1922..2257					g3135546	492	203	9.00E-52			(AF061918) Tn5 transposase [Plasposon pTnMod-OCm] ; (AF061919) Tn5 transposase [Plasposon pTnMod-OCm'] ; (AF061920) Tn5 transposase [Plasposon pTnMod-OGm] ; (AF061923) Tn5 transposase [Plasposon pTnMod-SmO] ; (AF061924) Tn5 transposase [Plasposon pTnMod-OTc] ; (AF061925) Tn5 transposase [Plasposon pTnMod-OTc'] ; (AF061926) Tn5 transposase [Plasposon pTnMod-OTp] ; (AF061927) Tn5 transposase [Plasposon pTnMod-CmOTc] ; (AF061928) Tn5 transposase [Plasposon pTnMod-Cm'OTc] ; (AF061929) Tn5 transposase [Plasposon pTnMod-RCm] ; (AF061930) Tn5 transposase [Plasposon pTnMod-RKm] ; (AF061931) Tn5 transposase [Plasposon pTnMod-RTp] DNA-directed RNA polymerase I largest subunit ; (Y09103) largest subunit of RNA polymerase I (A) [Drosophila melanogaster] 60S ribosomal protein L3-2 ; ribosomal protein L3 - fission yeast (Schizosaccharomyces pombe) ; (X57734) ribosomal protein L3 [Schizosaccharomyces pombe] chromosome region maintenance protein 1 ; (X15482) crml product [Schizosaccharomyces pombe]
23431	ENU07225	ANI61S907:3 52..1			LINAP		g3914818	131	57	0.000000 08			
23432	ENU07226	ANI61C7114: 482..1158			LINAP		g548771	577	117	1.00E-51	53	53	
23433	ENU07227	ANI61C7698: 23-45 3196..1151			LINAP		g399299	1580	225	5.00E-74	61	26	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23434	ENU07228	ANI61C8392: 40-60 507..884	40-60	454-475	LINAP		g131768	35	66	2.00E-10			quininate permease (quininate transporter) ; quininate transport protein - Emericella nidulans ; (X13525) quininate permease [Emericella nidulans] probable malate oxidoreductase (NAD) (malic enzyme) (ME) ; malate dehydrogenase homolog YKL029c - yeast (Saccharomyces cerevisiae) ; (Z28029) ORF YKL029c [Saccharomyces cerevisiae] beta-glucan synthesis-associated protein KRE6 ; (D88490) CaKRE6 [Candida albicans] (AL023634) hypothetical protein [Schizosaccharomyces pombe] (Y16675) aflatoxin B1-aldehyde reductase [Homo sapiens] putative transporter YIL166C ; probable membrane protein YIL166c - yeast (Saccharomyces cerevisiae) ; (Z46921) unknown [Saccharomyces cerevisiae] (AF030886) telomere-associated recQ-like helicase [Ustilago maydis] (L13655) membrane protein [Saccharum hybrid cultivar H65-7052] (AJ223998) PCZA361.18 [Amycolatopsis orientalis] (AL023634) protein kinase dsk1 [Schizosaccharomyces pombe] (AJ001909) transcriptional activator [Aspergillus niger] (AJ223504) amino acid transporter [Amanita muscaria] (X89442) peptide synthetase [Metarhizium anisopliae]
23435	ENU07229	ANI61C2616: 22-45 2660..4618	22-45	802-829	LINAP		g547888	1218	130	4.00E-46	40	38	
23436	ENU07230	ANI61C7114: 22-49 3961..4544	22-49	536-563	LINAP		g2498505	179	51	2.00E-14	43	21	
23437	ENU07231	ANI61C7710: 36-55 2928..3343	36-55	456-479	LINAP		g3150252	77	55	0.000000	27	21	
23438	ENU07232	ANI61C2641: 30-49 1214..2159	30-49	806-828	LINAP		g3378617	463	107	2.00E-41	44	78	
23439	ENU07233	ANI61C7128: 47-66 669..1472	47-66	682-703	LINAP		g731893	414	108	7.00E-40	47	37	
23440	ENU07234	ANI61C7693: 26-53 3032..1965	26-53	796-815	LINAP		g2642224	173	90	2.00E-17	28	36	
23441	ENU07235	ANI61C8379: 22-47 1661..911	22-47	702-729	LINAP		g294845	220	74	1.00E-20	33	64	
23442	ENU07236	ANI61C2649: 24-43 1079..1544	24-43	453-479	LINAP		g2894166	70	75	4.00E-13			
23443	ENU07237	ANI61C7110: 22-49 1636..43	22-49	768-786	LINAP		g3150261	1132	241	4.00E-63	56	37	
23444	ENU07238	ANI61C8381: 25-44 355..666	25-44	432-451	LINAP		g2808634	72	56	0.000000	29	13	
23445	ENU07239	ANI61C2655: 33-52 1026..1	33-52	770-789	LINAP		g4468097	516	131	3.00E-40	42	45	
23446	ENU07240	ANI61C351:2 29-48 822..1	29-48	712-730	LINAP		g2342601	1597	194	9.00E-49	40	5	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23447	ENU07241	ANI61C7141: 22-44 1134..2760	22-44	720-739	LINAP		g1351624	905	69	4.00E-11	45	23	hypothetical 122.9 KD protein C29E6.10C in chromosome I; (Z66525) unknown [Schizosaccharomyces pombe]
23448	ENU07242	ANI61C8385: 42-69 3918..3469	42-69	452-479	LINAP		g1723076	82	74	6.00E-13	32	27	hypothetical 57.3 KD protein GMC- type oxidoreductase CY50.03C; (Z77137) hypothetical protein Rv1279 [Mycobacterium tuberculosis] (U46857) vitellogenin [Anolis pulchellus] (D90917) eukaryotic protein kinase [Synechocystis sp.] (D42138) PIG-B [Homo sapiens]
23449	ENU07243	ANI61C7137: 60-79 1126..763	60-79	412-431	LINAP		g1197667	86	37	0.08			glycerate dehydrogenase (NADH- dependent hydroxypyruvate reductase) (HPR) (GDH) (hydroxypyruvate dehydrogenase) (glyoxylate reductase) (HPR-A)
23450	ENU07244	ANI61C8400: 45-64 1308..1782	45-64	430-449	LINAP		g1653955	94	43	0.001			hypothetical 72.2 KD protein C12C2.05C in chromosome II; (Z54140) hypothetical protein [Schizosaccharomyces pombe]
23451	ENU07245	ANI61C3600: 66-85 768..1717	66-85	778-801	LINAP		g1552169	145	71	1.00E-11			Pyrimidine pathway regulatory protein 1; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae); (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae]; (Z73186) ORF YLR014c [Saccharomyces cerevisiae]
23452	ENU07246	ANI61C7678: 25-44 2208..1435	25-44	710-729	LINAP		g2494084	259	147	7.00E-35	40	78	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium; (D83643) polyketide synthase [Colletotrichum lagenarium]
23453	ENU07247	ANI61C2687: 32-56 376..1	32-56	383-403	LINAP		g1175425	159	84	5.00E-16	30	25	
23454	ENU07248	ANI61C3566: 32-54 5338..6011	32-54	488-507	LINAP		g130784	85	61	0.000000 006			
23455	ENU07249	ANI61C7136: 36-55 827..1	36-55	698-725	LINAP		g2147662	535	209	2.00E-53	50	12	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23456	ENU07250	ANI61C7678: 22-47 5186..2864	22-47	797-824	LINAP	g136232	g136232	1429	285	3.00E-76	50	31	"potassium transport protein, low-affinity ; potassium transport protein TRK2, low-affinity - yeast (Saccharomyces cerevisiae) ; (M65215) TRK2 [Saccharomyces cerevisiae] ; (Z28275) ORF YKR050w [Saccharomyces cerevisiae] " (X62570) IFP53 [Homo sapiens]
23457	ENU07251	ANI61C3588: 22-47 1848..672	22-47	794-813	LINAP	g32709	g32709	1009	295	3.00E-79	59	54	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum " (AJ002894) OsGRP2 [Oryza sativa]
23458	ENU07252	ANI61C2675: 27-46 218..1168	27-46	802-829	LINAP	g3318897	g3318897	290	95	1.00E-19	39	33	"Erythronolide synthase, modules 5 and 6 (ORF 3) (6-deoxyerythronolide B synthase III) (DEBS 3) ; 6-deoxyerythronolide B synthase III - Saccharopolyspora erythraea ; (X62569) 6-deoxyerythronolide B synthase III [Saccharopolyspora erythraea] " (AL031262) hypothetical protein [Schizosaccharomyces pombe]
23459	ENU07253	ANI61C8388: 22-43 1335..1755	22-43	439-457	LINAP	g2624328	g2624328	125	43	2.00E-12			"Ankyrin, brain variant 2 (ankyrin B) (ankyrin, nonerythroid) " (hypothetical 269.9 KD protein in FKHI-MET18 intergenic region ; probable membrane protein YIL129c - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 2376, CAI: 0.14 [Saccharomyces cerevisiae] " (L35053) endonuclease [Magnaporthe grisea]
23460	ENU07254	ANI61C8388: 5001..3984			LINAP	g2506137	g2506137	281	123	1.00E-27	33	8	
23461	ENU07255	ANI61C7738: 941..1734			LINAP	g3417427	g3417427	144	35	0.73	30	57	
23462	ENU07256	ANI61C7743: 41-60 1610..1993	41-60	431-450	LINAP	g231551	g231551	146	53	0.000001	29	9	
23463	ENU07257	ANI61C7740: 36-55 3137..1	36-55	711-730	LINAP	g731871	g731871	790	136	3.00E-31	32	11	
23464	ENU07258	ANI61C8420: 1..1751			LINAP	g522302	g522302	866	187	1.00E-46	42	23	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23465	ENU07259	ANI61C3612: 28-47 749..1	28-47	608-632	LINAP		g2440190	166	113	2.00E-24	35	13	(Z98602) putative protein transport protein sec7 homolog [Schizosaccharomyces pombe]
23466	ENU07260	ANI61C7168: 22-43 1075..1	22-43	713-732	LINAP		g549738	128	51	1.00E-13			hypothetical amino-acid permease in STE3-GIN10 intergenic region ; probable transport protein YKL174c - yeast (Saccharomyces cerevisiae) ; (Z26878) unknown [Saccharomyces cerevisiae] ; (Z28174) ORF YKL174c [Saccharomyces cerevisiae] ; ORF [Saccharomyces cerevisiae]
23467	ENU07261	ANI61C7739: 71-90 777..1	71-90	646-673	LINAP		g2330791	457	171	9.00E-48	43	39	(Z98601) carboxypeptidase s precursor [Schizosaccharomyces pombe]
23468	ENU07262	ANI61C3597: 22-47 2921..2073	22-47	784-809	LINAP		g1652017	298	136	3.00E-31	33	87	(D90901) hypothetical protein [Synechocystis sp.]
23469	ENU07263	ANI61C7150: 83-107 321..2402	83-107	805-829	LINAP		g1213484	447	39	0.031			(U41740) trans-Golgi p230 [Homo sapiens] ; peripheral membrane protein p230 [Homo sapiens]
23470	ENU07264	ANI61C8351: 22-44 9042..8303	22-44	686-713	LINAP		g2132871	187	104	7.00E-22	36	47	probable membrane protein YOR059c - yeast (Saccharomyces cerevisiae) ; (Z74967) ORF YOR059c [Saccharomyces cerevisiae] ; (Z70678) YOR29-10 [Saccharomyces cerevisiae]
23471	ENU07265	ANI61C3638: 22-48 1001..600	22-48	452-479	LINAP		g3184056	90	78	3.00E-14			(AL023776) hypothetical protein [Schizosaccharomyces pombe]
23472	ENU07266	ANI61C7176: 24-48 1912..1502	24-48	424-448	LINAP		g3402751	120	79	2.00E-14	29	8	(AL031187) putative protein [Arabidopsis thaliana]
23473	ENU07267	ANI61C352:1 37-56 0337..11129	37-56	740-759	LINAP		g3023852	1460	268	3.00E-71	90	55	guanine nucleotide-binding protein beta subunit-like protein (cross-pathway control WD-repeat protein CPC-2) ; CPC2 protein - Neurospora crassa ; (X81875) CPC2 protein [Neurospora crassa]

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23474	ENU07268	ANI61C7151: 22-44 4911..4133	22-44	739-758	LINAP		g728850	166	43	0.002			"glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucohydrolase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, sta1, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus] "
23475	ENU07269	ANI61C8436: 22-47 1225..1548	22-47	459-479	LINAP		g731632	279	96	2.00E-19	53	20	hypothetical 57.0 KD protein in SOD2-RPL27 intergenic region ; hypothetical protein YHR009c - yeast (Saccharomyces cerevisiae) ; (U10400) Yhr009cp [Saccharomyces cerevisiae] (Z29098) transposase (putative) [Drosophila hydei] (Z98763) putative Inositol polyphosphate phosphatase [Schizosaccharomyces pombe] hypothetical 49.3 KD protein C30D11.06C in chromosome I ; hypothetical protein SPAC30D11.06c - fission yeast (Schizosaccharomyces pombe) ; (Z67961) hypothetical protein [Schizosaccharomyces pombe] hypothetical 70.2 KD protein C22E12.10C in chromosome I ; (Z70043) unknown [Schizosaccharomyces pombe] glycogen phosphorylase (EC 2.4.1.1) - yeast (Saccharomyces cerevisiae) ; (U28371) Glycogen phosphorylase (Swiss Prot. accession number P06738) [Saccharomyces cerevisiae] (Y17317) polyketide synthase [Aspergillus fumigatus]
23476	ENU07270	ANI61C7182: 1867..908			LINAP		g436464	187	102	4.00E-21			
23477	ENU07271	ANI61C7731: 57-76 1286..4662	57-76	805-823	LINAP		g2370558	1186	175	3.00E-52	46	22	
23478	ENU07272	ANI61C3629: 30-49 4217..3351	30-49	806-829	LINAP		g1351659	124	64	0.000000	32	50	
23479	ENU07273	ANI61C3668: 91-110 1190..445	91-110	703-725	LINAP		g1723522	566	212	2.00E-54	51	38	
23480	ENU07274	ANI61C3642: 37-63 2958..5308	37-63	709-736	LINAP		g2117720	1875	305	3.00E-82	56	31	
23481	ENU07275	ANI61C7178: 22-49 2739..278	22-49	803-829	LINAP		g3163925	609	108	7.00E-23	27	12	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23482	ENU07276	ANI61C8422: 104-123 360..1299	104-123	783-801	LINAP	g4097158	155	107	9.00E-23	26	12		(U46488) NtpS [Proteus mirabilis]
23483	ENU07277	ANI61C8422: 94-113 4025..4843	94-113	701-718	LINAP	g4499843	184	53	0.000003	27	37		(AJ011965) oxidoreductase [Claviceps purpurea]
23484	ENU07278	ANI61C843:1 101..1990			LINAP	g3618210	74	39	0.031	33	53		(AL031579) hypothetical protein [Schizosaccharomyces pombe]
23485	ENU07279	ANI61C7744: 22-46 4050..2553	22-46	804-829	LINAP	g482458	1195	167	2.00E-64	62	45		methionyl aminopeptidase (EC 3.4.11.18) 2 - rat ; (L10652) initiation factor 2 associated 67 kDa protein [Rattus rattus]
23486	ENU07280	ANI61C8417: 34-53 1..2024	34-53	804-829	LINAP	g2408035	750	73	2.00E-12	30	29		(Z99163) probable beta-adaptin clathrin assembly protein [Schizosaccharomyces pombe]
23487	ENU07281	ANI61C3674: 23-45 551..1	23-45	460-483	LINAP	g1352731	63	52	0.000004	27	28		putative protein disulfide isomerase C1F5.02 precursor ; (Z68136) unknown [Schizosaccharomyces pombe]
23488	ENU07282	ANI61C7744: 22-46 5017..5324	22-46	460-479	LINAP	g4567282	92	49	0.000000				(AC006841) putative DNAI protein [Arabidopsis thaliana]
23489	ENU07283	ANI61C7767: 22-45 2093..3226	22-45	807-829	LINAP	g2381494	1072	359	1.00E-98	60	47		(AB005589) Srw1 [Schizosaccharomyces pombe]
23490	ENU07284	ANI61C8444: 48-67 351..673	48-67	448-467	LINAP	g417106	91	54	0.000000	27	71		2-haloalkanoic acid dehalogenase I (L-2-haloacid dehalogenase I) (halocarboxylic acid halidohydrolyase I) (DEHC1) ; 2-haloacid dehalogenase (EC 3.8.1.2) I - Pseudomonas sp ; (M62908) 2-haloalkanoic acid dehalogenase I [Pseudomonas sp.] sericin MG-2 - greater wax moth (fragments)
23491	ENU07285	ANI61C3654: 31-50 2860..3613	31-50	703-726	LINAP	g1083944	136	38	0.06				(AE001142) glutamyl-tRNA synthetase (gltX) [Borrelia burgdorferi]
23492	ENU07286	ANI61C7794: 22-41 1411..267	22-41	784-811	LINAP	g2688265	622	191	5.00E-50	44	47		(AL034443) putative integral membrane efflux protein [Streptomyces coelicolor]
23493	ENU07287	ANI61C3645: 25-44 3080..3830	25-44	710-730	LINAP	g4007671	186	50	2.00E-12	26	43		

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23494	ENU07288	ANI61C7797: 1..319			LINAP		g731649	102	61	0.000000	28	22	hypothetical 53.4 KD protein in SLT2-PUT2 intergenic region ; hypothetical protein YHR036w - yeast (Saccharomyces cerevisiae) ; (U00062)
23495	ENU07289	ANI61C8443: 1..410	137-164	364-389	LINAP		g544191	109	68	2.00E-11	37	21	Yhr036wp [Saccharomyces cerevisiae] protein kinase DSK1 (DIS1-suppressing protein kinase) ; dis1-suppressing protein kinase dsk1 - fission yeast (Schizosaccharomyces pombe) ; (D13447) protein kinase [Schizosaccharomyces pombe] (Z95436) hypothetical protein Rv3633 [Mycobacterium tuberculosis] hypothetical 78.3 KD protein in RIP1-URA3 intergenic region ; hypothetical protein YEL023c - yeast (Saccharomyces cerevisiae) ; (U18530)
23496	ENU07290	ANI61C3624: 22-48	455-477		LINAP		g2105061	69	54	0.000000	29	40	Yel023cp [Saccharomyces cerevisiae] Topoisomerase I-related protein TRP4 ; topoisomerase I-related protein TRF4 - yeast (Saccharomyces cerevisiae) ; (Z48149) ORF [Saccharomyces cerevisiae] ; (U31355) Trf4p [Saccharomyces cerevisiae] ; (Z74857) ORF YOL115w [Saccharomyces cerevisiae]
23497	ENU07291	ANI61C3690: 22-49	713-730		LINAP		g731409	261	63	0.000000	22	36	(AC000133) ORF [Emericella nidulans] sodium/potassium-transporting ATPase alpha chain (sodium PUMP) (NA+/K+ ATPase) ; Na+/K+-exchanging ATPase (EC 3.6.1.37) alpha chain - white sucker ; (X58629)
23498	ENU07292	ANI61C7806: 23-45	611-630		LINAP		g1717744	299	152	3.00E-36	35	43	adenosinetriphosphatase [Catostomus commersoni] (L35601) ankyrin [Drosophila melanogaster] ; ankyrin [Drosophila melanogaster]
23499	ENU07293	ANI61C3682: 22-46	660-687		LINAP		g1870209	265	48	0.000000			
23500	ENU07294	ANI61C7809: 25-52	676-701		LINAP		g114386	221	57	4.00E-18	36	21	
23501	ENU07295	ANI61C3648: 22-41	762-789		LINAP		g557084	387	90	2.00E-17			

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23502	ENU07296	ANI61C7778: 32-51 7591..4646	32-51	768-788	LINAP		g2133248	2998	267	8.00E-71	66	26	chitin synthase (EC 2.4.1.16) C - Aspergillus fumigatus ; (X94245) chitin synthase C [Aspergillus fumigatus]
23503	ENU07297	ANI61C3644: 37-56 5841..6454	37-56	568-593	LINAP		g2645229	502	146	2.00E-34	37	41	(U78597) kinesin light chain [Plectonema boryanum]
23504	ENU07298	ANI61C7841: 22-45 1..460	22-45	372-391	LINAP		g1145799	61	48	0.00005	31	20	(U41806) p60 [Homo sapiens]
23505	ENU07299	ANI61C8492: 104-123 828..1277	104-123	315-338	LINAP		g1870209	625	231	2.00E-60	92	27	(AC000133) ORF [Emericella nidulans]
23506	ENU07300	ANI61C3677: 22-44 2990..1456	22-44	802-829	LINAP		g4107287	167	124	7.00E-28	30	54	(AL035076) putative allantoin permease [Schizosaccharomyces pombe]
23507	ENU07301	ANI61C8488: 22-44 2067..1752	22-44	419-438	LINAP		g2702312	60	49	0.00002			(U76556) antigen N54 [Neospora sp.]
23508	ENU07302	ANI61C3705: 102-120 1..655	102-120	590-609	LINAP		g464786	179	95	4.00E-19	33	33	SPT10 protein ; regulatory protein SPT10 - yeast (Saccharomyces cerevisiae) ; (L24435) SPT10 [Saccharomyces cerevisiae] ; (Z49402) ORF YJL127c [Saccharomyces cerevisiae]
23509	ENU07303	ANI61C7845: 24-44 1409..1091	24-44	267-294	LINAP		g3581903	189	84	3.00E-16	42	17	(AL031545) DEAD box ATP-dependent RNA helicase [Schizosaccharomyces pombe]
23510	ENU07304	ANI61C3693: 22-44 5491..6885	22-44	635-654	LINAP		g117619	305	77	2.00E-18	29	45	choline transport protein ; choline transport protein - yeast (Saccharomyces cerevisiae) ; (J05603) choline transport protein [Saccharomyces cerevisiae] ; (Z72599) ORF YGL077c [Saccharomyces cerevisiae]
23511	ENU07305	ANI61C7850: 28-51 814..1452	28-51	589-608	LINAP		g1805251	348	162	2.00E-39	40	38	(U58946) transposase [Aspergillus awamori]
23512	ENU07306	ANI61C7862: 671..286			LINAP		g1084952	88	76	1.00E-13			hypothetical protein YPR031w - yeast (Saccharomyces cerevisiae) ; (Z49274) unknown [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]

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23513	ENU07307	ANI61C7819: 48-72 1485..2608	807-829	LINAP		g1346290	364	72	3.00E-23	28	42	high-affinity glucoSE transporter ; (U22525) high affinity glucose transporter [Kluyveromyces lactis]
23514	ENU07308	ANI61C3737: 63-82 1184..287	765-784	LINAP		g2981103	202	65	6.00E-10	27	43	(AF052688) putative transmembrane transporter Liz1p [Schizosaccharomyces pombe] ; (AL023706) transmembrane transporter Liz1p [Schizosaccharomyces pombe]
23515	ENU07309	ANI61C8485: 25-52 5622..3617	804-829	LINAP		g2808753	601	112	4.00E-24	31	11	(AL021409) polyketide synthase [Streptomyces coelicolor]
23516	ENU07310	ANI61C3786: 22-44 932..1412	366-385	LINAP		g2132440	183	96	2.00E-19	33	37	probable membrane protein YDL133w - yeast (Saccharomyces cerevisiae) ; (X96876) putative ORF [Saccharomyces cerevisiae] ; (Z74181) ORF YDL133w [Saccharomyces cerevisiae]
23517	ENU07311	ANI61C7870: 31-51 1128..2120	808-825	LINAP		g584764	542	212	3.00E-54			aminopeptidase Y precursor ; aminopeptidase Y (EC 3.4.11.-) - yeast (Saccharomyces cerevisiae) ; (L31635) aminopeptidase Y [Saccharomyces cerevisiae] ; (X76053) YBR2024-ORF [Saccharomyces cerevisiae] ; (Z36155) ORF YBR286w [Saccharomyces cerevisiae] ; ORF YBR2024 [Saccharomyces cerevisiae] (Z69254) alpha-galactosidase [Hypocrea jecorina]
23518	ENU07312	ANI61C3744: 90-109 843..1	712-731	LINAP		g1580818	674	245	3.00E-69	55	33	(AF023132) choline monooxygenase [Beta vulgaris]
23519	ENU07313	ANI61C8510: 24-51 3106..2623	449-476	LINAP		g2522210	111	48	0.000000	03		"lignostilbene alphabeta-dioxygenase (EC 1.13.11.43) III isozyme beta chain - Pseudomonas paucimobilis ; (S80637) lignostilbene-alpha,beta-dioxygenase isozyme III, LSD-III [Pseudomonas paucimobilis, TMY1009, Peptide, 489 aa] [Sphingomonas paucimobilis] "
23520	ENU07314	ANI61C3730: 24-50 1373..619	686-713	LINAP		g2120665	447	189	1.00E-47	44	46	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23521	ENU07315	ANI61C787:1 418..3186	22-49	803-829	LINAP		g3581916	1423	250	7.00E-66	44	22	(AL031545) muts family DNA mismatch repair protein
23522	ENU07316	ANI61C7869: 22-46 2737..1530	22-46	799-817	LINAP		g3318897	95	80	2.00E-14	31	36	"Chain A, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain B, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain C, Phenol Hydroxylase From Trichosporon Cutaneum ; Chain D, Phenol Hydroxylase From Trichosporon Cutaneum "
23523	ENU07317	ANI61C3743: 39-59 1466..3481	39-59	774-793	LINAP		g1352290	916	157	9.00E-38	38	27	DNA ligase I (polydeoxyribonucleotide synthase (ATP)) ; DNA ligase (ATP) (EC 6.5.1.1) I - mouse ; (U19604) DNA ligase I [Mus musculus] ; (U04674) DNA ligase I [Mus musculus]
23524	ENU07318	ANI61C7892: 22-47 1050..591	22-47	443-462	LINAP		g1352493	224	95	4.00E-19	36	16	"type II inositol-1,4,5-trisphosphate 5-phosphatase precursor (5PTase) ; (M74161) inositol polyphosphate 5-phosphatase [Homo sapiens] "
23525	ENU07319	ANI61C7898: 451..1			LINAP		g3219812	69	56	0.000000	26	21	myo-inositol transporter 2 ; (Z95334) Itr2p [Schizosaccharomyces pombe]
23526	ENU07320	ANI61C7913: 22-42 1522..1	22-42	620-637	LINAP		g862488	847	42	0.000000	46	12	(U24167) PAK1 [Saccharomyces cerevisiae]
23527	ENU07321	ANI61C8507: 22-47 1205..896	22-47	438-457	LINAP		g1118141	51	32	3.1			(U41748) coded for by C. elegans cDNA yk16f8.5; coded for by C. elegans cDNA yk55f7.5; coded for by C. elegans cDNA yk16f8.3; coded for by C. elegans cDNA yk55f7.3; coded for by C. elegans cDNA yk72a5.5; coded for by C. elegans cDNA yk72a5.3...
23528	ENU07322	ANI61C7899: 23-50 1..1557	23-50	794-813	LINAP		g3004863	722	238	4.00E-62	45	33	"(AF029354) exo-beta-1,3-glucanase [Ampelomyces quisqualis] "
23529	ENU07323	ANI61C7929: 22-44 1461..2302	22-44	620-643	LINAP		g3914984	282	92	2.00E-28	30	7	Ferrichrome siderophore peptide synthetase ; (U62738) ferrichrome siderophore peptide synthetase [Ustilago maydis]

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23530	ENU07324	ANI61C8542: 1743..828	68-87	801-820	LINAP		g1350789	322	148	5.00E-35	36	62	"mitochondrial 60S ribosomal protein L3 precursor (YML3) ; ribosomal protein Yml3, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z49211) Mrip3p [Saccharomyces cerevisiae] " (AF008228) odd Oz protein [Drosophila melanogaster]
23531	ENU07325	ANI61C8533: 3468..3161	58-77	459-478	LINAP		g2266927	64	46	0.0001	27	3	"leucyl-TRNA synthetase, cytoplasmic (leucine--TRNA ligase) (LEURS) ; leucine--TRNA ligase (EC 6.1.1.4), cytosolic - Neurospora crassa ; (M30473) leucyl-tRNA synthetase [Neurospora crassa] "
23533	ENU07327	ANI61C8533: 4656..4194	81-103	419-442	LINAP		g3004662	110	50	6.00E-11	36	7	[AF017777] small optic lobes [Drosophila melanogaster]
23534	ENU07328	ANI61C8536: 3309..1177	66-85	782-804	LINAP		g1166378	840	205	3.00E-52	41	25	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "
23535	ENU07329	ANI61C858: 72..320	24-45	490-509	LINAP		g231902	95	41	0.000007			"cytochrome P450 XVIIA1 (P450-C17) (steroid 17-alpha-hydroxylase/17,20 lyase) ; steroid 17alpha-monooxygenase (EC 1.14.99.9) cytochrome P450 17 - rainbow trout ; (X65800) steroid 17-alpha-monooxygenase [Oncorhynchus mykiss] "
23536	ENU07330	ANI61C8544: 3861..2610	43-70	807-829	LINAP		g2132836	1101	322	1.00E-92	65	37	probable membrane protein YOL060c - yeast (Saccharomyces cerevisiae) ; (X91067) 01216; hypothetical protein [Saccharomyces cerevisiae] ; (Z74802) ORF YOL060c [Saccharomyces cerevisiae]
23537	ENU07331	ANI61C8586: 2116..1322	91-114	750-773	LINAP		g1352399	168	101	5.00E-21	32	26	"glucan 1,3-beta-glucosidase precursor (exo-beta 1,3 glucanase) (1,3-beta-D-glucanohydrolase) ; (L48994) exo-beta 1,3 glucanase [Cochliobolus carbonum] "
23538	ENU07332	ANI61C8567: 4390..6002	29-51	734-758	LINAP		g2388984	317	66	3.00E-10	31	25	(Z98980) hypothetical protein [Schizosaccharomyces pombe]

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23539	ENU07333	ANI61C8567: 1381..3558	22-44	810-829	LINAP	g2388584	g2388584	133	35	0.61			(AC000098) EST gb ATTS1136 comes from this gene. [Arabidopsis thaliana]
23540	ENU07334	ANI61C8572: 30-49 5330..6141	22-44	767-791	LINAP	g2507070	g2507070	236	91	8.00E-18	29	50	N amino acid transport system protein (methylcryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
23541	ENU07335	ANI61C8570: 28-55 3897..3529	28-55	436-457	LINAP	g1351653	g1351653	160	100	6.00E-21			hypothetical 103.2 KD protein C24B11.10C in chromosome I ; hypothetical protein SPAC24B11.10c - fission yeast (Schizosaccharomyces pombe) ; (Z67757) unknown [Schizosaccharomyces pombe]
23542	ENU07336	ANI61C8596: 22-43 3531..2592	22-43	806-827	LINAP	g1351714	g1351714	85	87	1.00E-16			putative transporter C11D3.18C ; (Z68166) unknown [Schizosaccharomyces pombe]
23543	ENU07337	ANI61C8593: 22-48 2431..3221	22-48	748-769	LINAP	g731532	g731532	813	164	2.00E-72	54	30	putative 90.2 KD zinc finger protein in CCA1-ADK2 intergenic region ; hypothetical protein YER169w - yeast (Saccharomyces cerevisiae) ; (U18922) Yer169wp [Saccharomyces cerevisiae] probable protein-tyrosine phosphatase YBR276C ; probable protein-tyrosine-phosphatase (EC 3.1.3.48) - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2013-ORF [Saccharomyces cerevisiae] ; (Z36145) ORF YBR276c [Saccharomyces cerevisiae] ; ORF YBR2013 [Saccharomyces cerevisiae]
23544	ENU07338	ANI61C8552: 31-51 516..1	31-51	391-413	LINAP	g586390	g586390	99	89	2.00E-17	36	16	

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23545	ENU07339	ANI61C8585: 23-47 6129..7445	23-47	775-794	LINAP		g114301	877	269	2.00E-71	61	25	calcium-transporting ATPase 1 (GOLGI CA2+-ATPase); Ca2+-transporting ATPase (EC 3.6.1.38) PMR1 - yeast (Saccharomyces cerevisiae); (M25488) PMR1 protein [Saccharomyces cerevisiae]; (X85757) calcium transporting ATPase 1 [Saccharomyces cerevisiae]; (Z72690) ORF YGL167c [Saccharomyces cerevisiae]
23546	ENU07340	ANI61C86:53 23-46 0..4337	23-46	768-787	LINAP		g4107308	1329	106	3.00E-22	29	18	(AL035075) hypothetical TPR domain-containing protein [Schizosaccharomyces pombe]
23547	ENU07341	ANI61C8621: 56-75 3687..3212	56-75	406-425	LINAP		g1708909	184	100	7.00E-21	30	35	malic acid transport protein (malate permease); C4-dicarboxylate transport protein mae1 - fission yeast (Schizosaccharomyces pombe); (U21002) malic acid transport protein [Schizosaccharomyces pombe]
23548	ENU07342	ANI61C8630: 41-61 584..1	41-61	456-475	LINAP		g1934614	139	106	1.00E-22	33	17	(U93874) cytochrome P450 102 [Bacillus subtilis]; (Z99117) similar to cytochrome P450 / NADPH-cytochrome P450 reductase [Bacillus subtilis]
23549	ENU07343	ANI61C864:1 39-59 ..337	39-59	296-315	LINAP		g119830	105	62	0.000000 001			"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41]; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum; (M37461) FAS2 protein [Penicillium patulum]" (AJ223999) PCZA363.3 [Amycolatopsis orientalis]
23550	ENU07344	ANI61C8641: 52-71 396..894	52-71	456-477	LINAP		g2894188	81	42	0.000002			hypothetical 54.3 KD TRP-ASP repeats containing protein C17H9.19C in chromosome I; (L75944) WD repeat protein [Schizosaccharomyces pombe]; (Z98597) beta-transducin [Schizosaccharomyces pombe]
23551	ENU07345	ANI61C8625: 72-92 1107..2494	72-92	789-808	LINAP		g3219975	283	87	1.00E-16	33	41	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23552	ENU07346	ANI61C1037 4:3791..4541	48-67	703-730	LINAP		g3876092	350	108	1.00E-35	43	30	Similarity to Drosophila white protein (SW:WHIT_DROME); cDNA EST EMBL:M89346 comes from this gene; cDNA EST yk311f2.3 comes from this gene; cDNA EST yk311f2.5 comes from this gene [Caenorhabditis elegans]
23553	ENU07347	ANI61C1038 3:4832..4388	22-49	458-476	LINAP		g2131767	116	55	0.000000 4	37	62	hypothetical protein YLR074c - yeast (Saccharomyces cerevisiae); (Z73246) ORF YLR074c [Saccharomyces cerevisiae]
23554	ENU07348	ANI61C1040 7:1418..1956			LINAP		g1346782	1092	201	2.00E-51			Serine/threonine protein phosphatase PP-X isozyme 1; phosphoprotein phosphatase (EC 3.1.3.16) X-1 (clone EP129) - Arabidopsis thaliana; (Z22587) protein phosphatase [Arabidopsis thaliana]; (AF030289) protein phosphatase X isoform 1 [Arabidopsis thaliana]; (AL035440) phosphoprotein phosphatase (PPX-1) [Arabidopsis thaliana]
23555	ENU07349	ANI61C1040 2:2381..2038	22-46	449-468	LINAP		g1078089	98	52	0.000004	26	33	hypothetical protein YLR423c - yeast (Saccharomyces cerevisiae); (U20939) Ylr423cp [Saccharomyces cerevisiae]
23556	ENU07350	ANI61C43:32 06..147	31-51	771-793	LINAP		g729230	1899	86	4.00E-25	24	20	chromosome segregation protein CUT3; cut3 protein - fission yeast (Schizosaccharomyces pombe); (D30788) cut3 protein [Schizosaccharomyces pombe]
23557	ENU07351	ANI61C1041 4:1..857			LINAP		g544369	474	200	9.00E-51	40	46	General amino-acid permease GAP1; amino acid transport protein GAP1 - yeast (Saccharomyces cerevisiae); (Z28264) ORF YKR039w [Saccharomyces cerevisiae]
23558	ENU07352	ANI61C1040 4:5613..5130	59-86	436-463	LINAP		g1166378	135	94	4.00E-19	31	14	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
23559	ENU07353	ANI61C1041 3:1682..783	22-42	802-829	LINAP		g626598	394	111	3.00E-36	42	53	hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae); (U10400) Ysc84p [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23560	ENU07354	ANI61C1041 3:2409..2019	51-70	457-479	LINAP		g4538664	180	71	7.00E-12	32	91	(AL049474) hypothetical protein [Schizosaccharomyces pombe]
23561	ENU07355	ANI61C4342: 1104..1732	22-48	588-608	LINAP		g2645229	241	87	5.00E-23	37	41	(U78597) kinesin light chain [Plectonema boryanum]
23562	ENU07356	ANI61C1041 0:3562..3158	45-64	363-382	LINAP		g1055333	111	68	6.00E-11	25	23	(U38821) pig1 [Magnaporthe grisea]
23563	ENU07357	ANI61C4349: 1384..628	22-47	714-733	LINAP		g2506204	265	94	2.00E-24	38	68	hypothetical 33.4 KD protein in MOEA-GRXA intergenic region precursor ; (AE000185) putative asparaginase [Escherichia coli] ; (D90720) Hypothetical protein in moeA-grxA intergenic region precursor . [Escherichia coli] ; (D90721) Hypothetical protein in moeA-grxA intergenic region precursor . [Escherichia coli]
23564	ENU07358	ANI61C1042 5:2784..2396	45-64	425-446	LINAP		g3025094	314	138	1.00E-32	51	50	hypothetical 32.5 KD protein in MSH6-BMH2 intergenic region ; thioredoxin homolog YDR098c - yeast (Saccharomyces cerevisiae) ; (Z47746) probable thioredoxin [Saccharomyces cerevisiae]
23565	ENU07359	ANI61C1040 9:4217..4878	24-43	616-635	LINAP		g1711596	212	134	7.00E-31	36	28	putative sulfate transporter YPR003C ; probable membrane protein YPR003c - yeast (Saccharomyces cerevisiae) ; (Z48951) unknown [Saccharomyces cerevisiae] ; (U31900) Lpz3p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae] (AF024618) cyclin H [Drosophila melanogaster]
23566	ENU07360	ANI61C1043: 2600..3276	22-47	602-621	LINAP		g2570798	222	53	0.000000	30	51	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
23567	ENU07361	ANI61C1038 8:9158..8406	47-65	684-703	LINAP		77				25		
23568	ENU07362	ANI61C433:5 523..6762	47-66	805-829	LINAP		g2497056	613	131	2.00E-46	44	57	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23569	ENU07363	ANI61C4387: 415..1	22-49	455-474	LINAP		g3169083	124	84	7.00E-16	37	42	(AL023705) hypothetical protein
23570	ENU07364	ANI61C4384: 1566..2087	67-86	468-487	LINAP		g3023956	166	76	2.00E-13	36	11	[Schizosaccharomyces pombe] vegetative incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina] (AL035159) putative oxidoreductase [Mycobacterium leprae] (Z99113) polyketide synthase [Bacillus subtilis] (U68040) polyketide synthase [Cochliobolus heterostrophus] (X89442) peptidase synthetase [Metarhizium anisopliae] (AL031825) putative membrane transport protein [Schizosaccharomyces pombe]
23571	ENU07365	ANI61C1043 4:4998..4685	70-89	320-339	LINAP		g4154042	123	65	3.00E-10	34	33	lipase 5 precursor ; triacylglycerol lipase (EC 3.1.1.3) 5 precursor - yeast (Candida rugosa) (AJ224324) cp31BHv [Hordeum vulgare] (AF016585) polyketide synthase module 6 [Streptomyces caelestis] alpha-glucosidase (maltase) ; (AF042494) alpha-glucosidase [Sulfolobus solfataricus] (Z98602) putative protein transport protein sec7 homolog [Schizosaccharomyces pombe] DNAJ protein ; heat shock protein dnaJ - Clostridium acetobutylicum ; (X69050) DnaJ [Clostridium acetobutylicum] (AB008771) beta-N-Acetylglucosaminidase [Streptomyces thermoviolaceus] (AL023517) putative secreted protease [Streptomyces coelicolor]
23572	ENU07366	ANI61C436:3 921..3166	38-57	689-708	LINAP		g2634106	189	121	6.00E-27	29	9	
23573	ENU07367	ANI61C436:6 570..5307	29-48	804-823	LINAP		g1546072	275	211	6.00E-54	43	10	
23574	ENU07368	ANI61C4410: 1381..3045	22-47	782-801	LINAP		g2342601	1238	213	9.00E-55	36	5	
23575	ENU07369	ANI61C4402: 2740..3699	95-114	726-745	LINAP		g3702646	193	68	3.00E-19			
23576	ENU07370	ANI61C4429: 1..704	110-137	645-664	LINAP		g417253	136	73	3.00E-12	41	24	
23577	ENU07371	ANI61C1046 4:1629..1300	48-73	449-468	LINAP		g3550483	80	54	0.000000			
23578	ENU07372	ANI61C4444: 602..208	22-44	454-479	LINAP		g2558841	172	99	2.00E-20	41	8	
23579	ENU07373	ANI61C1044 1:3768..4364	51-70	508-527	LINAP		g3912992	122	92	3.00E-18			
23580	ENU07374	ANI61C4446: 1415..392	25-45	719-743	LINAP		g2440190	372	78	1.00E-29	36	15	
23581	ENU07375	ANI61C1045 1:2702..2370	23-46	442-461	LINAP		g1169369	40	50	0.00001	35	23	
23582	ENU07376	ANI61C1100 0:2307..3900	22-45	804-827	LINAP		g3426176	354	52	0.000004			
23583	ENU07377	ANI61C1104 2:1321..657	109-128	622-644	LINAP		g3130007	147	43	0.002			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23584	ENU07378	ANI61C4476: 258..558	36-57	277-300	LINAP		g4097335	89	47	0.00009	36	50	(U57524) I kappa B alpha [Mus musculus]
23585	ENU07379	ANI61C1104 0:1..460	47-70	401-419	LINAP		g1708078	81	50	0.00001	28	7	"endoglucanase A precursor (endo-1,4-beta-glucanase A) (cellulase A) ; (L32742) cellulase [Caldocellum saccharolyticum] "
23586	ENU07380	ANI61C4496: 1..886	112-131	804-829	LINAP		g4503355	109	104	8.00E-22	26	15	dedicator of cyto-kinesis 1 ; (D50857) DOCK180 protein [Homo sapiens] (AC005966) Similar to gi 2829865 F3I6.4 from Arabidopsis thaliana BAC gb AC002396. [Arabidopsis thaliana] (AB010810) phospholipase D [Candida albicans]
23587	ENU07381	ANI61C1046 2:4242..4589	36-59	457-479	LINAP		g4249377	124	42	0.000000	37	25	"methionyl-TRNA synthetase, cytoplasmic (methionine--TRNA ligase) (METRS) ; methionine--TRNA ligase (EC 6.1.1.10), cytosolic - yeast (Saccharomyces cerevisiae) ; (Z73049) ORF YGR264c [Saccharomyces cerevisiae] ; (Y07777) methionine--tRNA ligase [Saccharomyces cerevisiae] "
23588	ENU07382	ANI61C439:1..473	130-157	432-452	LINAP		g3413518	417	118	3.00E-26	37	9	retrograde regulation protein 2 ; RTG2 protein - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRF588; EMBL:SCRTG2X:M97691; PIR:B44344;B44344 [Saccharomyces cerevisiae] ; (M97691) Rtg2p [Saccharomyces cerevisiae] ; (Z72774) ORF YGI.252c [Saccharomyces cerevisiae]
23589	ENU07383	ANI61C1102 9:4141..4735	22-49	501-525	LINAP		g1711639	663	275	2.00E-73	72	23	molybdopterin biosynthesis CNX1 protein (molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] ; (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]
23590	ENU07384	ANI61C45:1..535	102-122	404-423	LINAP		g1710803	150	52	1.00E-12	36	29	
23591	ENU07385	ANI61C1046 8:1..831	102-125	782-803	LINAP		g2497953	347	143	3.00E-37	45	37	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23592	ENU07386	ANI61C45:15 62..1195	22-49	454-479	LINAP		g1911486	159	45	0.000000	38	38	"(S80872) putative Tc1-mariner class transposase/IS630-Tc1 homolog [Aspergillus niger, chlorate-resistant mutant 46, transposon Ant1, Peptide Transposon, 325 aa] [Aspergillus niger]"
23593	ENU07387	ANI61C4537: 40-59 1259..2507	40-59	805-825	LINAP		g2132480	553	124	9.00E-28	43	33	probable membrane protein YDR205w - yeast (Saccharomyces cerevisiae) ; (Z68194) unknown [Saccharomyces cerevisiae]
23594	ENU07388	ANI61C1046 5:2048..718	22-42	800-827	LINAP		g2131433	692	244	7.00E-64	44	40	hypothetical protein YDR332w - yeast (Saccharomyces cerevisiae) ; (U32517) Ydr332wp [Saccharomyces cerevisiae]
23595	ENU07389	ANI61C4532: 22-48 2747..726	22-48	810-829	LINAP		g3913674	217	46	0.0002			Fer1 reductase transmembrane component 3 precursor ; probable membrane protein YOR381w - yeast (Saccharomyces cerevisiae) ; (Z75289) ORF YOR381w [Saccharomyces cerevisiae]
23596	ENU07390	ANI61C1046 5:7103..6296	26-45	764-783	LINAP		g4220848	609	169	7.00E-48	49	16	(AF033823) moira [Drosophila melanogaster]
23597	ENU07391	ANI61C4588: 55-79 413..1	55-79	452-479	LINAP		g2131783	706	88	3.00E-26	46	31	hypothetical protein YLR116w - yeast (Saccharomyces cerevisiae) ; (U53877) Ylr116wp [Saccharomyces cerevisiae] ; (X89514) putative orf [Saccharomyces cerevisiae] ; (Z73288) ORF YLR116w [Saccharomyces cerevisiae]
23598	ENU07392	ANI61C1047 8:2773..3779	24-42	801-828	LINAP		g121967	81	33	2.3			histone H2A.1 ; histone H2A.1 - yeast (Saccharomyces cerevisiae) ; (V01304) histone H2A1 [Saccharomyces cerevisiae] ; (U13239) histone H2A1 [Saccharomyces cerevisiae] ; (Z48612) H2a1p [Saccharomyces cerevisiae]
23599	ENU07393	ANI61C5459: 178-202 1128..550	178-202	535-558	LINAP		g2440180	187	37	0.13			(Z99531) ubiquitin system protein [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23600	ENU07394	ANI61C1103 2:6045..6458	68-95	455-479	LINAP		g1710802	121	75	3.00E-13	35	45	RTA1 protein ; RTA1 protein - yeast (Saccharomyces cerevisiae) ; (Z72998) ORF YGR213c [Saccharomyces cerevisiae] ; (X84736) RTA1 [Saccharomyces cerevisiae] (AB025252) reverse transcriptase [Magnaporthe grisea] (U43704) ketoreductase [Streptomyces sp. C5] (AC004392) Contains similarity to gb U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus. [Arabidopsis thaliana] (AF111172) lysosomal pepstatin insensitive protease precursor [Mus musculus] Transmission-blocking target antigen S230 precursor ; transmission-blocking target antigen Pfs230 - Plasmodium falciparum ; (L08135) Pfs230 [Plasmodium falciparum] ; (L04162) s230 [Plasmodium falciparum] ; (AE001393) transmission blocking target antigen PfS230 [Plasmodium falciparum] (AL021046) putative mitotic spindle protein [Schizosaccharomyces pombe] "Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1 ; (L43920) microsomal omega-6 desaturase [Glycine max] " lymphocyte specific helicase - mouse ; (U25691) lymphocyte specific helicase [Mus musculus]
23601	ENU07395	ANI61C532:4 143..3695	22-46	457-479	LINAP		g4586458	133	89	2.00E-17	32	57	
23602	ENU07396	ANI61C1103 5:2574..3119	22-49	499-525	LINAP		g1163927	108	75	3.00E-13			
23603	ENU07397	ANI61C532:1 1195..11988	22-49	750-773	LINAP		g3367519	96	72	4.00E-12	30	20	
23604	ENU07398	ANI61C4578: 2040..1151	62-88	810-829	LINAP		g4106913	285	46	0.00005	33	17	
23605	ENU07399	ANI61C5492: 1..785	51-70	716-735	LINAP		g730413	118	52	0.000004			
23606	ENU07400	ANI61C5469: 1442..576	22-48	803-829	LINAP		g2706463	297	125	4.00E-28	27	19	
23607	ENU07401	ANI61C1107 5:2077..2843	23-49	689-706	LINAP		g1345976	371	187	8.00E-47	44	59	
23608	ENU07402	ANI61C4539: 3779..5452	22-49	809-829	LINAP		g2137490	700	266	1.00E-70	50	44	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23609	ENU07403	ANI61C5517: 24-47 876..1	24-47	776-798	LINAP		g1346360	638	201	3.00E-54	53	43	probable serine/threonine-protein kinase C24B11.11C; hypothetical protein SPAC24B11.11c - fission yeast (Schizosaccharomyces pombe) ; (Z67757) unknown
23610	ENU07404	ANI61C1048 2:2761..4048	22-49	810-829	LINAP		g1168808	446	155	5.00E-37	39	40	[Schizosaccharomyces pombe] cell division control protein 18 ; cell division control protein CDC18+ - fission yeast (Schizosaccharomyces pombe) ; (L16793) cell division cycle protein [Schizosaccharomyces pombe] ; (AL022305) cell division control protein 18 [Schizosaccharomyces pombe]
23611	ENU07405	ANI61C4614: 57-83 1..458	57-83	411-437	LINAP		g4063383	174	61	7.00E-10	53	30	(AF096285) serine-threonine kinase receptor-associated protein [Mus musculus]
23612	ENU07406	ANI61C5521: 22-45 455..1028	22-45	360-379	LINAP		g586352	474	137	1.00E-44	56	15	hypothetical 124.0 KD protein in PCS60-ABD1 intergenic region ; probable membrane protein YBR235w - yeast (Saccharomyces cerevisiae) ; (Z36104) ORF YBR235w [Saccharomyces cerevisiae]
23613	ENU07407	ANI61C4601: 55-72 330..1	55-72	444-463	LINAP		g3023267	109	61	0.000000	37	10	alpha-glucosidase precursor (maltase) ; (D45356) alpha-glucosidase [Aspergillus niger]
23614	ENU07408	ANI61C5535: 22-40 388..982	22-40	550-574	LINAP		g4104775	96	57	0.000000	31	37	(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
23615	ENU07409	ANI61C4618: 45-64 887..481	45-64	431-453	LINAP		g1723476	204	99	2.00E-20	47	57	hypothetical 22.2 KD protein C17G8.03C in chromosome I ; (Z69795) unknown
23616	ENU07410	ANI61C1049 4:3226..2619	116-135	469-488	LINAP		g4493697	43	71	9.00E-12			[Schizosaccharomyces pombe] (Y18863) Pop4 protein [Homo sapiens]
23617	ENU07411	ANI61C5529: 36-55 1940..700	36-55	801-828	LINAP		g2342601	95	59	0.000000			(X89442) peptide synthetase [Metarhizium anisopliae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23618	ENU07412	ANI61C1106 5:6587..6241	37-56	456-475	LINAP		g3219959	211	128	3.00E-29	47	32	"probable zinc metallopeptidase C17A5.04C precursor ; (Z98849) probable zinc metallopeptidase, disintegrin [Schizosaccharomyces pombe] "
23619	ENU07413	ANI61C8968: 22-48 932..2028	22-48	809-828	LINAP		g2501739	204	123	1.00E-27	31	19	"putative 151.3 KD transcriptional regulatory protein ; probable membrane protein YLR278c - yeast (Saccharomyces cerevisiae) ; (U17243) Serine, glutamine, asparagine rich central portion of protein [Saccharomyces cerevisiae] "
23620	ENU07414	ANI61C1108: 26-49 3803..3001	26-49	760-782	LINAP		g3334796	217	131	5.00E-30	34	52	(AL031107) putative secreted glucosidase [Streptomyces coelicolor] (AB018321) KIAA0778 protein [Homo sapiens]
23621	ENU07415	ANI61C4622: 37-57 210..1318	37-57	657-678	LINAP		g3882277	259	112	3.00E-24	37	38	[AL031536] fnx1p. [Schizosaccharomyces pombe]
23622	ENU07416	ANI61C5567: 22-44 1..1008	22-44	805-829	LINAP		g3560207	275	141	6.00E-33			[U66283] dihydropteroate synthase [Pneumocystis carinii f. sp. muris] (Z99708) putative protein [Arabidopsis thaliana]
23623	ENU07417	ANI61C893:5 38-57 964..4504	38-57	800-827	LINAP		g2270900	869	235	2.00E-61	48	97	(Y09899) sensory histidine protein kinase [Calothrix viguieri]
23624	ENU07418	ANI61C1110 3:331..652			LINAP		g4006889	72	49	0.00002	33	32	pyrroline-5-carboxylate reductase (P5CR) (P5C reductase) ; pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Zalerion arboricola ; (U33266) pyrroline carboxylate reductase [Zalerion arboricola]
23625	ENU07419	ANI61C1051 22-43 3:446..782	22-43	456-475	LINAP		g2765035	106	69	2.00E-11	38	12	(AB010714) salicylate hydroxylase [Pseudomonas putida]
23626	ENU07420	ANI61C1111 22-49 0:2185..1270	22-49	794-813	LINAP		g3024443	362	149	3.00E-35	34	82	(AL009197) hypothetical ubiquitin conjugating enzyme [Schizosaccharomyces pombe] (Z82044) hypothetical 54.4 kd protein [Bacillus subtilis]
23627	ENU07421	ANI61C1047 22-42 7:2007..3198	22-42	809-829	LINAP		g2826168	224	109	2.00E-23	31	64	
23628	ENU07422	ANI61C5574: 23-50 2915..3635	23-50	678-699	LINAP		g2661610	436	168	1.00E-43	49	90	
23629	ENU07423	ANI61C1107 25-44 3:2565..3336	25-44	717-736	LINAP		g1673402	118	47	0.000000	30	46	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23630	ENU07424	ANI61C1047 7:9261..10917	22-45	660-679	LINAP		g3023956	1264	282	5.00E-81	54	20	vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [Podospora anserina]
23631	ENU07425	ANI61C558:1 ..424	36-63	366-385	LINAP		g11166378	109	66	1.00E-10	34	12	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata] "
23632	ENU07426	ANI61C1107 3:8638..9147	35-54	460-487	LINAP		g1150442	134	81	5.00E-15			"(Z46869) exo-1,3-beta-glucanase/1,3-beta-D-Glucan glucanohydrolase [Kluyveromyces lactis] "
23633	ENU07427	ANI61C1050 9:2651..3170	54-73	387-406	LINAP		g2462678	108	34	0.003	32	40	(Z99568) recombinational dna repair protein rhp55p. [Schizosaccharomyces pombe] ; (AF053410) recombinational DNA repair protein Rhp55p [Schizosaccharomyces pombe]
23634	ENU07428	ANI61C5640: 527..17	22-49	335-357	LINAP		g1352987	275	121	3.00E-27	40	41	BTN1 protein ; probable membrane protein YJL059w - yeast (Saccharomyces cerevisiae) ; (Z49334) ORF YJL059w [Saccharomyces cerevisiae]
23635	ENU07429	ANI61C8997: 1040..656	48-70	314-333	LINAP		g3901117	193	92	1.00E-18	38	20	(AJ012752) maltose permease [Saccharomyces cerevisiae]
23636	ENU07430	ANI61C4607: 2725..2293	35-55	426-445	LINAP		g2959337	95	61	0.000000	23	71	(AJ224767) hypothetical protein [Acinetobacter sp. ADP1]
23637	ENU07431	ANI61C5576: 5415..4439	50-69	799-817	LINAP		g2645229	365	150	9.00E-36	35	49	(U78597) kinesin light chain [Plectonema boryanum]
23638	ENU07432	ANI61C1109 9:2053..2776	38-57	680-703	LINAP		g3184386	149	35	0.66			(AF043102) surface glycoprotein A [Pneumocystis carinii]
23639	ENU07433	ANI61C4629: 1396..180	22-46	620-643	LINAP		g2414656	613	191	4.00E-48	38	55	(Z99261) putative aminotransferase [Schizosaccharomyces pombe]
23640	ENU07434	ANI61C5639: 695..384	87-111	308-332	LINAP		g2555098	234	58	0.000000	45	27	(AF019407) GTP-binding protein [Caulobacter crescentus]
23641	ENU07435	ANI61C1109 9:4414..4960	22-40	464-483	LINAP		g3489	204	62	0.000000	36	79	(X03449) unidentified reading frame [Saccharomyces cerevisiae]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23642	ENU07436	ANI61C1051 5:1440..1	22-47	721-740	LINAP		g2498346	1342	351	4.00E-96	59	44	probable electron transfer flavoprotein-ubiquinone oxidoreductase precursor (ETF-QO) (ETF-ubiquinone oxidoreductase) (ETF dehydrogenase) (electron-transferring-flavoprotein dehydrogenase) ; hypothetical protein YOR356w - yeast (Saccharomyces cerevisiae) ; (Z75264) ORF YOR356w [Saccharomyces cerevisiae]
23643	ENU07437	ANI61C460:5 253..4307	22-48	805-827	LINAP		g2133702	326	93	3.00E-28			phosphorylase kinase (EC 2.7.1.38) gamma chain - fruit fly (Drosophila melanogaster) ; (U13014) phosphorylase kinase gamma [Drosophila melanogaster] (Y17317) polyketide synthase [Aspergillus fumigatus]
23644	ENU07438	ANI61C4647: 49-67 1379..1	22-42	762-780	LINAP		g3163925	307	114	7.00E-25	29	13	Diatom spindle kinesin 1 ; (U51680) diatom spindle kinesin 1 [Cylindrotheca fusiformis] (Z35639) cDNA EST CEMSD23F comes from this gene; cDNA EST CEESE24F comes from this gene; cDNA EST EMBL:D33683 comes from this gene; cDNA EST EMBL:D36566 comes from this gene; cDNA EST EMBL:D36682 comes from this gene; cDNA EST ... (X69481) GTPase [Saccharomyces cerevisiae]
23645	ENU07439	ANI61C1051 1:2645..2166	22-42	453-479	LINAP		g2497529	113	65	4.00E-10	38	21	(AC004684) putative ribitol dehydrogenase [Arabidopsis thaliana]
23646	ENU07440	ANI61C8980: 22-45 3812..2877	22-45	776-795	LINAP		g4008344	153	39	0.054			
23647	ENU07441	ANI61C5655: 46-65 636..1524	46-65	625-644	LINAP		g4006	289	129	3.00E-29	32	49	
23648	ENU07442	ANI61C1113 0:977..541	23-42	457-479	LINAP		g3236237	53	47	0.00007			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23649	ENU07443	ANI61C5641: 23-42 2234..1359	23-42	806-828	LINAP		g1175036	188	99	5.00E-20	35	52	"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase) / alpha-L-arabinofuranosidase (arabinosidase) ; xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Butyrivibrio fibrisolvens ; (M55537) beta-D-xylosidase/alpha-L-arabinofuranosidase [Butyrivibrio fibrisolvens] "
23650	ENU07444	ANI61C8978: 46-65 1484..1879	46-65	457-479	LINAP		g1377890	65	61	0.000000			(L77083) cdc2 gene product [Nicotiana tabacum]
23651	ENU07445	ANI61C1051 22-47 1:3430..2845	22-47	532-551	LINAP		g2978452	96	73	2.00E-12			(AE001274) MCAK; L549.3 [Leishmania major]
23652	ENU07446	ANI61C4646: 23-42 3587..2915	23-42	626-652	LINAP		g543754	212	85	4.00E-16	40	29	acetylcholinesterase precursor (ACHE)
23653	ENU07447	ANI61C1110 34-53 0:3330..2673	34-53	611-630	LINAP		g1352996	184	79	7.00E-20	38	24	hypothetical 68.8 KD protein in EXO70-ARP4 intergenic region ; hypothetical protein YJL083w - yeast (Saccharomyces cerevisiae) ; (X88851) hypothetical protein [Saccharomyces cerevisiae] ; (X83502) J1002 [Saccharomyces cerevisiae] ; (Z49358) ORF YJL083w [Saccharomyces cerevisiae]
23654	ENU07448	ANI61C8986: 22-42 2620..3097	22-42	457-477	LINAP		g731862	82	75	3.00E-13	34	10	"Nucleoporin NUP159 (nuclear pore protein NUP159) ; nucleoporin RAT7 - yeast (Saccharomyces cerevisiae) ; (Z38125) orf, len: 1460,CAI: 0.15 [Saccharomyces cerevisiae] ; (L40634) nucleoporin [Saccharomyces cerevisiae] "
23655	ENU07449	ANI61C1052 161-182 5:5633..4932	161-182	639-658	LINAP		g1172047	107	79	3.00E-14	34	33	Lysosomal pro-X carboxypeptidase precursor (prolylcarboxypeptidase) (PRCP) (proline carboxypeptidase) (angiotensinase C) (lysosomal carboxypeptidase C) ; lysosomal Pro-X carboxypeptidase (EC 3.4.16.2) - human ; (L13977) prolylcarboxypeptidase [Homo sapiens]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23656	ENU07450	ANI61C5629: 3467..1943	23-43	806-828	LINAP	g3121733	1250	243	2.00E-66	56	34	"aconitate hydratase, mitochondrial precursor (citrate hydro-lyase) (aconitase) ; (Z98601) aconitate hydratase. [Schizosaccharomyces pombe] "	
23657	ENU07451	ANI61C1055: 871..104	22-43	580-602	LINAP	g3925783	538	237	6.00E-62	52	55	(AL034353) glutamate n-acetyltransferase precursor [Schizosaccharomyces pombe]	
23658	ENU07452	ANI61C459:1 002..1	27-46	801-828	LINAP	g2119802	366	105	4.00E-36	37	40	probable membrane protein YDL247w - yeast (Saccharomyces cerevisiae) ; (Z74295) ORF YDL247w [Saccharomyces cerevisiae]	
23659	ENU07453	ANI61C9012: 1882..1172	22-47	665-684	LINAP	g541082	164	77	1.00E-13	36	63	GutQ homolog - Escherichia coli	
23660	ENU07454	ANI61C1116 3:4552..3479	197-216	777-796	LINAP	g3738162	549	203	1.00E-51	49	53	(AL031856) putative involvement in protein glycosylation in the golgi [Schizosaccharomyces pombe]	
23661	ENU07455	ANI61C1054 5:677..283	23-43	413-432	LINAP	g2494853	43	59	0.000000	02		probable hydroxyacylglutathione hydrolase (glyoxalase II) (GLX II) ; (D83536) unknown [Escherichia coli] ; (U70214) hypothetical protein [Escherichia coli] ; (AE000130) probable hydroxyacylglutathione hydrolase [Escherichia coli]	
23662	ENU07456	ANI61C4681: 1354..669	49-73	524-546	LINAP	g4514622	222	109	2.00E-23	37	61	(AB011211) pectin methylesterase [Aspergillus oryzae]	
23663	ENU07457	ANI61C9019: 1260..397	22-49	690-714	LINAP	g3560143	481	198	3.00E-51	58	42	(AL031534) putative vacuolar protein sorting-associated protein [Schizosaccharomyces pombe]	
23664	ENU07458	ANI61C1115: 1340..3049	59-81	808-829	LINAP	g1346099	1100	197	8.00E-50	47	45	Glycolipid anchored surface protein precursor (glycoprotein GP115) ; glycopospholipid-anchored surface glycoprotein GAS1 precursor - yeast (Saccharomyces cerevisiae) ; (X56399) glycoprotein gp115 [Saccharomyces cerevisiae] ; (Z49212) Gas1p [Saccharomyces cerevisiae]	

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23665	ENU07459	ANI61C4696: 101-123 1134..477	101-123	612-637	LINAP		g731945	129	80	1.00E-14	30	23	putative 86.7 KD transcriptional regulatory protein in NUC1-NCE1 intergenic region ; finger protein YJL206c - yeast (Saccharomyces cerevisiae) ; (X77688) hypothetical protein J0316 [Saccharomyces cerevisiae] ; (Z49481) ORF YJL206c [Saccharomyces cerevisiae]
23666	ENU07460	ANI61C4709: 532..1			LINAP		g1705462	125	68	6.00E-12	37	26	"adenosylmethionine-8-amino-7-oxonanoate aminotransferase (7,8-diamino-pelargonic acid aminotransferase) (DAPA aminotransferase) ; BIO3 protein - yeast (Saccharomyces cerevisiae) ; (Z71673) ORF YNR058w [Saccharomyces cerevisiae] "
23667	ENU07461	ANI61C5635: 43-70 1715..495	43-70	794-817	LINAP		g1084961	197	41	7.00E-11			lipase - yeast (Geotrichum candidum) ; (U02387) lipase [Geotrichum candidum] ; lipase I [Galactomyces geotrichum]
23668	ENU07462	ANI61C1050 27-54 5:9182..10097	27-54	809-828	LINAP		g3915140	306	78	1.00E-13	32	37	isotrichodermin C-15 hydroxylase (cytochrome P450 65A1) ; (AF011355) isotrichodermin C-15 hydroxylase [Fusarium sporotrichioides]
23669	ENU07463	ANI61C464:4 48-67 64..1102	48-67	577-596	LINAP		g130784	68	72	4.00E-12			Pyrimidine pathway regulatory protein 1 ; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae) ; (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae] ; (Z73186) ORF YLR014c [Saccharomyces cerevisiae]
23670	ENU07464	ANI61C464:5 44-71 802..6738	44-71	805-829	LINAP		g1171129	104	81	9.00E-15	25	10	(U24657) saframycin Mx1 synthetase A [Myxococcus xanthus]
23671	ENU07465	ANI61C1476: 22-41 2762..1351	22-41	805-823	LINAP		g4507551	177	76	3.00E-13	32	16	transmembrane protein 1 ; epilepsy holoprosencephaly candidate-1 protein (EHOC-1) (transmembrane protein 1) ; probable transmembrane protein - human ; (U19252) putative transmembrane protein [Homo sapiens]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23672	ENU07466	ANI61C9001: 38-64 3362..1	38-64	804-828	LINAP		g1834342	3543	329	e-119	76	19	(Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
23673	ENU07467	ANI61C1476: 5187..4809			LINAP		g3859670	154	82	2.00E-15	38	19	(AL033502) hypothetical membrane protein [Candida albicans]
23674	ENU07468	ANI61C5635: 66-85 4748..4091	66-85	614-637	LINAP		g544191	144	67	3.00E-18	41	25	protein kinase DSK1 (DIS1-suppressing protein kinase); dis1-suppressing protein kinase dsk1 - fission yeast (Schizosaccharomyces pombe); (D13447) protein kinase [Schizosaccharomyces pombe]
23675	ENU07469	ANI61C1115 49-68 7:5462..5836	49-68	458-479	LINAP		g417770	328	143	1.00E-33	45	21	zinc finger protein SFPI1; split zinc finger protein 1 - yeast (Saccharomyces cerevisiae); (U19729) Sfp1p [Saccharomyces cerevisiae]
23676	ENU07470	ANI61C9031: 30-50 1..938	30-50	806-829	LINAP		g544368	189	91	1.00E-19	29	54	Galactose-proton symport (galactose transporter); (U28377) ORF_o464 [Escherichia coli]; (AE000377) galactose-proton symport of transport system [Escherichia coli] (AL022304) putative galactosyltransferase associated protein kinase [Schizosaccharomyces pombe]
23677	ENU07471	ANI61C1571: 22-49 637..1	22-49	510-536	LINAP		g3006192	649	200	6.00E-51	58	39	probable membrane protein YPL260w - yeast (Saccharomyces cerevisiae); (Z73617) ORF YPL260w [Saccharomyces cerevisiae]
23678	ENU07472	ANI61C4717: 22-48 260..1027	22-48	724-744	LINAP		g2133011	318	99	4.00E-20	45	39	(AL021409) polyketide synthase [Streptomyces coelicolor]
23679	ENU07473	ANI61C5710: 38-57 1706..2075	38-57	426-445	LINAP		g2808753	206	115	3.00E-25	38	7	"hypothetical 78.1 KD protein in TIP20-MRF1 intergenic region; hypothetical protein YGL144c - yeast (Saccharomyces cerevisiae); (Z72666) ORF YGL144c [Saccharomyces cerevisiae]; (X99960) putative, YGL144c [Saccharomyces cerevisiae]"
23680	ENU07474	ANI61C904:5 55-74 30..1	55-74	395-414	LINAP		g1723926	298	115	3.00E-25	48	18	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23681	ENU07475	ANI61C1578: 1..419	22-45	358-377	LINAP		g134968	320	152	9.00E-37	54	25	serine/threonine protein kinase STE7 ; regulatory protein STE7 - yeast (Saccharomyces cerevisiae) ; (M14097) STE7 protein [Saccharomyces cerevisiae] ; (Z67750) regulatory protein STE7 [Saccharomyces cerevisiae] ; (Z74207) ORF YDL159w [Saccharomyces cerevisiae] probable membrane protein YOR320c - yeast (Saccharomyces cerevisiae) ; (X90565) orf 06145 [Saccharomyces cerevisiae] ; (Z75228) ORF YOR320c [Saccharomyces cerevisiae] (AB014885) HrPOPK-1 [Halocynthia roretzi] hypothetical 89.2 KD protein in RAR1-SCJ1 intergenic region ; probable membrane protein YMR212c - yeast (Saccharomyces cerevisiae) ; (Z49809) unknown [Saccharomyces cerevisiae] (AB007927) KIAA0458 protein [Homo sapiens] "glucoamylase S1/S2 precursor (glucan 1,4-alpha-glucosidase) (1,4-alpha-D-glucan glucosylase) ; glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae) ; (Z38061) mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 glucoamylase S1 (EC 3.2.1.3) [Saccharomyces cerevisiae] ; (U30626) glucoamylase [Saccharomyces cerevisiae var. diastaticus] " glycoprotein GP100 precursor (P29F8) ; (L04286) glycoprotein gp100 [Dictyostelium discoideum] (AF059534) severin kinase [Dictyostelium discoideum]
23682	ENU07476	ANI61C9003: 22-48 763..247	22-48	448-467	LINAP		g2132946	156	89	3.00E-17	35	29	
23683	ENU07477	ANI61C1555: 22-47 1..1288	22-47	805-824	LINAP		g3172111	657	185	3.00E-46	43	30	
23684	ENU07478	ANI61C1118 29-56 8:5374..3784	29-56	803-829	LINAP		g2497190	175	38	0.07			
23685	ENU07479	ANI61C4702: 22-47 1643..1059	22-47	532-551	LINAP		g3413878	110	37	0.001			
23686	ENU07480	ANI61C9003: 22-43 5306..7862	22-43	809-828	LINAP		g728850	574	40	0.024			
23687	ENU07481	ANI61C1598: 122-141 800..468	122-141	285-304	LINAP		g544411	71	45	0.0002			
23688	ENU07482	ANI61C1057 22-44 8:603..1764	22-44	805-824	LINAP		g3075511	342	104	2.00E-26	37	45	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23689	ENU07483	ANI61C4702: 3622..3185	25-48	452-479	LINAP	g4499843	131	55	0.000000	3	34	30	(AJ011965) oxidoreductase [Claviceps purpurea]
23690	ENU07484	ANI61C1120 2:242..1069	22-47	752-771	LINAP	g732206	394	101	9.00E-21	41	78		Autophagocytosis protein AUT1; hypothetical protein YNR007c - yeast (Saccharomyces cerevisiae); (X77395) N2040 [Saccharomyces cerevisiae]; (Z71622) ORF YNR007c [Saccharomyces cerevisiae]
23691	ENU07485	ANI61C1059 4:1..1061			LINAP	g1723076	321	71	2.00E-26	35	46		hypothetical 57.3 KD protein GMC-type oxidoreductase CY50.03C; (Z77137) hypothetical protein Rv1279 [Mycobacterium tuberculosis]
23692	ENU07486	ANI61C4730: 953..1	22-41	743-764	LINAP	g2133023	495	208	4.00E-53	39	32		probable membrane protein YPR091c - yeast (Saccharomyces cerevisiae); (U51033) Similar in central region to C. elegans hypothetical protein F55C12.5 (GenBank accession number U41107) [Saccharomyces cerevisiae] (AJ133651) conidiospore surface protein [Trichoderma harzianum] (AB014886) typeII DNA topoisomerase [Emicella nidulans] (AL033127) hypothetical protein [Schizosaccharomyces pombe]
23693	ENU07487	ANI61C9036: 3594..2846	25-44	708-728	LINAP	g4585623	183	39	0.046		17		"beta-xylosidase (1,4-beta-D-xylan xylohydrolase) (xylan 1,4-beta-xylosidase); xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Bacillus pumilus; (X05793) xylan 1,4-beta-xylosidase [Bacillus pumilus]"
23694	ENU07488	ANI61C16:29 5..1437	122-141	744-763	LINAP	g3172113	1741	559	e-159	95	25		(AF030554) class V chitin synthase [Ustilago maydis] (L40632) ankyrin 3 [Mus musculus]
23695	ENU07489	ANI61C1059 3:1..1731	68-87	764-784	LINAP	g3821332	240	98	8.00E-20	29	30		(D90914) beta-glucosidase [Synechocystis sp.]
23696	ENU07490	ANI61C5643: 4851..4395	22-48	452-479	LINAP	g465491	261	68	2.00E-26	46			
23697	ENU07491	ANI61C1118 3:5396..7922	22-47	777-795	LINAP	g2613108	2260	345	e-104	65	24		
23698	ENU07492	ANI61C57:41 8..2193	22-45	808-828	LINAP	g710551	163	78	1.00E-13				
23699	ENU07493	ANI61C1120 3:4450..3389	54-72	786-813	LINAP	g1653521	200	103	1.00E-21	27	51		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23700	ENU07494	ANI61C1059 8:2380..882	22-43	807-829	LINAP		g549643	775	161	1.00E-49	43	29	hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region ; hypothetical protein YKR089c - yeast (Saccharomyces cerevisiae) ; (Z27116) ORF YKR409 [Saccharomyces cerevisiae] ; (Z28314) ORF YKR089c [Saccharomyces cerevisiae] (M94916) ubiquitin-specific processing protease [Saccharomyces cerevisiae] delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5C dehydrogenase) ; (X95584) 1-pyrroline-5-carboxylate dehydrogenase [Agaricus bisporus] (AF107264) glutamate synthase large subunit [Rhizobium etli] Metal homeostatis protein BSD2 ; metal homeostatis protein BSD2 - yeast (Saccharomyces cerevisiae) ; (X76053) YBR2037-ORF [Saccharomyces cerevisiae] ; (L33783) metal homeostatis protein [Saccharomyces cerevisiae] ; (Z36159) ORF YBR290w [Saccharomyces cerevisiae] ; ORF YBR2037 [Saccharomyces cerevisiae] (AL035247) ion transporter [Schizosaccharomyces pombe] pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 ; (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster] hypothetical 47.8 KD protein in HSP26-TTF32 intergenic region ; aminopeptidase Y homolog - yeast (Saccharomyces cerevisiae) ; (X76294) ORF YBRO718 [Saccharomyces cerevisiae] ; (Z35943) ORF YBR074w [Saccharomyces cerevisiae]
23701	ENU07495	ANI61C465:2 478..4468	22-49	804-829	LINAP		g173128	510	123	1.00E-27			
23702	ENU07496	ANI61C5689: 3897..4786	40-59	730-754	LINAP		g2494072	558	150	7.00E-57	48	46	
23703	ENU07497	ANI61C1060 0:2213..2711	36-55	367-387	LINAP		g4038458	230	53	1.00E-14	45	7	
23704	ENU07498	ANI61C465:9 120..9481	64-83	453-479	LINAP		g586358	172	72	2.00E-15			
23705	ENU07499	ANI61C1058 6:2054..1345	29-47	668-688	LINAP		g4164420	644	117	9.00E-26	41	59	
23706	ENU07500	ANI61C4751: 871..1704	34-53	749-773	LINAP		g85105	316	101	5.00E-21	39	13	
23707	ENU07501	ANI61C6475: 1453..2048	22-49	419-438	LINAP		g586511	187	99	6.00E-22	41	43	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23708	ENU07502	ANI61C9037: 22-45 1753..1442	22-45	457-476	LINAP		g3879015	95	52	0.000003	39	100	"(Z81108) similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST EMBL:D73942 comes from this gene; cDNA EST yk257f10.5 comes from this gene; cDNA EST EMBL:D70930 comes from this gene; cDNA EST EMBL:D73476 come..."
23709	ENU07503	ANI61C1611: 46-65 1330..376	46-65	725-746	LINAP		g2131263	873	196	1.00E-77	65	11	GLT1 protein - yeast (Saccharomyces cerevisiae) ; (Z67750) putative protein [Saccharomyces cerevisiae] ; (Z74219) ORF YDL171c [Saccharomyces cerevisiae]
23710	ENU07504	ANI61C6464: 36-54 666..332	36-54	456-479	LINAP		g557084	38	55	0.000000	2		(L35601) ankyrin [Drosophila melanogaster] ; ankyrin [Drosophila melanogaster]
23711	ENU07505	ANI61C9056: 97-116 2136..1496	97-116	595-620	LINAP		g3581879	366	116	1.00E-25	43	21	(AL031540) hypothetical ATP binding protein [Schizosaccharomyces pombe]
23712	ENU07506	ANI61C1557: 22-47 4403..2640	22-47	802-829	LINAP		g116453	720	36	0.35			"sodium channel protein, skeletal muscle alpha-subunit (MU-1) ; sodium channel protein mu1 alpha chain, skeletal muscle - rat ; (M26643) voltage-sensitive sodium channel alpha subunit [Rattus norvegicus] "
23713	ENU07507	ANI61C5732: 22-46 516..1	22-46	386-413	LINAP		g1351672	106	65	3.00E-10	28	16	putative 89.3 KD transcriptional regulatory protein CIF7.11C ; hypothetical protein SPAC1F7.11c - fission yeast (Schizosaccharomyces pombe) ; (Z67998) unknown [Schizosaccharomyces pombe]
23714	ENU07508	ANI61C6469: 41-60 1051..174	41-60	803-829	LINAP		g2612904	322	109	2.00E-23	35	79	(AF015825) malate dehydrogenase-like protein [Bacillus subtilis] ; (Z99110) similar to malate dehydrogenase [Bacillus subtilis]
23715	ENU07509	ANI61C1619: 48-69 648..1090	48-69	459-478	LINAP		g4519535	217	91	4.00E-18	34	31	(AB015306) Leukotriene B4 omega-hydroxylase [Homo sapiens]
23716	ENU07510	ANI61C567:1 32-51 213..866	32-51	456-479	LINAP		g3319757	64	58	0.000000	33	13	(AL031035) putative ATP /GTP-binding protein [Streptomyces coelicolor]

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23717	ENU07511	ANI61C6430: 30-51 6653..6314	57-76	443-470	LINAP	g3257375	91	37	0.08				(AP000004) 275aa long hypothetical translation initiation factor eIF-2 alpha chain [Pyrococcus horikoshii]
23718	ENU07512	ANI61C9058: 57-76 1..509	458-477		LINAP	g1351343	48	75	3.00E-13	28	15		positive regulator of purine utilisation ; positive regulator of purine utilisation - Emericella nidulans ; (X84015)
23719	ENU07513	ANI61C568:2 22-48 880..3595	670-695		LINAP	g127338	149	48	4.00E-11	30	18		positive regulator of purine utilisation [Emericella nidulans]
23720	ENU07514	ANI61C9070: 1118..1			LINAP	g2832315	1046	356	e-101	69	38		morphogenesis-related protein (multicopy suppression of a budding defect 1) ; morphogenesis-related protein MSB1 - yeast (Saccharomyces cerevisiae) ; (M37767) multicopy suppressor of a budding defect [Saccharomyces cerevisiae] ; (Z75096) ORF YOR188w [Saccharomyces cerevisiae]
23721	ENU07515	ANI61C1617: 25-52 1583..2072	457-479		LINAP	g1834342	439	154	4.00E-37	66	10		(AF045014) translation release factor eRF3 [Podospira anserina] (Z68905) ATP-binding cassette multidrug transporter [Emericella nidulans]
23722	ENU07516	ANI61C4767: 102-127 318..1	453-479		LINAP	g3913990	57	50	0.00001	29	14		ATP-dependent protease LA ; (AF030688) ATP-dependent proteinase [Mycobacterium smegmatis]
23723	ENU07517	ANI61C568:7 28-47 265..6706	502-528		LINAP	g2981452	299	127	6.00E-29	45	91		(AF052482) germinating protein [Erysiphe graminis]
23724	ENU07518	ANI61C6462: 70-89 4185..3107	804-829		LINAP	g134388	373	91	1.00E-35	42	78		L-serine dehydratase (L-serine deaminase) ; L-serine dehydratase (EC 4.2.1.13) SDL1 - yeast (Saccharomyces cerevisiae) ; (X52657) L-serine dehydratase (AA 1-338)
23725	ENU07519	ANI61C9042: 22-41 1623..912	646-665		LINAP	g4499843	270	83	2.00E-15	42	40		[Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea]
23726	ENU07520	ANI61C1628: 25-50 2453..2797	331-350		LINAP	g98686	28	49	0.00002				internalin B - Listeria monocytogenes

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23727	ENU07521	ANI61C1060 4:1987..1325	24-51	611-629	LINAP		g3924850	99	59	2.00E-14			"(Z81586) predicted using Genefinder; similar to Alcohol/other dehydrogenases, short chain type [Caenorhabditis elegans]"
23728	ENU07522	ANI61C4780: 54-81 94..516	54-81	451-470	LINAP		g3873652	112	73	1.00E-12			(Z71177) Similarity with human nuclear autoantigen (PIR accession number JC2522); cDNA EST EMBL:D65093 comes from this gene; cDNA EST EMBL:D68406 comes from this gene; cDNA EST yk297d9.5 comes from this gene; cDNA EST yk353f10...; (Z71181) Similarity with human nuclear autoantigen (PIR accession number JC2522); cDNA EST EMBL:D65093 comes from this gene; cDNA EST EMBL:D68406 comes from this gene; cDNA EST yk297d9.5 comes from this gene; cDNA EST yk353f10...
23729	ENU07523	ANI61C5751: 31-50 1204..1	31-50	721-740	LINAP		g2440206	1023	272	3.00E-72	51	36	putative integral membrane protein [Schizosaccharomyces pombe]
23730	ENU07524	ANI61C6462: 22-49 5222..5951	22-49	685-709	LINAP		g1351719	102	61	0.000000	34	71	hypothetical 30.0 KD protein C18G6.01C in chromosome I; (Z68198) hypothetical protein [Schizosaccharomyces pombe]
23731	ENU07525	ANI61C9042: 5892..5338			LINAP		g114959	220	87	6.00E-21	40	22	Thermotable beta-glucosidase B (gentiobiase) (cellobiase) (beta-D-glucoside glucosidase) (beta-D-glucosidase (EC 3.2.1.21) B - Clostridium thermocellum; (X15644) bglB gene (AA1-754) [Clostridium thermocellum]
23732	ENU07526	ANI61C1062 22-46 1:1..406	22-46	346-365	LINAP		g710552	126	75	2.00E-13	40	6	(L40632) ankyrin 3 [Mus musculus]
23733	ENU07527	ANI61C4785: 22-48 764..1211	22-48	444-463	LINAP		g1546072	248	52	2.00E-13	40	5	(U68040) polyketide synthase [Cochliobolus heterostrophus]

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23734	ENU07528	ANI61C6502: 22-47 240..779	22-47	422-448	LINAP	g2132816	256	130	8.00E-30	53			probable membrane protein YOL002c - yeast (Saccharomyces cerevisiae); (U43491) hypothetical protein UND327 [Saccharomyces cerevisiae]; (Z74744) ORF YOL002c [Saccharomyces cerevisiae]
23735	ENU07529	ANI61C4789: 1093..1483			LINAP		30				29		
23736	ENU07530	ANI61C5728: 1182..1849			LINAP	g729781	159	45	0.000000				probable glucoSE transporter HXT5; hexose transport protein HXT5 - yeast (Saccharomyces cerevisiae); (X77961) hexose transporter [Saccharomyces cerevisiae]; (U00060) Hxt5p: Hexose transporter [Saccharomyces cerevisiae] A-agglutinin attachment subunit precursor; a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae); (M60590) a-agglutinin core subunit [Saccharomyces cerevisiae]; (Z71659) ORF YNR044w [Saccharomyces cerevisiae] (AF009417) cytochrome P450 [Myrothecium roridum] (Z97052) hypothetical protein [Schizosaccharomyces pombe] hypothetical protein MJ0301; hypothetical protein MJ0301 - Methanococcus jannaschii; (U67485) conserved hypothetical protein [Methanococcus jannaschii] (L35053) endonuclease [Magnaporthe grisea]
23737	ENU07531	ANI61C6472: 82-108 2582..2106	82-108	452-479	LINAP	g416592	101	42	0.003				
23738	ENU07532	ANI61C907:8 45-71 2..1854	45-71	807-829	LINAP	g2267601	474	109	2.00E-23	39			
23739	ENU07533	ANI61C1652: 57-74 1249..2315	57-74	720-741	LINAP	g2213557	682	176	2.00E-43	40			
23740	ENU07534	ANI61C1060 40-62 3:4136..3828	40-62	450-477	LINAP	g2495901	124	69	2.00E-11	32			
23741	ENU07535	ANI61C5782: 179-206 1..1467	179-206	673-700	LINAP	g522302	755	219	2.00E-56	44			
23742	ENU07536	ANI61C6429: 37-56 4404..2930	37-56	789-808	LINAP	g1703215	74	80	2.00E-14				general alpha-glucoside permease; alpha-glucoside transport protein - yeast (Saccharomyces cerevisiae); (Z73074) ORF YGR289c [Saccharomyces cerevisiae]

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23743	ENU07537	ANI61C9091: 1571..756	26-47	757-776	LINAP		g2494090	174	82	6.00E-15	27	86	hypothetical 33.3 KD protein in PERR-ARGF intergenic region ; (AE000134) putative lyase/synthase [Escherichia coli]
23744	ENU07538	ANI61C1675: 1739..2203	47-66	431-454	LINAP		g1723643	355	153	7.00E-37	52	37	hypothetical 44.9 KD protein in SEC9-MSB2 intergenic region ; probable membrane protein YGR010w - yeast (Saccharomyces cerevisiae) ; (Z72795) ORF YGR010w [Saccharomyces cerevisiae]
23745	ENU07539	ANI61C1061 22-49	774-797	LINAP			g3757672	148	70	2.00E-11	25	26	(AJ010902) inversin [Mus musculus]
23746	ENU07540	ANI61C4814: 104-125	558-576	LINAP			g2920706	498	242	3.00E-63	51	28	(Y13568) beta-xylosidase [Emericella nidulans]
23747	ENU07541	ANI61C4817: 1225..914	71-90	438-457	LINAP		g3413872	168	33	1.6			(AB007924) KIAA0455 protein [Homo sapiens]
23748	ENU07542	ANI61C566: 860..7865	106-133	796-823	LINAP		g1363735	84	32	5.3			probable membrane protein YLR242c - yeast (Saccharomyces cerevisiae) ; (U20865) Arv1p [Saccharomyces cerevisiae]
23749	ENU07543	ANI61C4815: 1691..415	32-52	806-829	LINAP		g549443	547	210	1.00E-53	37	14	conidial green pigment synthase ; probable polyketide synthase - Emericella nidulans ; (X65866) putative polyketide or fatty acid synthase [Emericella nidulans] ; wA gene [Emericella nidulans]
23750	ENU07544	ANI61C1062 2-4990..5304	22-48	458-479	LINAP		g465533	166	36	0.14			hypothetical 11.5 KD protein in HTB2-NTH2 intergenic region ; hypothetical protein YBL001c - yeast (Saccharomyces cerevisiae) ; (Z26494) unknown [Saccharomyces cerevisiae] ; (Z35762) ORF YBL001c [Saccharomyces cerevisiae] ; ORF YBL0105 [Saccharomyces cerevisiae]

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23751	ENU07545	ANI61C9597: 46-72 848..1	46-72	712-738	LINAP		g4505499	421	148	6.00E-35	38	25	O-GlcNAc transferase (uridine diphospho-N-acetylglucosamine:polypeptide beta-N-acetylglucosaminyl transferase) ; (U77413) O-linked GlcNAc transferase [Homo sapiens]
23752	ENU07546	ANI61C9593: 22-44 2213..3056	22-44	779-806	LINAP		g2133786	89	39	0.053			NF-180 - sea lamprey ; (U19361) NF-180 [Petromyzon marinus]
23753	ENU07547	ANI61C6503: 57-76 2076..449	57-76	615-637	LINAP		g1077259	837	171	6.00E-42	39	23	probable membrane protein YPL006w - yeast (Saccharomyces cerevisiae) ; (Z48483) unknown [Saccharomyces cerevisiae] ; (U33335) Lpa1p [Saccharomyces cerevisiae] ; (Z71255) unknown [Saccharomyces cerevisiae]
23754	ENU07548	ANI61C1674: 22-48 892..300	22-48	529-548	LINAP		g2498563	280	139	2.00E-32	53	46	MLO2 protein ; (L42550) ORF [Schizosaccharomyces pombe]
23755	ENU07549	ANI61C9034: 25-52 4999..5519	25-52	480-499	LINAP		g2689471	95	85	2.00E-16	37	30	(U62774) cytochrome P450 monooxygenase [Aspergillus parasiticus]
23756	ENU07550	ANI61C650:2 080..2671			LINAP		g3150139	108	66	2.00E-10	32	22	(AL023594) amino-acid permease [Schizosaccharomyces pombe]
23757	ENU07551	ANI61C909:4 71..1308	28-47	793-817	LINAP		g1437475	315	106	2.00E-34	33	80	"(D86544) hydroxyquinol-1, 2-dioxygenase [Ralstonia pickettii] "
23758	ENU07552	ANI61C9556: 59-78 1162..1997	59-78	795-814	LINAP		g171963	293	162	4.00E-39	41	53	(M15991) rRNA isopentenyl transferase [Saccharomyces cerevisiae]
23759	ENU07553	ANI61C5675: 40-59 6149..4744	40-59	809-828	LINAP		g1546072	394	63	3.00E-22	41	10	(U68040) polyketide synthase [Cochliobolus heterostrophus]
23760	ENU07554	ANI61C1122 8:6103..6779	26-45	635-656	LINAP		g2497056	85	55	0.000000	30	35	putative dioxygenase YLL057C ; hypothetical protein YLL057c - yeast (Saccharomyces cerevisiae) ; (Z47973) ORF L0572 [Saccharomyces cerevisiae] ; (Z73162) ORF YLL057c [Saccharomyces cerevisiae]
23761	ENU07555	ANI61C9102: 22-42 1863..942	22-42	800-819	LINAP		g3036840	378	106	3.00E-22	39	67	(AJ222967) cystinosin [Homo sapiens] ; (Y15924) cystinosin [Homo sapiens]

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23762	ENU07556	ANI61C9556: 23-47 3868..3127	23-47	694-721	LINAP		g1723981	296	59	6.00E-13	32	53	hypothetical 44.5 KD protein in PDE1-RTF1 intergenic region ; hypothetical protein YGL246c - yeast (Saccharomyces cerevisiae) ; (X94357) ORF NRE387 [Saccharomyces cerevisiae] ; (Z72768) ORF YGL246c [Saccharomyces cerevisiae] (AL023587) putative kinesin-like protein [Schizosaccharomyces pombe] ; quinate permease (quinate transporter) ; quinate transport protein - Emericella nidulans ; (X13525) quinate permease [Emericella nidulans] "probable calcium-transporting ATPase 3 (endoplasmic reticulum CA2+-ATPase) ; probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) ; (L01795) ATPase [Saccharomyces cerevisiae] ; (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae] "
23763	ENU07557	ANI61C6476: 22-49 4571..5242	22-49	627-651	LINAP		g3136023	469	168	2.00E-48	54	26	Start control protein CDC10 ; cdc10 start control protein - fission yeast (Schizosaccharomyces pombe) ; (X02175) cdc10 polypeptide [Schizosaccharomyces pombe] (U78597) kinesin light chain [Plectonema boryanum] (AL031798) putative leucine permease transcriptional regulator. [Schizosaccharomyces pombe] (AB018344) KIAA0801 protein [Homo sapiens] (AF102265) N-acetylglucosamine-phosphate mutase [Homo sapiens]
23764	ENU07558	ANI61C1685: 22-47 298..1945	22-47	806-828	LINAP		g131768	381	128	4.00E-29			
23765	ENU07559	ANI61C1127 25-44 6:342..642	25-44	439-466	LINAP		g728905	304	140	7.00E-33	63	7	
23766	ENU07560	ANI61C5756: 66-85 2056..3660	66-85	805-823	LINAP		g115906	375	135	3.00E-31	35	34	
23767	ENU07561	ANI61C1127 29-51 1:669..1	29-51	610-637	LINAP		g2645229	225	85	6.00E-16	29	45	
23768	ENU07562	ANI61C9579: 22-47 6751..5631	22-47	808-829	LINAP		g3687460	402	157	7.00E-38	40	25	
23769	ENU07563	ANI61C65:35 33-52 11..4969	33-52	721-748	LINAP		g3882323	1206	386	e-106	69	26	
23770	ENU07564	ANI61C5811: 22-47 646..1	22-47	546-573	LINAP		g3851711	286	119	2.00E-26	44	32	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23771	ENU07565	ANI61C1123 1:338..1	52-74	439-458	LINAP		g131768	87	61	6.00E-10	31	31	quininate permease (quininate transporter) ; quininate transport protein - Emericella nidulans ; (X13525) quininate permease [Emericella nidulans]
23772	ENU07566	ANI61C5803: 22-48 312..1387	22-48	767-786	LINAP		g2500587	621	100	4.00E-30	47	51	Spliceosome associated protein 49 (SAP 49) (SF3B53) ; spliceosome-associated protein SAP-49 - human ; (L35013) spliceosomal protein [Homo sapiens]
23773	ENU07567	ANI61C1703: 38-57 1542..994	38-57	506-525	LINAP		g2132865	170	58	0.000000 06			probable membrane protein YOR034c - yeast (Saccharomyces cerevisiae) ; (X87331) AKR1 homologue; overlaps with L31407 [Saccharomyces cerevisiae] ; (Z74942) ORF YOR034c [Saccharomyces cerevisiae]
23774	ENU07568	ANI61C1123 22-43 1:2054..1750	22-43	455-479	LINAP		g2808662	42	55	0.000000 4			(AJ223459) PnaA protein [Emericella nidulans]
23775	ENU07569	ANI61C9063: 22-44 8556..7615	22-44	810-829	LINAP		g2132036	104	106	1.00E-24			hypothetical protein YOR049c - yeast (Saccharomyces cerevisiae) ; (Z74957) ORF YOR049c [Saccharomyces cerevisiae]
23776	ENU07570	ANI61C4823: 22-48 4928..3780	22-48	810-829	LINAP		g3023275	926	107	1.00E-42	41	27	alpha-glucosidase precursor (maltase) ; alpha-glucosidase (EC 3.2.1.20) - barley ; (U22450) alpha-glucosidase [Hordeum vulgare]
23777	ENU07571	ANI61C9110: 22-45 1874..1306	22-45	526-548	LINAP		g1711494	65	37	0.095			"Immunoglobulin G binding protein H precursor (protein H) ; protein H precursor - Streptococcus sp. (group A, strain 40/58) ; (M29398) protein H precursor [Streptococcus sp.] "
23778	ENU07572	ANI61C9578: 23-45 4522..4933	23-45	458-479	LINAP		g1263187	72	46	0.0002	26	46	(U24215) HOMODA hydrolase [Pseudomonas putida] ; HOMODA hydrolase [Pseudomonas putida]
23779	ENU07573	ANI61C4906: 22-45 2268..1	22-45	726-749	LINAP		g126929	745	139	3.00E-33	48	12	multiDRUG resistance protein 2 (P-glycoprotein 2) ; multidrug resistance protein 2 - mouse ; (J03398) multidrug resistance protein [Mus musculus]

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23780	ENU07574	ANI61C1715: 1..354	114-133	312-332	LINAP		g2281979	117	50	0.000006			(Z98056) putative glyoxylate pathway regulator [Schizosaccharomyces pombe]
23781	ENU07575	ANI61C9108: 22-47 3744..2763	22-47	807-826	LINAP		g1805251	914	339	1.00E-92	55	51	(U58946) transposase [Aspergillus awamori]
23782	ENU07576	ANI61C5784: 22-45 3592..3988	22-45	455-479	LINAP		g4165298	85	56	0.000000	28	20	(AL035254) putative transcriptional regulator [Schizosaccharomyces pombe]
23783	ENU07577	ANI61C4909: 23-43 1329..2684	23-43	787-806	LINAP		g3913676	405	143	2.00E-33	32	42	Ferric reductase transmembrane component 7 precursor ; probable membrane protein YOL152w - yeast (Saccharomyces cerevisiae) ; (Z48239) orf1 [Saccharomyces cerevisiae] ; (Z74894) ORF YOL152w [Saccharomyces cerevisiae]
23784	ENU07578	ANI61C1127 22-48 5:1524..1185	22-48	297-319	LINAP		g4468913	210	95	1.00E-19	41	14	(AJ131720) alpha integrin binding protein 80 [Homo sapiens]
23785	ENU07579	ANI61C1709: 102-123 1..367	102-123	319-346	LINAP		g769829	143	63	9.00E-10	49	14	(M80674) hydroxylase [Streptomyces glaucescens]
23786	ENU07580	ANI61C5854: 23-46 1..1173	23-46	803-829	LINAP		g3242253	494	181	6.00E-45	39	11	(Z83857) ppsC [Mycobacterium tuberculosis]
23787	ENU07581	ANI61C1127 53-72 8:607..1	53-72	398-420	LINAP		g3025210	85	46	0.0003			"hypothetical 43.0 KD protein in cut-GLNX intergenic region ; (AE000170) orf, hypothetical protein [Escherichia coli] ; (D90706) VisC protein [Escherichia coli] "
23788	ENU07582	ANI61C4930: 32-51 989..1	32-51	714-741	LINAP		g4467980	127	34	1.8			(AJ133272) atrophin-1 [Pongo pygmaeus]
23789	ENU07583	ANI61C1127: 32-51 2453..3163	32-51	651-670	LINAP		g3875304	370	164	8.00E-40	42	65	(Z74030) predicted using Genefinder; cDNA EST EMBL: C07609 comes from this gene; cDNA EST EMBL: C09023 comes from this gene; cDNA EST yk505e9.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 comes...

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23790	ENU07584	ANI61C9603: 1311..2844	32-51	807-829	LINAP		g548585	602	165	4.00E-40	47	23	poly [ADP-ribose] polymerase (PARP) (ADPRT) (NAD(+)) ADP-riboyltransferase) poly[ADP-ribose] synthetase) ; NAD+ ADP-riboyltransferase (EC 2.4.2.30) - fruit fly (Drosophila melanogaster) ; (D13806) poly(ADP-ribose) polymerase [Drosophila melanogaster] ; (AF051548) poly(ADP-ribose) polymerase [Drosophila melanogaster] hypothetical protein YDL201w - yeast (Saccharomyces cerevisiae) ; (X99000) ORF D1075 [Saccharomyces cerevisiae] ; (Z74249) ORF YDL201w [Saccharomyces cerevisiae] hypothetical 42.2 KD protein C17G8.11C in chromosome I ; (Z69795) unknown [Schizosaccharomyces pombe] lactose permease ; lactose permease - yeast (Kluyveromyces marxianus var. lactis) ; (X06997) lactose permease (AA 1-587) [Kluyveromyces lactis] (Z98533) phosphoribosylformylglycinamide synthase [Schizosaccharomyces pombe]
23791	ENU07585	ANI61C6528: 2266..1157	23-43	806-825	LINAP		g2131358	535	166	1.00E-40	58	66	
23792	ENU07586	ANI61C9619: 91..512	22-45	456-479	LINAP		g1723483	97	68	4.00E-11	27	38	
23793	ENU07587	ANI61C6539: 1..1262	24-43	800-822	LINAP		g125935	574	124	3.00E-45	39	48	
23794	ENU07588	ANI61C5850: 1559..3577	22-45	727-746	LINAP		g2330857	1810	260	4.00E-69	64	20	
23795	ENU07589	ANI61C1130: 0:1245..1	22-45	726-745	LINAP		g3850110	948	185	1.00E-71	52	32	
23796	ENU07590	ANI61C9114: 1..3099	23-50	806-828	LINAP		g3850108	3130	356	8.00E-98	63	22	
23797	ENU07591	ANI61C6538: 1591..2558	22-42	796-815	LINAP		g4588918	353	75	7.00E-29	29	44	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23798	ENU07592	ANI61C1131 4:689..1089	26-53	376-399	LINAP		g130784	126	74	8.00E-13	25	18	Pyrimidine pathway regulatory protein PPR1 - yeast 1 ; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae) ; (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae] ; (Z73186) ORF YLR014c [Saccharomyces cerevisiae] (M57453) sterol carrier protein-x [Rattus norvegicus] transaldolase ; (D90900) transaldolase [Synchocystis sp.] probable sucrose utilization protein SUC1 (Z98529) putative cytoskeleton assembly control protein [Schizosaccharomyces pombe] "fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum] " (U43200) antifreeze glycopeptide AFGP polypeptide precursor [Boreogadus saida] (AJ010902) inversin [Mus musculus] hypothetical 102.7 KD protein in PRP16-SRP40 intergenic region ; hypothetical protein YKR089c - yeast (Saccharomyces cerevisiae) ; (Z27116) ORF YKR409 [Saccharomyces cerevisiae] ; (Z28314) ORF YKR089c [Saccharomyces cerevisiae] probable calcium-transporting ATPase 4 ; probable ATPase (EC 3.6.1.-) YDR093w - yeast (Saccharomyces cerevisiae) ; (Z47746) probable ATPase [Saccharomyces cerevisiae]
23799	ENU07593	ANI61C1711: 22-47 5137..3884	22-47	788-807	LINAP		g206877	980	177	4.00E-65	52	48	
23800	ENU07594	ANI61C9114: 22-49 4111..4459	22-49	454-479	LINAP		g2501349	89	61	0.000000	34	33	
23801	ENU07595	ANI61C5845: 22-47 4587..3480	22-47	809-828	LINAP		g1174472	181	60	0.000000	28	47	
23802	ENU07596	ANI61C9134: 22-47 1..1382	22-47	796-815	LINAP		g2330690	481	146	1.00E-34	35	16	
23803	ENU07597	ANI61C1119: 26-53 9244..11350	26-53	728-748	LINAP		g119830	1655	185	2.00E-52	44	15	
23804	ENU07598	ANI61C9134: 47-67 1439..2299	47-67	808-827	LINAP		g2078483	129	35	0.61	26	53	
23805	ENU07599	ANI61C9625: 24-47 443..1412	24-47	807-829	LINAP		g3757672	248	125	5.00E-28			
23806	ENU07600	ANI61C1131 102-129 8:2481..1732	102-129	705-729	LINAP		g549643	284	41	0.000000			
23807	ENU07601	ANI61C1721: 22-49 800..2490	22-49	622-649	LINAP		g2493010	1141	320	9.00E-87	55	17	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23808	ENU07602	ANI61C9117: 2011..2352	23-44	451-472	LINAP		g3560261	328	156	1.00E-37	48	29	(AL031535) RNA binding protein [Schizosaccharomyces pombe]
23809	ENU07603	ANI61C9635: 258..934	38-57	633-656	LINAP		g2842505	191	112	3.00E-24	42	46	(AL021748) adenosine deaminase [Schizosaccharomyces pombe]
23810	ENU07604	ANI61C6489: 4892..4135	48-67	709-730	LINAP		g3236250	140	59	0.000000	36	48	(AC004684) hypothetical protein [Arabidopsis thaliana]
23811	ENU07605	ANI61C5883: 3020..2339	23-42	639-661	LINAP		g1168610	379	99	2.00E-41			"Asparagine-rich zinc finger protein AZFI; finger protein AZFI, asparagine-rich - yeast (Saccharomyces cerevisiae); (Z26253) zinc finger protein of 101170 Da [Saccharomyces cerevisiae]; (X90518) ORF O3244 [Saccharomyces cerevisiae]; (X94335) YOR3244w [Saccharomyces cerevisiae]; (Z75021) ORF YOR113w [Saccharomyces cerevisiae]"
23812	ENU07606	ANI61C1718: 4412..3576	22-49	792-815	LINAP		g171106	195	101	9.00E-21	26	83	(M61773) ATP12 [Saccharomyces cerevisiae]
23813	ENU07607	ANI61C6547: 493..988	22-46	452-479	LINAP		g1208874	87	70	9.00E-12	30	8	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans]; (U39847) AO66 ankyrin [Caenorhabditis elegans]
23814	ENU07608	ANI61C1132 6:1590..2375			LINAP		g3417437	227	65	5.00E-10	36	73	(AL031263) putative GTPase-activator protein for Rho-like GTPases [Schizosaccharomyces pombe]
23815	ENU07609	ANI61C1735: 1650..417	22-43	699-721	LINAP		g1705871	1276	335	e-104	88	48	"citrate synthase, mitochondrial precursor; (D63376) citrate synthase precursor [Aspergillus niger]"
23816	ENU07610	ANI61C1745: 3133..2756	34-59	446-465	LINAP		g4567277	104	49	0.00002	34	11	(AC006841) putative pol protein with Zn finger CCHC type domain [Arabidopsis thaliana]
23817	ENU07611	ANI61C5888: 4057..3501	156-183	448-467	LINAP		g1083757	323	112	1.00E-31	43	15	plasma membrane Ca2+-ATPase isoform 4 - rat; (U15408) plasma membrane Ca2+-ATPase isoform 4 [Rattus norvegicus]

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23818	ENU07612	ANI61C1135 3:746..396	22-45	451-478	LINAP		g586486	99	48	0.00005	29	23	hypothetical 77.3 KD protein in FIG1-hypothetical intergenic region ; probable GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912)
23819	ENU07613	ANI61C2700: 27-45 639..1	27-45	566-585	LINAP		g4176520	524	219	1.00E-56	51	55	ORF YBR043c [Saccharomyces cerevisiae] (AL035263) homoserine dehydrogenase [Schizosaccharomyces pombe]
23820	ENU07614	ANI61C6547: 22-49 2952..2523	22-49	452-479	LINAP		g3169083	115	92	2.00E-18	34	48	(AL023705) hypothetical protein [Schizosaccharomyces pombe] (AB004537) methionyl-tRNA synthetase [Schizosaccharomyces pombe]
23821	ENU07615	ANI61C9647: 50-70 1..368	50-70	309-328	LINAP		g2257528	54	52	0.000000 03			(U07187) Mlh1p [Saccharomyces cerevisiae] (M33703) Hex2 protein [Saccharomyces cerevisiae] (Z98979) putative phosphatidylserine decarboxylase proenzyme [Schizosaccharomyces pombe]
23822	ENU07616	ANI61C658:3 30-57 00..755	30-57	376-399	LINAP		g460627	231	125	3.00E-28	43	20	UV radiation resistance associated gene ; (X99050) p63 (processed form) [Homo sapiens]
23823	ENU07617	ANI61C1736: 58-77 1872..1548	58-77	422-441	LINAP		g171666	185	94	2.00E-21	47	10	(U29156) involved in signaling by the epidermal growth factor receptor; Method: conceptual translation supplied by author. [Mus musculus]
23824	ENU07618	ANI61C2666: 60-79 361..1	60-79	432-451	LINAP		g2388966	107	62	0.000000 002	26	16	(AF000975) 7-O-methyltransferase [Medicago sativa] probable membrane protein YOR019w - yeast (Saccharomyces cerevisiae) ; (X87331) ORF OR26.09 [Saccharomyces cerevisiae] ; (Z74927) ORF YOR019w [Saccharomyces cerevisiae]
23825	ENU07619	ANI61C9142: 22-47 452..1659	22-47	802-829	LINAP		g4507861	260	108	4.00E-23	27	43	
23826	ENU07620	ANI61C9630: 22-43 4371..2964	22-43	781-800	LINAP		g968973	309	124	7.00E-28	29	30	
23827	ENU07621	ANI61C6496: 35-55 6254..5908	35-55	455-475	LINAP		g2580582	95	65	4.00E-10			
23828	ENU07622	ANI61C5884: 30-53 2369..1036	30-53	800-819	LINAP		g1078035	101	32	4			
23829	ENU07623	ANI61C9145: 102-120 1..814	102-120	694-713	LINAP		g1335892	212	79	3.00E-19	33	10	(U49439) ASH1 [Drosophila melanogaster]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23830	ENU07624	ANI61C9601: 35-55 930..1297	55-55	452-479	LINAP		g1351343	103	36	0.23	30	11	positive regulator of purine utilisation ; positive regulator of purine utilisation - [Emicella nidulans ; (X84015) positive regulator of purine utilisation [Emicella nidulans] (Z82044) hypothetical 54.4 kd protein [Bacillus subtilis] (AB014596) KIAA0696 protein [Homo sapiens] ANKYRIN ; ankyrin - mouse ; (M84756) ankyrin [Mus musculus] (U46069) fertilin alpha subunit [Oryctolagus cuniculus] Pyrimidine pathway regulatory protein 1 ; regulatory protein PPR1 - yeast (Saccharomyces cerevisiae) ; (X01739) regulatory protein (AA 1-904) [Saccharomyces cerevisiae] ; (Z73186) ORF YLR014c [Saccharomyces cerevisiae] (Z74697) ppsA [Mycobacterium tuberculosis] (AL023777) hypothetical protein [Schizosaccharomyces pombe] (U43720) Sug2p [Saccharomyces cerevisiae] (AC000098) EST gb/ATTS1136 comes from this gene. [Arabidopsis thaliana] hypothetical 44.9 KD protein C18B11.02C in chromosome I ; hypothetical protein SPAC18B11.02c - fission yeast (Schizosaccharomyces pombe) ; (Z50728) hypothetical protein [Schizosaccharomyces pombe]
23831	ENU07625	ANI61C6553: 24-43 3275..2800	24-43	452-479	LINAP		g1673402	145	65	3.00E-10			
23832	ENU07626	ANI61C1734: 47-74 5554..4663	47-74	806-828	LINAP		g3327206	300	150	9.00E-36	39	41	
23833	ENU07627	ANI61C2767: 27-46 651..1125	27-46	375-394	LINAP		g1168457	101	85	2.00E-16	35	8	
23834	ENU07628	ANI61C9145: 22-49 2397..1682	22-49	671-695	LINAP		g1245061	78	55	0.000000			
23835	ENU07629	ANI61C9601: 55-74 1822..2247	55-74	422-442	LINAP		g130784	79	74	8.00E-13	31	18	
23836	ENU07630	ANI61C1131: 22-45 2884..1508	22-45	805-827	LINAP		g3261605	579	146	6.00E-43	41	13	
23837	ENU07631	ANI61C1757: 22-45 1867..2501	22-45	568-590	LINAP		g3184102	185	127	7.00E-29	37	32	
23838	ENU07632	ANI61C2764: 65-91 1339..358	65-91	803-829	LINAP		g1147800	1005	254	e-101	78	57	
23839	ENU07633	ANI61C9144: 22-46 2094..2560	22-46	458-479	LINAP		g2388584	69	38	0.046			
23840	ENU07634	ANI61C6543: 22-49 659..1663	22-49	808-827	LINAP		g1175381	773	251	5.00E-66	50	63	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23841	ENU07635	ANI61C5903: 496..1	121-142	461-479	LINAP		g115875	155	85	2.00E-16	33	48	CBP3 protein precursor ; membrane protein CBP3 - yeast (Saccharomyces cerevisiae) ; (J04830) CBP3 protein [Saccharomyces cerevisiae] ; (Z73571) ORF YPL215w [Saccharomyces cerevisiae] (X97001) LR8B [Gallus gallus]
23842	ENU07636	ANI61C1747: 2322..1833	31-50	430-450	LINAP		g1595750	34	59	0.000000			Pectate lyase L precursor ; (L42248)
23843	ENU07637	ANI61C2775: 806..1	22-48	682-705	LINAP		g3914287	134	69	2.00E-16	30	50	pectate lyase [Erwinia chrysanthemi] "AC002292" similar to "Mx" GTP-binding proteins [Arabidopsis thaliana]
23844	ENU07638	ANI61C9628: 2250..2782	23-46	493-512	LINAP		g2462747	44	49	0.00002	32	17	"
23845	ENU07639	ANI61C5931: 277..690	29-48	438-457	LINAP		g1723807	161	54	0.000000	21	25	hypothetical 70.6 KD protein in PGD1-SIT3 intergenic region ; hypothetical protein YGL023c - yeast (Saccharomyces cerevisiae) ; (Z72545) ORF YGL023c [Saccharomyces cerevisiae]
23846	ENU07640	ANI61C1135: 7:407..1430	28-48	805-829	LINAP		g2894292	68	63	0.000000			"(AL021837) SPBC947.05c, ferric reductase transmembrane component, (possibility of intron between 15640-15725 but FASTA suggests not), len:564aa, similar eg. to S. pombe, FRP1_SCHPO, Q04800, ferric reductase transmembrane compon..." (AE000948) 3-hydroxyacyl-CoA dehydrogenase (hbd-10) [Archaeoglobus fulgidus] (AL031740) putative calcium dependant serine-threonine protein kinase. [Schizosaccharomyces pombe] Quinic acid utilization activator ; regulatory protein QUTA - Emeritella nidulans ; (X06252) QUTA protein (AA 1 - 825) [Emeritella nidulans] (AL023533) hypothetical protein [Schizosaccharomyces pombe]
23847	ENU07641	ANI61C1747: 3506..2751	109-128	710-735	LINAP		g2648250	178	97	1.00E-19	31	33	
23848	ENU07642	ANI61C9161: 1266..1	22-48	722-744	LINAP		g3650382	579	190	8.00E-48	38	28	
23849	ENU07643	ANI61C9628: 3696..4135	43-61	459-478	LINAP		g131767	63	53	0.000001			
23850	ENU07644	ANI61C2801: 1..321	115-132	270-289	LINAP		g3130058	167	47	2.00E-11	51	11	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23851	ENU07645	ANI61C6552: 22-44 5929..4882	22-44	803-822	LINAP		g1208874	430	167	8.00E-41	34	15	(U50071) <i>C. elegans</i> ankyrin-related unc-44 (GB:U21734) [<i>Caenorhabditis elegans</i>] ; (U39847) AO66 ankyrin [<i>Caenorhabditis elegans</i>] vegetable incompatibility protein HET-E-1 ; (L28125) beta transducin-like protein [<i>Podospira anserina</i>] vacuolar protein sorting-associated protein VPS5 ; (U73512) Vps5p [<i>Saccharomyces cerevisiae</i>] ; (U84735) Vps5p [<i>Saccharomyces cerevisiae</i>] hypothetical 85.0 KD protein in HLJ1-SMP2 intergenic region ; hypothetical protein YMR164c - yeast (<i>Saccharomyces cerevisiae</i>) ; (Z49705) unknown [<i>Saccharomyces cerevisiae</i>] TRNA splicing protein SPL1 ; (AF000115) tRNA splicing protein [<i>Candida maltosa</i>] (Z99104) similar to cell-cycle protein [<i>Bacillus subtilis</i>] (X71807) uric acid-xanthine permease [<i>Emicella nidulans</i>] (AJ012627) haloalkane dehalogenase [<i>Mycobacterium</i> sp.] (AL021839) putative nuclear pore protein [<i>Schizosaccharomyces pombe</i>] (AC000133) ORF [<i>Emicella nidulans</i>] (AL035065) putative urea active transporter [<i>Schizosaccharomyces pombe</i>] hypothetical 59.1 KD protein ZK637.1 in chromosome III "(X80835) len: 676, CAI: 0.13 [<i>Saccharomyces cerevisiae</i>]" (AL049498) rho1 gdp-gtp exchange protein 1 [<i>Schizosaccharomyces pombe</i>]
23852	ENU07646	ANI61C1137 9:4059..4439	22-48	375-397	LINAP		g3023956	87	75	3.00E-13			
23853	ENU07647	ANI61C1765: 75-94 864..1	75-94	729-749	LINAP		g2499128	220	79	4.00E-18	34	38	
23854	ENU07648	ANI61C2801: 79-98 959..1393	79-98	356-380	LINAP		g2497170	97	44	0.0008			
23855	ENU07649	ANI61C6608: 75-94 254..836	75-94	359-381	LINAP		g2492879	698	290	6.00E-78	72	39	
23856	ENU07650	ANI61C1139 5:204..1067	32-59	803-829	LINAP		g2632334	75	61	0.000000			
23857	ENU07651	ANI61C1807: 480..1820			LINAP		g3286685	1908	392	e-121	92	39	
23858	ENU07652	ANI61C9140: 22-49 1710..2011	22-49	449-468	LINAP		g3860531	94	41	0.000000	28	37	
23859	ENU07653	ANI61C1806: 23-42 1773..2999	23-42	721-740	LINAP		g2894271	326	112	3.00E-24	30	69	
23860	ENU07654	ANI61C9147: 49-68 3471..4684	49-68	805-824	LINAP		g1870209	245	111	5.00E-24	28	50	
23861	ENU07655	ANI61C59:11 36..361	22-41	537-556	LINAP		g4106690	339	109	2.00E-28	48	30	
23862	ENU07656	ANI61C1140 3:689..292	24-47	448-467	LINAP		g586797	57	70	1.00E-11			
23863	ENU07657	ANI61C7181: 25-52 1094..1718	25-52	584-603	LINAP		g530340	141	65	4.00E-10	25	30	
23864	ENU07658	ANI61C7196: 1384..1			LINAP		g4539279	1069	346	2.00E-94	64	20	

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23865	ENU07659	ANI61C2840: 2281..1	32-58	713-732	LINAP		g2500542	1356	79	1.00E-18			putative ATP-dependent RNA helicase YMR128W ; probable membrane protein YMR128w - yeast (Saccharomyces cerevisiae) ; (Z48622)
23866	ENU07660	ANI61C9655: 1827..1442	56-76	314-333	LINAP		g4499843	124	52	0.000001			unknown [Saccharomyces cerevisiae] (AJ011965) oxidoreductase [Claviceps purpurea]
23867	ENU07661	ANI61C6602: 829..1979	22-49	808-829	LINAP		g2144437	640	178	2.00E-69	55	57	choline-phosphate cytidylyltransferase (EC 2.7.7.15) - yeast (Saccharomyces cerevisiae) ; (Z49133)
23868	ENU07662	ANI61C2875: 978..595	28-50	266-289	LINAP		g728783	204	126	1.00E-28	41	21	cholinephosphate cytidylyltransferase [Saccharomyces cerevisiae] ; (Z72987) ORF YGR202c [Saccharomyces cerevisiae]
23869	ENU07663	ANI61C9645: 2268..3125	45-64	785-803	LINAP		g4008556	296	111	2.00E-32	40	69	putative aconitase in PRP21-UBP12 intergenic region ; aconitate hydratase homolog YJL200c - yeast (Saccharomyces cerevisiae) ; (X77688)
23870	ENU07664	ANI61C183:1 137..1	22-42	729-749	LINAP		g3182891	1746	513	e-145	98	70	hypothetical protein J0327 [Saccharomyces cerevisiae] ; (Z49475)
23871	ENU07665	ANI61C2835: 1..2645	23-50	798-817	LINAP		g3510629	525	123	1.00E-27	32	2	ORF YJL200c [Saccharomyces cerevisiae]
23872	ENU07666	ANI61C9163: 616..1967	22-49	805-829	LINAP		g4099313	386	161	3.00E-40	42	2	(AL034490) putative lectin precursor [Schizosaccharomyces pombe]
23873	ENU07667	ANI61C6535: 9996..9601	22-44	429-448	LINAP		g630885	124	71	4.00E-12	32	39	Actin ; (AJ000335) actin [Botryotinia fuckeliana] (AF047828) syringomycin synthetase [Pseudomonas syringae pv. syringae] (U85909) peptide synthetase [Aureobasidium pullulans]
23874	ENU07668	ANI61C1758: 1213..565	23-50	609-628	LINAP		g2459421	312	94	6.00E-29	47	74	"Sp1/egr-like zinc-finger protein - fruit fly (Drosophila sp.) ; (S71230) Sp1/egr-like zinc-finger protein=hkb [Drosophila, 0-4 hr embryos, Peptide, 296 aa] [Drosophila sp.] ; huckebein gene [Drosophila melanogaster]" (AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

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23875	ENU07669	ANI61C9146: 1..595	222-241	363-380	LINAP		g128831	641	200	5.00E-67			"mitochondrial nuclease ; nuclease NUC1 (EC 3.1.30.-) precursor, mitochondrial - yeast (Saccharomyces cerevisiae) ; (X06670) nuclease [Saccharomyces cerevisiae] ; (Z34098) ORF [Saccharomyces cerevisiae] ; (X77688) mitochondrial nuclease [Saccharomyces cerevisiae] ; (Z49483) ORF YJL208c [Saccharomyces cerevisiae] "
23876	ENU07670	ANI61C9678: 1001..1846	22-45	795-815	LINAP		g730615	139	118	6.00E-26			DNA-directed RNA polymerase mitochondrial precursor ; (L25087) mitochondrial RNA polymerase [Neurospora crassa] ; cyt-5 gene [Neurospora crassa]
23877	ENU07671	ANI61C6535: 9039..8508	110-137	491-510	LINAP		g1345773	116	35	0.33			Chromodomain-helicase-DNA-binding protein 1 (CHD-1) ; (L10410) DNA-binding protein [Mus musculus]
23878	ENU07672	ANI61C59:45 75..5192	22-45	561-580	LINAP		g2851420	181	103	9.00E-22	27	26	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region ; (AE000443) orf, hypothetical protein [Escherichia coli] "
23879	ENU07673	ANI61C7187: 3306..2556	36-53	622-641	LINAP		g586312	107	55	6.00E-14	24	37	hypothetical 63.4 KD protein in SMY2-RPS101 intergenic region ; probable resistance protein - yeast (Saccharomyces cerevisiae) ; (Z36049) ORF YBR180w [Saccharomyces cerevisiae]
23880	ENU07674	ANI61C6605: 485..850	22-49	422-441	LINAP		g2132942	67	65	4.00E-10			probable membrane protein YOR306c - yeast (Saccharomyces cerevisiae) ; (Z75214) ORF YOR306c [Saccharomyces cerevisiae]
23881	ENU07675	ANI61C5928: 3691..2752	26-53	744-767	LINAP		g2414637	988	332	2.00E-90	58	37	(Z99260) probable na(+)-h(+) antiporter [Schizosaccharomyces pombe]

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23882	ENU07676	ANI61C1139 7:4176..2829	23-42	808-829	LINAP		g729417	403	142	3.00E-41	38	42	GAA1 protein ; membrane protein END2 - yeast (Saccharomyces cerevisiae) ; (X79409) Gaa1 [Saccharomyces cerevisiae] ; (U53880) Gaa1p [Saccharomyces cerevisiae] ; (Z73260) ORF YLR088w [Saccharomyces cerevisiae] (AJ223999) PCA363.5 [Amycolatopsis orientalis] (M77661) putative pol polypeptide [Magnaporthe grisea] hypothetical 50.6 KD protein in RPL14B-GPA1 intergenic region ; hypothetical protein YHR004c - yeast (Saccharomyces cerevisiae) ; (U10555) Yhr004cp [Saccharomyces cerevisiae] (AL049521) hypothetical protein [Schizosaccharomyces pombe] (AB015510) FIL-CMCase [Aspergillus aculeatus] hypothetical 65.3 KD protein in PRE3- SAG1 intergenic region ; hypothetical protein YJR001w - yeast (Saccharomyces cerevisiae) ; (X87611) ORF YJR83.4 [Saccharomyces cerevisiae] ; (Z49501) ORF YJR001w [Saccharomyces cerevisiae] (AL023592) rna binding protein [Schizosaccharomyces pombe] "N2,N2-dimethylguanosine TRNA methyltransferase precursor ; N2,N2- dimethylguanine tRNA methyltransferase - yeast (Saccharomyces cerevisiae) ; (M17193) tRNA dimethyltransferase [Saccharomyces cerevisiae] ; (Z48758) Trm1p [Saccharomyces cerevisiae]"
23883	ENU07677	ANI61C6605: 22-49 1777..2165		451-470	LINAP		g2894190	71	58	0.000000 04	30	6	
23884	ENU07678	ANI61C1136: 63-90 2200..906		733-760	LINAP		g538067	463	176	2.00E-43	39	20	
23885	ENU07679	ANI61C2838: 28-47 4406..5240		781-808	LINAP		g731630	339	94	5.00E-34	41	53	
23886	ENU07680	ANI61C9153: 35-54 3411..2201		771-790	LINAP		g4539592	458	115	1.00E-41	35	46	
23887	ENU07681	ANI61C6623: 117-137 430..1		453-479	LINAP		g3242653	262	87	2.00E-23	57	27	
23888	ENU07682	ANI61C5970: 107-127 378..1		454-478	LINAP		g1353046	302	134	4.00E-31	39	27	
23889	ENU07683	ANI61C1139 22-41 9:3306..4594		723-749	LINAP		g3136059	194	98	1.00E-19	27	19	
23890	ENU07684	ANI61C7223: 29-50 1606..1		611-630	LINAP		g136242	781	146	1.00E-34	42	42	

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23891	ENU07685	ANI61C6601: 22-45 3930..3485	22-45	445-465	LINAP		g1176495	94	111	4.00E-24	36	22	hypothetical 79.4 KD protein in PRP16-SRP40 intergenic region ; (Z28315) ORF YKR090w [Saccharomyces cerevisiae]
23892	ENU07686	ANI61C9170: 22-42 3667..4819	22-42	772-799	LINAP		g3876393	843	138	5.00E-47	53	68	(Z79695) Similarity to Human 2-oxoisovalerate dehydrogenase (SW:ODBB_HUMAN) [Caenorhabditis elegans]
23893	ENU07687	ANI61C9674: 22-47 807..441	22-47	452-471	LINAP		g3912958	128	44	0.000003	47	24	alpha-L-arabinofuranosidase precursor (arabinosidase) ; (AL021411) arabinofuranosidase [Streptomyces coelicolor]
23894	ENU07688	ANI61C1139: 34-53 1905..1591	34-53	452-479	LINAP		g1934826	71	50	0.000008	30	47	(Z93938) unknown [Bacillus subtilis]
23895	ENU07689	ANI61C9184: 30-57 2382..2699	30-57	457-479	LINAP		g3947870	52	36	0.23			(AL034382) hypothetical protein [Schizosaccharomyces pombe]
23896	ENU07690	ANI61C6633: 39-58 627..969	39-58	448-475	LINAP		g3646455	436	88	3.00E-17	73	43	(AL031603) 60s ribosomal protein [Schizosaccharomyces pombe]
23897	ENU07691	ANI61C5982: 56-75 1258..541	56-75	665-684	LINAP		g1730644	271	120	1.00E-26	32	36	hypothetical 73.4 KD protein in ERG24-MET2 intergenic region ; probable membrane protein YNL279w - yeast (Saccharomyces cerevisiae) ; (Z71555) ORF YNL279w [Saccharomyces cerevisiae]
23898	ENU07692	ANI61C1139: 68-87 2758..2293	68-87	430-449	LINAP		g3915558	122	73	1.00E-12	33	44	hypothetical 36.5 KD protein in GBSA-TLPB intergenic region ; (Z99119) similar to hypothetical proteins [Bacillus subtilis]
23899	ENU07693	ANI61C1869: 26-45 662..1	26-45	519-546	LINAP		g2492777	413	113	5.00E-35	47	59	hypothetical zinc-type alcohol dehydrogenase-like protein in PRE5-FET4 intergenic region ; hypothetical protein YMR318c - yeast (Saccharomyces cerevisiae) ; (Z54141) unknown [Saccharomyces cerevisiae]
23900	ENU07694	ANI61C5985: 44-64 512..1	44-64	453-480	LINAP		g3885836	196	67	8.00E-11	41	24	(AF091042) putative cercosporin transporter [Cercospora kikuchii]
23901	ENU07695	ANI61C1907: 52-71 534..1	52-71	456-475	LINAP		g2315274	159	88	4.00E-17	40	46	(Y11113) endoglucanase IV [Hypocrea jecorina]

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23902	ENU07696	ANI61C9180: 1991..1668	23-50	452-479	LINAP		g3925783	263	130	6.00E-30	49	24	(AL034353) glutamate n-acetyltransferase precursor [Schizosaccharomyces pombe]
23903	ENU07697	ANI61C5987: 32-51	457-479		LINAP		g4501925	252	75	6.00E-13	40	41	adducin 1 (alpha) ; (Z68280) Human tetracycline transporter-like protein mRNA [Homo sapiens]
23904	ENU07698	ANI61C1143 22-46	578-603		LINAP		g4502601	168	82	3.00E-15	32	53	carboxyl reductase 3 ; (AB004854) carboxyl reductase 3 [Homo sapiens] ; (AB003151) carboxyl reductase 3 [Homo sapiens]
23905	ENU07699	ANI61C1142 26-45	458-477		LINAP		g2133058	178	87	6.00E-17	33	41	probable transcription factor YPL230w - yeast (Saccharomyces cerevisiae) ; (X94561) transcription factor [Saccharomyces cerevisiae] ; (Z73586) ORF YPL230w [Saccharomyces cerevisiae]
23906	ENU07700	ANI61C9663: 5432..5009			LINAP		g476334	220	71	1.00E-21	44	33	(U07801) serine/threonine/tyrosine kinase [Ustilago maydis]
23907	ENU07701	ANI61C2977: 106-124	454-479		LINAP		g2853097	130	69	2.00E-11	48	56	(AL021767) hypothetical protein [Schizosaccharomyces pombe]
23908	ENU07702	ANI61C7261: 1363..1008			LINAP		g2984067	51	60	0.000000	35	18	(AE000755) transketolase [Aquifex aeolicus]
23909	ENU07703	ANI61C6642: 25-52	454-481		LINAP		g1350795	254	126	1.00E-28	40	64	"mitochondrial 60S ribosomal protein L24 precursor (YML24) ; ribosomal protein YmL24, mitochondrial - yeast (Saccharomyces cerevisiae) ; (Z47815) ribosomal protein [Saccharomyces cerevisiae]"
23910	ENU07704	ANI61C2968: 54-74	420-439		LINAP		g450864	939	286	3.00E-88	61	47	(L27993) alkaline phosphatase [Neurospora crassa]
23911	ENU07705	ANI61C6595: 22-46	722-741		LINAP		g1654028	178	61	0.000000	27	50	(Z81360) hypothetical protein Rv1726 [Mycobacterium tuberculosis]
23912	ENU07706	ANI61C5991: 26-48	644-663		LINAP		g2851420	1248	178	6.00E-79	56	33	"hypothetical 88.1 KD protein in GLTS-SELC intergenic region ; (AE000443) orf, hypothetical protein [Escherichia coli]"
23913	ENU07707	ANI61C1894: 38-57	731-750		LINAP								
		2439..4124											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
23914	ENU07708	ANI61C9673: 24-43 5828..5111	24-43	481-502	LINAP		g1806234	134	68	4.00E-17	31	78	(Z84498) hypothetical protein Rv1928c [Mycobacterium tuberculosis]
23915	ENU07709	ANI61C5961: 22-45 2804..2047	22-45	705-732	LINAP		g4501975	80	43	0.002			beta3A-adaptin ; (U91931) AP-3 complex beta3A subunit [Homo sapiens]
23916	ENU07710	ANI61C1036 22-49 3:1246..1693	22-49	453-479	LINAP		g3417427	94	45	0.0005			(AL031262) hypothetical protein [Schizosaccharomyces pombe]
23917	ENU07711	ANI61C2978: 63-90 668..1	63-90	557-582	LINAP		g1706559	118	54	0.000000 31 003	31	32	Ethanolamine kinase (easily shocked protein) ; (L35603) ethanolamine kinase [Drosophila melanogaster]
23918	ENU07712	ANI61C9701: 27-47 3206..3928	27-47	585-604	LINAP		g3850091	319	128	2.00E-37	43	42	(AL033389) putative aminotransferase [Schizosaccharomyces pombe]
23919	ENU07713	ANI61C6593: 2302..1			LINAP		g586510	1022	118	1.00E-35	45	28	hypothetical 108.0 KD helicase in HSP26-TTF32 intergenic region ; probable DNA repair protein - yeast (Saccharomyces cerevisiae) ; (X76294) ORF YBRO715; homologous to Rad54 Snf2 and Sth1 of S.cerevisiae [Saccharomyces cerevisiae] ; (Z35942) ORF YBR073w [Saccharomyces cerevisiae]
23920	ENU07714	ANI61C599:2 23-48 247..1	23-48	719-737	LINAP		g1174555	1182	170	5.00E-49	43	28	putative transcription initiation factor TFIID 111 KD subunit (TBP-associated factor 111 KD) (TAFII-111) ; hypothetical protein SPAC2G11.14 - fission yeast (Schizosaccharomyces pombe) ; (Z54354) putative transcription initiation factor tffiid subunit [Schizosaccharomyces pombe]
23921	ENU07715	ANI61C1044 38-57 3:2002..2587	38-57	531-551	LINAP		g624076	80	45	0.0004			"(U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X); similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13993 [Paramecium bursaria Chlorella virus 1]"
23922	ENU07716	ANI61C9675: 24-43 5744..6242	24-43	454-478	LINAP		g1085697	123	80	1.00E-14	29	36	chitin deacetylase - Mucor rouxii (fragment)
23923	ENU07717	ANI61C5953: 24-43 993..555	24-43	453-479	LINAP		g4456816	371	126	9.00E-29	34	17	(AL035548) hypothetical protein [Schizosaccharomyces pombe]

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23924	ENU07718	ANI61C2959: 22-48 1..1071		778-798	LINAP		g3877858	130	41	0.008	21	24	Similarity with drosophila (Z34801) MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans] ; (Z66514) Similarity with drosophila MSP-300 protein (PIR acc. no. S30431) [Caenorhabditis elegans] (X93302) Msn5 protein [Saccharomyces cerevisiae] (AF111068) DNA polymerase gamma [Neurospora crassa] "alcohol dehydrogenase (ADH-T) ; alcohol dehydrogenase (EC 1.1.1.1), thermostable - Bacillus stearothermophilus ; (D90421) alcohol dehydrogenase [Bacillus stearothermophilus] " (AB001895) B120 [Homo sapiens] (AL023534) hypothetical protein [Schizosaccharomyces pombe] (AF051140) putative glucose transporter protein [Schizosaccharomyces pombe] "(AE001002) ATP-dependent RNA helicase, putative [Archaeoglobus fulgidus] " hypothetical 93.9 KD helicase C19G10.02 in chromosome I ; (Z69909) dna repair protein [Schizosaccharomyces pombe] (AL022600) hypothetical protein [Schizosaccharomyces pombe] hypothetical 187.1 KD protein in OGG1-CNA2 intergenic region ; probable membrane protein YML059c - yeast (Saccharomyces cerevisiae) ; (Z46729) unknown [Saccharomyces cerevisiae]
23925	ENU07719	ANI61C9693: 29-56 3518..378		805-829	LINAP		g1246837	411	61	0.000000			
23926	ENU07720	ANI61C7224: 22-49 3886..663		802-829	LINAP		g4455007	3371	377	e-104	67	21	
23927	ENU07721	ANI61C6624: 41..971			LINAP		g1168347	270	53	9.00E-17	34	65	
23928	ENU07722	ANI61C1059 24-43 0:2443..1234		804-823	LINAP		g2588991	148	38	0.12			
23929	ENU07723	ANI61C3017: 102-120 1011..410		471-490	LINAP		g3130035	348	129	2.00E-32	40	29	
23930	ENU07724	ANI61C9716: 22-44 947..1		773-796	LINAP		g3746450	135	59	0.000000	27	36	
23931	ENU07725	ANI61C6617: 40-59 1820..3569		791-810	LINAP		g2649107	798	119	3.00E-31	33	35	
23932	ENU07726	ANI61C6009: 87-106 1244..451		666-685	LINAP		g1723497	371	187	6.00E-47	47	27	
23933	ENU07727	ANI61C6621: 39-62 4620..3659		761-780	LINAP		g3080533	258	145	5.00E-34	42	33	
23934	ENU07728	ANI61C600:1 26-53 273..1		723-742	LINAP		g2501686	596	207	9.00E-53	42	16	

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23935	ENU07729	ANI61C6011: 34-53 610..1027	34-53	413-432	LINAP		g2120949	94	64	5.00E-10	36	22	lipase-like enzyme - Alcaligenes eutrophus ; (L36817) lipase-like enzyme [Alcaligenes eutrophus] ; ORF 8 [Ralstonia eutropha]
23936	ENU07730	ANI61C6030: 22-47 340..640	22-47	427-454	LINAP		g4098421	132	71	7.00E-12	35	19	(U77581) sugar transporter 3 [Pichia stipitis]
23937	ENU07731	ANI61C3004: 22-49 392..3781	22-49	737-764	LINAP		g1169440	5402	321	e-135	96	6	"Dynein heavy chain, cytosolic (DYHC) ; cytoplasmic dynein heavy chain - Emericella nidulans ; (U03904) cytoplasmic dynein [Emericella nidulans] "
23938	ENU07732	ANI61C972:1 37-58 53..568	37-58	409-433	LINAP		g2842510	204	106	1.00E-22	45	15	(AL021748) hypothetical protein [Schizosaccharomyces pombe]
23939	ENU07733	ANI61C9702: 68-87 3294..4074	68-87	735-759	LINAP		g2497203	164	48	3.00E-13	26	15	hypothetical 180.2 KD protein in FAA4-HOR7 intergenic region ; probable membrane protein YMR247c - yeast (Saccharomyces cerevisiae)
23940	ENU07734	ANI61C6675: 918..1244			LINAP		g1723187	107	39	0.00005			"112.3 KD protein in PYK1-SNC1 intergenic region ; FUN12 protein - yeast (Saccharomyces cerevisiae) ; (U12980) Fun12p: 97kDa protein, function unknown [Saccharomyces cerevisiae] "
23941	ENU07735	ANI61C1136 122-145 7:322..1	122-145	442-467	LINAP		g1764098	51	41	0.004			(U81794) putative permease [Uromyces fabae]
23942	ENU07736	ANI61C9235: 32-52 1457..1992	32-52	403-425	LINAP		g3929366	714	155	1.00E-50	77	73	40S ribosomal protein S7 ; (U73847) ribosomal protein [Neurospora crassa]
23943	ENU07737	ANI61C7286: 33-52 1067..2864	33-52	655-673	LINAP		g625653	575	136	3.00E-51	54	27	ATP-dependent proteinase BsgA - Myxococcus xanthus
23944	ENU07738	ANI61C9700: 22-48 4965..5613	22-48	439-466	LINAP		g121649	150	51	8.00E-17	31	17	GRR1 protein ; GRR1 protein - yeast (Saccharomyces cerevisiae) ; (M59247) putative [Saccharomyces cerevisiae] ; (Z49590) ORF YJR090c
23945	ENU07739	ANI61C1500: 22-45 1..428	22-45	366-385	LINAP		g2257705	141	71	3.00E-12	31	11	[Saccharomyces cerevisiae] ; (L47993) ORF YJR090c [Saccharomyces cerevisiae]
													(D63905) ubiquitin ligase [Saccharomyces cerevisiae]

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23946	ENU07740	ANI61C7292: 1197..496	22-49	639-658	LINAP	g2887409	90	60	0.000000	02	30	27	(AB007877) KIAA0417 [Homo sapiens]
23947	ENU07741	ANI61C6688: 907..1343	116-135	381-399	LINAP	g4582195	195	100	8.00E-21	34	17		[Z99532] hypothetical protein [Schizosaccharomyces pombe]
23948	ENU07742	ANI61C1432: 3416..3809	47-73	262-289	LINAP	g1166378	80	44	0.0008	26	14		"[L76169] reverse transcriptase, RNaseH [Glomerella cingulata]"
23949	ENU07743	ANI61C9221: 592..1377	22-40	745-765	LINAP	g1711542	80	48	0.00007	23	76		SSO2 protein; syntaxin-related protein SSO2 - yeast [Saccharomyces cerevisiae]; (Z49808) unknown [Saccharomyces cerevisiae]
23950	ENU07744	ANI61C9697: 4700..4381	62-81	414-433	LINAP	g4100623	97	62	0.000000	32	27		(AF001630) SH3P18-like WASP associated protein [Homo sapiens]
23951	ENU07745	ANI61C7292: 1644..1233	22-43	457-476	LINAP	g115573	46	41	0.004				CAMP binding protein CABP1A/CABP1B (CABP1 protein); CABP1 protein - slime mold [Dictyostelium discoideum]; (X52688) CABP1 protein [Dictyostelium discoideum]; (M36176) cAMP binding protein [Dictyostelium discoideum] (AL033497) unknown hypothetical protein [Candida albicans]
23952	ENU07746	ANI61C6692: 1..345	102-126	293-312	LINAP	g3859703	104	48	0.00002	34	12		ryanodine receptor [Oryctolagus cuniculus]
23953	ENU07747	ANI61C1726: 903..1554	40-59	594-613	LINAP	g226386	88	45	0.0004	28	2		(Z99714) bK1048E9.2 (similar to CE02118) [Homo sapiens]
23954	ENU07748	ANI61C6692: 954..1488	44-68	413-434	LINAP	g4455408	137	78	6.00E-14	22	31		6-hydroxy-D-nicotine oxidase (6-HDNO); (X05999) 6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]
23955	ENU07749	ANI61C3030: 1689..1370	39-58	277-299	LINAP	g122805	170	62	0.000000	39	23		melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium; (D83643) polyketide synthase [Colletotrichum lagenarium] (U53876) Cdc45p: assembles into a complex with Cdc46p/Mcm5p [Saccharomyces cerevisiae]
23956	ENU07750	ANI61C923:3 457..2487	50-69	809-829	LINAP	g2147662	86	64	0.000000	21	10		transcription factor nft1 - fission yeast (Schizosaccharomyces pombe)
23957	ENU07751	ANI61C9750: 1120..549	70-92	520-539	LINAP	g1256852	202	34	0.85				
23958	ENU07752	ANI61C7276: 717..341	22-42	457-477	LINAP	g626072	69	54	0.000000	26	16		

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23959	ENU07753	ANI61C9246: 29-52 1072..1418	29-52	451-470	LINAP		g1173005	163	88	5.00E-17	43	61	60S ribosomal protein L27 ; ribosomal protein L27 - fungus (Filobasidium floriforme) ; (L37877) ribosomal protein L27 [Filobasidiella neoformans]
23960	ENU07754	ANI61C9740: 32-51 1..2223	32-51	797-816	LINAP		g2414649	909	131	5.00E-31	31	10	(Z99296) hypothetical protein [Schizosaccharomyces pombe]
23961	ENU07755	ANI61C6597: 22-41 748..1	22-41	624-647	LINAP		g2257530	502	213	8.00E-55	50	50	(AB004537) hypothetical protein YPL063w [Schizosaccharomyces pombe]
23962	ENU07756	ANI61C1963: 23-50 398..1	23-50	459-479	LINAP		g83245	96	64	5.00E-10			"transcription factor HCM1 - yeast (Saccharomyces cerevisiae) ; (X59720) YCR065w, len:532 [Saccharomyces cerevisiae]"
23963	ENU07757	ANI61C9246: 122-144 2842..2487	122-144	281-307	LINAP		g1449177	79	58	0.000000	32	14	(D86478) Crb2 [Schizosaccharomyces pombe]
23964	ENU07758	ANI61C9698: 102-121 1..685	102-121	629-656	LINAP		g2731568	196	107	7.00E-23	35	38	(AF025410) cephalosporin esterase precursor [Rhodosporidium toruloides]
23965	ENU07759	ANI61C9209: 102-121 1..611	102-121	553-580	LINAP		g2749755	72	62	0.000000	33	17	(AL021086) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=150.57; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AI238311; 2-match_description=GH14334.5prime GH Drosophila melanogaste...
23966	ENU07760	ANI61C3796: 43-62 491..1252	43-62	699-718	LINAP		g2132293	118	84	1.00E-15			hypothetical protein YPR128c - yeast (Saccharomyces cerevisiae) ; (U40829) Similar to mitochondrial ADP/ATP carrier protein (Swiss Prot. accession number P12235) and mitochondrial phosphate carrier protein (Swiss Prot. accession number Q00325) [Saccharomyces cerevisiae]
23967	ENU07761	ANI61C3052: 622..1558			LINAP		g3702646	339	126	9.00E-31	34	43	(AL031825) putative membrane transport protein [Schizosaccharomyces pombe]

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23968	ENU07762	ANI61C3806: 22-49 1576..2142	22-49	528-546	LINAP		g586486	114	65	4.00E-10	23	24	hypothetical 77.3 KD protein in FIG1-GIP1 intergenic region ; probable membrane protein YBR043c - yeast (Saccharomyces cerevisiae) ; (Z35912) ORF YBR043c [Saccharomyces cerevisiae]
23969	ENU07763	ANI61C6661: 22-49 1080..1751	22-49	627-649	LINAP		g2257523	319	159	2.00E-38	43	57	(AB004537) lipoate-protein ligase A [Schizosaccharomyces pombe]
23970	ENU07764	ANI61C297:9 744..10255	22-49		LINAP		g4160573	125	60	4.00E-11	34	16	(AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]
23971	ENU07765	ANI61C3818: 22-41 2391..1914	22-41	440-459	LINAP		g3006139	352	100	2.00E-37	54	37	(AL022299) hypothetical protein [Schizosaccharomyces pombe]
23972	ENU07766	ANI61C9698: 22-43 8097..8486	22-43	427-451	LINAP		g1708501	84	49	0.000000	34	7	Integrin alpha chain-like protein (alpha-INT1) ; (U35070) integrin-like protein alpha Int1p [Candida albicans]
23973	ENU07767	ANI61C7307: 67-94 523..1333	67-94	768-790	LINAP		g136125	166	94	9.00E-19	30	30	putative AC transposase (ORFA) ; (X05424) ORFa [Zea mays]
23974	ENU07768	ANI61C6716: 111-130 2520..2076	111-130	341-360	LINAP		g731872	66	65	2.00E-10			"putative 108.8 KD transcriptional regulatory protein in FKH1-STH1 intergenic region ; probable membrane protein YTL130w - yeast (Saccharomyces cerevisiae) ; (Z38059) orf, len: 964, CAl: 0.15, possible regulatory protein [Saccharomyces cerevisiae] "
23975	ENU07769	ANI61C1918: 22-40 2568..660	22-40	796-815	LINAP		g113449	1374	168	4.00E-41	55	25	"probable ATP-dependent permease precursor ; ATP-dependent permease ADP1 precursor - yeast (Saccharomyces cerevisiae) ; (X59720) YCR011c, len: 1049 [Saccharomyces cerevisiae] "
23976	ENU07770	ANI61C3066: 22-44 879..134	22-44	660-679	LINAP		g2246452	106	50	0.00002	31	34	(U71107) S-adenosyl-methionine-sterol-C-methyltransferase homolog [Nicotiana tabacum]
23977	ENU07771	ANI61C9727: 33-53 642..1451	33-53	758-779	LINAP		g2656003	734	271	4.00E-72	69	74	(Z98980) hypothetical protein [Schizosaccharomyces pombe]

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23978	ENU07772	ANI61C6686: 22-49 981..219	22-49	563-584	LINAP		g731298	219	59	5.00E-16	36	35	probable transporter SEO1 ; probable membrane protein YAL067c - yeast (Saccharomyces cerevisiae) ; (U12980) Scd1p: putative membrane protein [Saccharomyces cerevisiae]
23979	ENU07773	ANI61C3047: 23-50 1105..347	23-50	592-611	LINAP		g2801701	405	106	1.00E-22	36	22	(AF042379) spindle pole body protein spc97 homolog GCP2 [Homo sapiens] "(U80668) homogenisate 1,2-dioxygenase [Arabidopsis thaliana] " (D87686) KIAA0017 protein [Homo sapiens]
23980	ENU07774	ANI61C3850: 117-136 1..334	117-136	282-303	LINAP		g4098647	159	85	2.00E-16	43	24	hypothetical protein KIAA0210 ; (D86965) similar to a putative protein coded in Caenorhabditis elegans cosmid B0393. [Homo sapiens]
23981	ENU07775	ANI61C311:1 380..679	61-84	549-576	LINAP		g3540219	705	217	8.00E-56	51	19	hypothetical protein YLR357w - yeast (Saccharomyces cerevisiae) ; (U19102) Ylr357wp [Saccharomyces cerevisiae]
23982	ENU07776	ANI61C7345: 61-84 1..597	61-84	549-576	LINAP		g2495720	173	69	6.00E-20	35	20	probable N-end-recognizing protein (ubiquitin-protein ligase E3 component) (N-recognin) ; (AL023859) putative ubiquitin protein ligase [Schizosaccharomyces pombe]
23983	ENU07777	ANI61C6723: 1583..570	43-62	811-829	LINAP		g1077415	529	239	2.00E-62	40	31	alpha-glucosidase precursor (maltase) ; (D86624) alpha-glucosidase precursor [Spinacia oleracea]
23984	ENU07778	ANI61C1952: 43-62 1269..2376	43-62	811-829	LINAP		g3915187	902	170	9.00E-49	40	14	G1/S-specific cyclin PCL1 (cyclin HCS26) ; cyclin G1 homolog HCS26 - yeast (Saccharomyces cerevisiae) ; (M73966) G1 cyclin [Saccharomyces cerevisiae] ; (Z71565) ORF YNL289w [Saccharomyces cerevisiae]
23985	ENU07779	ANI61C9727: 22-46 4681..5583	22-46	724-749	LINAP		g3023260	426	115	6.00E-48	48	23	N amino acid transport system protein (methyltryptophan resistance protein) ; neutral amino acid permease - Neurospora crassa ; (L34605) neutral amino acid permease [Neurospora crassa]
23986	ENU07780	ANI61C7285: 25-48 3265..3862	25-48	363-383	LINAP		g116149	297	139	2.00E-32	47	63	
23987	ENU07781	ANI61C298:5 891..4773	22-42	784-803	LINAP		g2507070	182	65	7.00E-10	31	50	

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23988	ENU07782	ANI61C3844: 57-76 379..1042		620-643	LINAP		g1363740	157	76	2.00E-13	36	81	probable membrane protein YLR251w - yeast (Saccharomyces cerevisiae) ; (U20865) Ylr251 wp [Saccharomyces cerevisiae]
23989	ENU07783	ANI61C9748: 23-42 561..1		513-540	LINAP		g3874557	356	166	1.00E-40	45	25	(Z81041) predicted using Genefinder; Similarity to E.coli L-asparaginase (SW:P18840); cDNA EST EMBL:D34586 comes from this gene; cDNA EST EMBL:D35768 comes from this gene; cDNA EST EMBL:D64950 comes from this gene; cDNA EST EMB...
23990	ENU07784	ANI61C6697: 42-61 3617..5527		799-825	LINAP		g671684	1353	200	1.00E-50	40	32	(U20346) H antigen precursor [Ajellomyces capsulatus]
23991	ENU07785	ANI61C2019: 22-45 374..72		443-469	LINAP		g2660584	111	39	0.021			(Y11823) colicin U [Shigella boydii]
23992	ENU07786	ANI61C298:7 23-50 839..831		440-467	LINAP		g118239	117	52	0.000004	35	53	"dihydrodipicolinate synthase (DHDPs) ; (X53993) L-2,3-dihydrodipicolinate synthetase [Corynebacterium glutamicum] "
23993	ENU07787	ANI61C9755: 40-59 1197..511		637-656	LINAP		g550095	296	145	2.00E-34	43	18	(D38310) Boi2p [Saccharomyces cerevisiae]
23994	ENU07788	ANI61C3107: 22-42 1458..2133		621-643	LINAP		g4490979	136	83	2.00E-15			(AL035707) CDA peptide synthetase III [Streptomyces coelicolor]
23995	ENU07789	ANI61C6711: 30-54 3450..4811		709-730	LINAP		g2739028	115	57	0.000000			(AF023919) PK-120 precursor [Mus musculus]
23996	ENU07790	ANI61C9731: 38-58 4153..4547		436-455	LINAP		g114866	55	57	0.000000	33	49	Magnesium-chelataase 30 KD subunit ; bchO protein - Rhodobacter capsulatus ; (Z11165) 284 aa (30 kD) Mg chelataase subunit [Rhodobacter capsulatus]
23997	ENU07791	ANI61C2060: 28-50 600..1		508-535	LINAP		g2408014	186	106	1.00E-22	33	41	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
23998	ENU07792	ANI61C3860: 47-66 2937..774		789-808	LINAP		g2147662	987	145	3.00E-34	36	12	melanin biosynthetic polyketide synthase PKS1 - Colletotrichum lagenarium ; (D83643) polyketide synthase [Colletotrichum lagenarium]

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23999	ENU07793	ANI61C7926: 2051..472	24-43	804-829	LINAP		g541015	265	32	4			hypothetical protein 471 - Rhizobium leguminosarum ; (X77198) orf471; homologous to NodT [Rhizobium leguminosarum]
24000	ENU07794	ANI61C7335: 2014..2622	22-44	535-554	LINAP		g729344	138	104	4.00E-22			"DLTE protein ; hypothetical protein - Bacillus subtilis ; dltE product[putative cytosolic oxidoreductase [Bacillus subtilis, Peptide, 252 aa] ; (X73124) ipa-1r [Bacillus subtilis] ; (Z99123) alternate gene name: ipa-1r [Bacillus subtilis]"
24001	ENU07795	ANI61C3863: 2806..1	22-45	707-730	LINAP		g2414649	471	116	1.00E-25	29	10	(Z99296) hypothetical protein [Schizosaccharomyces pombe]
24002	ENU07796	ANI61C7355: 1301..2388	22-41	771-790	LINAP		g131777	868	232	3.00E-60	47	24	DNA repair protein RAD13 ; excision repair protein - fission yeast (Schizosaccharomyces pombe) ; (X66795) excision repair protein [Schizosaccharomyces pombe]
24003	ENU07797	ANI61C380:1..376	112-131	330-349	LINAP		g1122901	39	39	0.013			(X94215) MSP8 [Saccharomyces cerevisiae]
24004	ENU07798	ANI61C7962: 1..473	51-70	407-426	LINAP		g1166378	44	108	2.00E-23	36	14	"(L76169) reverse transcriptase, RNaseH [Glomerella cingulata]"
24005	ENU07799	ANI61C6708: 1..380	121-140	311-330	LINAP		g3818605	166	68	2.00E-11	44	3	"(AF091251) Ybt peptide/polyketide synthetase HMWP1 [Yersinia pestis] ; (AL031866) ORF68, len=3163 aa, irp1, function=synthesis of siderophore yersiniabactin, product=HMWP1 protein, 97.9% identity in 3163 aa overlap to YEIRPOP_1
24006	ENU07800	ANI61C31:1..949	32-51	804-826	LINAP		g861336	170	75	2.00E-13	40	69	Y.enterocolitica irp1, FastA scores: opt: 2088, E0: 0 [Yersinia pestis]" (U28943) similar to hydrtase-dehydrogenase-epimerase (HDE) [Caenorhabditis elegans]
24007	ENU07801	ANI61C9759: 1593..957	22-44	571-590	LINAP		g1729996	244	112	3.00E-24	38	68	TOXD protein ; (X92391) unique to isolates that make the cyclic peptide HC-toxin [Cochliobolus carbonum]

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24008	ENU07802	ANI61C2070: 1017..451			LINAP		g123338	414	63	1.00E-18			3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 (HMG-CoA reductase 2) ; hydroxymethylglutaryl-CoA reductase (EC 1.1.1.88) II - yeast (Saccharomyces cerevisiae) ; (M22255) 3-hydroxy-3-methyl glutaryl coenzyme A reductase [Saccharomyces cerevisiae] ; (U22382) Hmg2p: 3-hydroxy-3-methylglutaryl-coenzyme A (HMG-CoA) reductase [Saccharomyces cerevisiae] (AF079317) unknown [Spingomonas aromaticivorans] geranylgeranyl transferase type I beta subunit (type I protein geranylgeranyltransferase beta subunit) (GGTASE-I-beta) ; geranylgeranyl-diphosphate geranylgeranyltransferase (EC 2.5.1.32) I beta chain - rat ; (L24116) geranylgeranyltransferase type I [Rattus norvegicus] probable kynureninase (L-kynurenine hydrolase) ; (U56965) similar to R. norvegicus kynureninase (PIR:PS0370) [Caenorhabditis elegans] (AL031644) RAD16 nucleotide excision repair protein homolog [Schizosaccharomyces pombe] (AL031764) putative helicase [Schizosaccharomyces pombe] fumarate reductase (NADH) (EC 1.3.1.6) - yeast (Saccharomyces cerevisiae) (X97581) spalt protein [Mus musculus] hypothetical 17.3 KD protein in ERP5-ORC6 intergenic region ; hypothetical protein YHR116w - yeast (Saccharomyces cerevisiae) ; (U00059) Yhr116wp [Saccharomyces cerevisiae]
24009	ENU07803	ANI61C31:35 29-48 29..2201		796-815	LINAP		g3378265	502	164	9.00E-40	34	63	
24010	ENU07804	ANI61C3888: 29-52 479..12		453-479	LINAP		g1730527	110	49	0.000000 001	35	34	
24011	ENU07805	ANI61C7983: 25-52 584..1		526-552	LINAP		g3913983	340	116	5.00E-36	53	34	
24012	ENU07806	ANI61C7368: 39-66 1492..1		699-726	LINAP		g3647341	615	92	8.00E-21	43	22	
24013	ENU07807	ANI61C2088: 53-72 226..1027		757-781	LINAP		g3668152	142	113	1.00E-24			
24014	ENU07808	ANI61C3109: 206-233 384..1066		633-660	LINAP		g2131257	249	120	1.00E-26	39	47	
24015	ENU07809	ANI61C3867: 32-51 1045..1509		455-479	LINAP		g1296845	68	48	0.00005			
24016	ENU07810	ANI61C6714: 22-46 572..872		459-479	LINAP		g731704	84	46	0.0002	41	42	

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24017	ENU07811	ANI61C2045: 22-40 660..1	532-559	LINAP			g115689	472	96	5.00E-47	58	55	nuclear protein SNF4 (regulatory protein CAT3); CAT3 protein - yeast (Saccharomyces cerevisiae); (M21760) regulatory protein CAT3 [Saccharomyces cerevisiae]; (M30470) SNF4 protein [Saccharomyces cerevisiae]; (Z72637) ORF YGL115w [Saccharomyces cerevisiae] "(AL031852) valyl-trna synthetase, mitochondrial precursor [Schizosaccharomyces pombe]; (AL031856) valyl-trna synthetase, mitochondrial precursor [Schizosaccharomyces pombe] " probable sterigmatoctystin biosynthesis P450 monooxygenase STCB (cytochrome P450 62); (U34740) putative p450 monooxygenase [Emeritella nidulans] (AF013216) unknown [Myxococcus xanthus] hypothetical 65.3 KD protein in SUN4-MASS intergenic region; probable membrane protein YNL065w - yeast (Saccharomyces cerevisiae); (U12141) membrane protein [Saccharomyces cerevisiae]; (Z71341) ORF YNL065w [Saccharomyces cerevisiae] cytochrome B5
24018	ENU07812	ANI61C3092: 26-53 4451..5044	438-461	LINAP			g3738140	516	219	1.00E-56	56	20	
24019	ENU07813	ANI61C9741: 5356..6142		LINAP			g2493391	209	70	2.00E-11	32	26	
24020	ENU07814	ANI61C6714: 23-42 6661..7031	423-450	LINAP			g2384693	100	31	4.6			
24021	ENU07815	ANI61C2101: 670..1		LINAP			g1730741	143	61	3.00E-12	25	38	
24022	ENU07816	ANI61C3893: 45-64 1669..1973	450-477	LINAP			g117808	158	81	6.00E-15	48	55	
24023	ENU07817	ANI61C9739: 28-54 4457..2354	800-819	LINAP			g3243033	251	83	3.00E-15	27	40	(AF069765) signal recognition particle 72 [Homo sapiens]; (AF077019) signal recognition particle 72 [Homo sapiens]
24024	ENU07818	ANI61C7925: 4042..3499		LINAP			g1174472	126	66	1.00E-10	29	35	probable sucrose utilization protein SUC1
24025	ENU07819	ANI61C6769: 22-46 1062..258	728-754	LINAP			g2443355	207	76	2.00E-13	37	26	(AB003395) ent-Kaurene synthase [Phacosphaeria sp. L487]

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24026	ENU07820	ANI61C2111: 316..685			LINAP		g4038642	265	87	3.00E-20	54	29	(D87063) chitinase [Emericella nidulans]
24027	ENU07821	ANI61C3136: 211-238	455-479		LINAP		g2239197	137	80	8.00E-15	32	76	(Z97209) ureidoglycolate hydrolase [Schizosaccharomyces pombe]
24028	ENU07822	ANI61C9770: 37-57 3123..3644	468-495		LINAP		g1730641	159	146	1.00E-34	48	26	hypothetical 65.0 KD protein in MET2-SEC2 intergenic region ; probable membrane protein YNL275w - yeast (Saccharomyces cerevisiae) ; (Z71551) ORF YNL275w [Saccharomyces cerevisiae]
24029	ENU07823	ANI61C7336: 52-71 1..3069	807-829		LINAP		g119830	2976	299	1.00E-80	52	15	"fatty acid synthase, subunit alpha [contains: EC 1.1.1.100; EC 2.3.1.41] ; fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum ; (M37461) FAS2 protein [Penicillium patulum] " (AC003952) putative histidine kinase [Arabidopsis thaliana]
24030	ENU07824	ANI61C2130: 22-43 581..97	420-439		LINAP		g2708752	74	60	0.000000			[AF016696] peptide synthetase module [Streptomyces fradiae]
24031	ENU07825	ANI61C3134: 101-127 2089..1338	706-731		LINAP		g2738765	82	102	2.00E-21			DNA polymerase alpha/PRIMASE associated subunit (P86 subunit) ; probable membrane protein YBL035c - yeast (Saccharomyces cerevisiae) ; (X74738) ORF YBL0415 [Saccharomyces cerevisiae] ; (Z35796) ORF YBL035c [Saccharomyces cerevisiae] ; ORF YBL0415 [Saccharomyces cerevisiae]
24032	ENU07826	ANI61C9760: 22-42 741..1	618-639		LINAP		g585063	415	150	1.00E-35	39	34	hypothetical 50.2 KD protein in CPT1-SPC98 intergenic region ; probable tyrosine phosphatase YNL128w - yeast (Saccharomyces cerevisiae) ; (Z46843) tyrosine phosphatase (putative) [Saccharomyces cerevisiae] ; (Z71404) ORF YNL128w [Saccharomyces cerevisiae]
24033	ENU07827	ANI61C6776: 35-54 1436..1979	472-494		LINAP		g1730775	98	42	0.000000	35	32	ORF YBL0415 [Saccharomyces cerevisiae]
24034	ENU07828	ANI61C3146: 24-42 1603..2092	264-283		LINAP		g3559814	312	118	2.00E-26	58	16	hypothetical 50.2 KD protein in CPT1-SPC98 intergenic region ; probable tyrosine phosphatase YNL128w - yeast (Saccharomyces cerevisiae) ; (Z46843) tyrosine phosphatase (putative) [Saccharomyces cerevisiae] ; (Z71404) ORF YNL128w [Saccharomyces cerevisiae]

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24035	ENU07830	ANI61C1460: 363..79			GTBX	AFUc04191				1.4E-57			
24036	ENU07831	ANI61C2191: 6033..2276			GTBX	"AFUc11304, AFUc11498, AFUc11616, AFUc15909, FGRc06071, FGRc10768, FGRc16185"				"4.8e-14, 1.9e-37, 4.7e-31, 4.5e-41, 4.6e-13, 3.6e-12, 6.2e-19"			
24037	ENU07832	ANI61C1464: 793..74			GTBX	AFUc11953				2.2E-73			
24038	ENU07833	ANI61C1466: 193..825			GTBX	AFUc10467				2.8E-31			
24039	ENU07834	ANI61C1468: 478..158			GTBX	AFUc15379				2.2E-24			
24040	ENU07835	ANI61C1469: 740..1360			GTBX	AFUc03772				3.4E-28			
24041	ENU07836	ANI61C2198: 878..9			GTBX	"AFUc06520, FGRc12926"				"1.7e-59, 2.2e-35"			
24042	ENU07837	ANI61C1474: 1..420			GTBX	AFUc04846				2.4E-41			
24043	ENU07838	ANI61C302:2 275..1774			GTBX	AFUc03198				4.2E-41			
24044	ENU07839	ANI61C304:5 59..966			GTBX	FGRc09646				1.7E-25			
24045	ENU07840	ANI61C305:2 799..474			GTBX	"AFUc13219, AFUc19102, CALc06130"				"7.3e-143, 8.3e-57, 1.7e-156"			
24046	ENU07841	ANI61C1027 0:6065..7449			GTBX	"AFUc12274, AFUc19270, AFUc19270"				"3.8e-63, 7.1e-10, 7.4e-08"			

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24047	ENU07842	ANI61C1027 3:250..1270			GTBX	"AFUc01302, AFUc18982, FGRc04116"				"1.6e-111, 6.2e-14, 1.2e-30"			
24048	ENU07843	ANI61C1027 4:2845..3490			GTBX	"AFUc05575, AFUc07542"				"4.3e-09, 9.4e-21"			
24049	ENU07844	ANI61C1027 5:2551..4131			GTBX	"AFUc01701, AFUc09710, AFUc09710, AFUc12211, AFUc20787, AFUc21939, Z71256"				"7.0e-23, 3.3e-23, 3.9e-14, 3.9e-24, 1.9e-13, 3.3e-25, 2.7e-07" 3.9E-33			
24050	ENU07845	ANI61C1027 9:79..1101			GTBX	FGRc22675							
24051	ENU07846	ANI61C1481: 592..54			GTBX	"AFUc10211, AFUc15427"				"4.2e-36, 6.7e-28"			
24052	ENU07847	ANI61C1487: 963..1571			GTBX	"AFUc04386, CALc02388"				"3.3e-81, 1.6e-08"			
24053	ENU07848	ANI61C1489: 487..281			GTBX	AFUc14845				8.1E-30			
24054	ENU07849	ANI61C1028 0:1900..466			GTBX	"AFUc01505, AFUc06388, FGRc05792, FGRc08715, FGRc10632"				"7.8e-46, 1.3e-45, 1.0e-20, 3.2e-18, 9.6e-14" 1.3E-129			
24055	ENU07850	ANI61C1028 2:1207..1860			GTBX	AFUc14473							
24056	ENU07851	ANI61C1028 5:548..831			GTBX	"CALc03391, Y13137"				"9.0e-29, 6.1e-39"			
24057	ENU07852	ANI61C1028 7:1684..2097			GTBX	U00092				6.0e-55			

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24058	ENU07853	ANI61C1493:117..1265			GTBX	"AFUc19753, FGRc23159"				"2.0e-25, 7.6e-27"			
24059	ENU07854	ANI61C1495:294..538			GTBX	U00094				1.6e-51			
24060	ENU07855	ANI61C1496:741..115			GTBX	AFUc03226				1.3E-38			
24061	ENU07856	ANI61C320:251..612			GTBX	AFUc12957				1.1E-40			
24062	ENU07857	ANI61C321:7229..6601			GTBX	AFUc21833				5E-31			
24063	ENU07858	ANI61C322:3260..3635			GTBX	"AFUc20332, FGRc09045"				"4.5e-25, 5.0e-15"			
24064	ENU07859	ANI61C327:400..34			GTBX	FGRc11552				3E-22			
24065	ENU07860	ANI61C10296:2669..18			GTBX	"AFUc15183, CALc05935"				"1.6e-85, 5.4e-262"			
24066	ENU07861	ANI61C10296:11566..1224			GTBX	AFUc15911				7E-93			
24067	ENU07862	ANI61C10297:23..1444			GTBX	AFUc15769				9.4E-113			
24068	ENU07863	ANI61C10299:1537..3212			GTBX	"AFUc21263, FGRc09112"				"3.8e-55, 6.6e-63"			
24069	ENU07864	ANI61C10299:4892..3860			GTBX	AFUc12138				5.7E-25			
24070	ENU07865	ANI61C10299:5928..6774			GTBX	AFUc03113				5.7E-64			
24071	ENU07866	ANI61C1:30..683			GTBX	AFUc09360				4.1E-27			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24072	ENU07867	ANI61C1:104 7..769			GTBX	AFUc18004				7.5E-30			
24073	ENU07868	ANI61C2:458 ..5			GTBX	"AFUc04176, FGRc07928"				"3.7e-38, 1.7e-22"			
24074	ENU07869	ANI61C330:2 112..1395			GTBX	AFUc02133				2.9E-65			
24075	ENU07870	ANI61C333:6 49..911			GTBX	AFUc06176				7.7E-23			
24076	ENU07871	ANI61C340:9 66..691			GTBX	AFUc04374				1.7E-27			
24077	ENU07872	ANI61C343:6 76..13			GTBX	AFUc12179				7E-45			
24078	ENU07873	ANI61C345:2 853..1498			GTBX	AFUc12264				1.2E-94			
24079	ENU07874	ANI61C352:1 1341..11766			GTBX	"AFUc12377, X59720"				"1.8e-70, 2.1e-12"			
24080	ENU07875	ANI61C352:1 2904..12374			GTBX	AFUc12377				2E-59			
24081	ENU07876	ANI61C362:1 70..1977			GTBX	"AFUc12101, AFUc14601, FGRc23569"				"6.3e- 111, 9.1e-18, 2.5e-38"			
24082	ENU07877	ANI61C7202: 1145..858			GTBX	"AFUc05840, AFUc05840, CALc06220"				"4.0e-26, 7.6e-12, 2.2e-58"			
24083	ENU07878	ANI61C7204: 1288..1623			GTBX	AFUc14370				7.4E-25			
24084	ENU07879	ANI61C373:4 8..451			GTBX	AFUc17629				5.7E-30			
24085	ENU07880	ANI61C379:4 01..66			GTBX	Y13135				3.8e-21			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24086	ENU07881	ANI61C379:4 245..5557			GTBX	"AFUc04762, FGRc21465"				"7.2e-41, 2.0e-37"			
24087	ENU07882	ANI61C379:7 058..6858			GTBX	AFUc15378				1.4E-23			
24088	ENU07883	ANI61C382:1 430..510			GTBX	"AFUc10214, AFUc13687"				"1.0e-56, 4.9e-33"			
24089	ENU07884	ANI61C383:3 030..3578			GTBX	AFUc06191				1.1E-56			
24090	ENU07885	ANI61C7223: 6059..5046			GTBX	"CALc05044, FGRc18203"				"2.8e-67, 1.6e-41"			
24091	ENU07886	ANI61C395:1 29..502			GTBX	FGRc01389				7.2E-34			
24092	ENU07887	ANI61C7231: 571..130			GTBX	AFUc06018				5.9E-32			
24093	ENU07888	ANI61C7232: 1188..2754			GTBX	"AFUc15564, AFUc20293"				"2.5e-99, 1.8e-34"			
24094	ENU07889	ANI61C7232: 6257..6705			GTBX	AFUc02538				1E-33			
24095	ENU07890	ANI61C6504: 15..1182			GTBX	AFUc12291				3.4E-21			
24096	ENU07891	ANI61C7234: 1359..273			GTBX	"AFUc07075, AFUc15048"				"2.8e-85, 4.2e-17"			
24097	ENU07892	ANI61C7236: 3414..1523			GTBX	"AFUc04239, AFUc09737"				"7.5e- 119, 1.4e-36"			
24098	ENU07893	ANI61C7242: 1515..1201			GTBX	FGRc19758				1.1E-23			
24099	ENU07894	ANI61C6518: 848..1501			GTBX	AFUc09603				1.7E-54			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24100	ENU07895	ANI61C7249: 1489..574			GTBX	"FGRc17352, U00092"				"9.7e-37, 2.3e-30"			
24101	ENU07896	ANI61C6521: 103..759			GTBX	"AFUc06725, AFUc09341"				"2.4e-12, 1.1e-35"			
24102	ENU07897	ANI61C7251: 609..10			GTBX	AFUc13794				8.5E-76			
24103	ENU07898	ANI61C7252: 785..43			GTBX	"AFUc11055, FGRc22632"				"3.1e-95, 4.2e-07"			
24104	ENU07899	ANI61C6526: 4472..3329			GTBX	"AFUc00779, FGRc05727, FGRc22503"				"2.2e-24, 2.1e-14, 3.0e-17"			
24105	ENU07900	ANI61C6527: 6158..6573			GTBX	"AFUc12900, FGRc14925"				"2.5e- 164, 9.5e-14"			
24106	ENU07901	ANI61C6532: 3..497			GTBX	AFUc01942				2.9E-60			
24107	ENU07902	ANI61C6532: 3956..6787			GTBX	"AFUc05806, AFUc12778, AFUc19750"				"2.6e-52, 5.2e- 157, 1.0e-21"			
24108	ENU07903	ANI61C6535: 4190..5827			GTBX	"AFUc16901, FGRc10006"				"6.8e-44, 4.9e-23"			
24109	ENU07904	ANI61C6535: 10281..9997			GTBX	AFUc03224				3.4E-43			
24110	ENU07905	ANI61C5807: 670..1293			GTBX	"AFUc08318, AFUc08318, FGRc09465"				"3.6e-82, 4.6e-80, 2.3e-35"			
24111	ENU07906	ANI61C5808: 514..1299			GTBX	"AFUc04514, AFUc13919, CALc05514, D50167"				"1.2e-76, 1.0e-07, 4.8e-25, 4.5e-08"			
24112	ENU07907	ANI61C5809: 284..6			GTBX	AFUc16862				3.8E-27			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24113	ENU07908	ANI61C5810: 819..47			GTBX	"AFUc08467, CALc05923"				"4.4e-09, 8.3e-56"			
24114	ENU07909	ANI61C6540: 3119..3417			GTBX	AFUc08906				9E-44			
24115	ENU07910	ANI61C5813: 460..1074			GTBX	AFUc12201				7.9E-95			
24116	ENU07911	ANI61C7273: 960..2083			GTBX	AFUc10281				1.1E-47			
24117	ENU07912	ANI61C7274: 1136..206			GTBX	AFUc03210				2.9E-57			
24118	ENU07913	ANI61C7276: 3527..4341			GTBX	"AFUc01802, FGRC10582"				"1.6e-22, 1.3e-15"			
24119	ENU07914	ANI61S207:5 43..121			GTBX	AFUc07853				3.8E-25			
24120	ENU07915	ANI61C7280: 335..1938			GTBX	"FGRC08244, FGRC16187"				"1.3e-71, 2.0e-46"			
24121	ENU07916	ANI61C6552: 3134..4669			GTBX	"AFUc13978, AFUc16716, AFUc19617, FGRC15557"				"1.1e-31, 1.4e-29, 2.0e-44, 6.2e-18"			
24122	ENU07917	ANI61C6553: 3869..4420			GTBX	AFUc11116				5.8E-30			
24123	ENU07918	ANI61C6556: 441..97			GTBX	AFUc13317				1.2E-36			
24124	ENU07919	ANI61C7285: 916..1315			GTBX	FGRC02595				1.9E-36			
24125	ENU07920	ANI61C7285: 7900..8248			GTBX	AFUc15172				4.4E-69			
24126	ENU07921	ANI61C5829: 736..359			GTBX	AFUc08971				4.2E-34			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24127	ENU07922	ANI61S219:484..9			GTBX	AFUc08358				1.5E-60			
24128	ENU07923	ANI61C5831:903..18			GTBX	AFUc14499				6.3E-77			
24129	ENU07924	ANI61C7290:909..336			GTBX	Y13134				3.0e-28			
24130	ENU07925	ANI61C6562:1020..89			GTBX	"AFUc01328, AFUc04061"				"6.1e-55, 3.1e-53"			
24131	ENU07926	ANI61C5834:536..1960			GTBX	CALc03151				8.9E-171			
24132	ENU07927	ANI61C5835:1327..116			GTBX	"AFUc02187, AFUc12580, AFUc16794"				"1.4e-14, 1.9e-07, 4.2e-61"			
24133	ENU07928	ANI61C6564:16..965			GTBX	"AFUc16593, FGRc03157"				"4.2e-43, 1.2e-11"			
24134	ENU07929	ANI61C5836:693..5			GTBX	"CALc04906, FGRc04099"				"2.4e-48, 8.5e-59"			
24135	ENU07930	ANI61C5837:3117..648			GTBX	AFUc14040				8.4E-26			
24136	ENU07931	ANI61C7298:592..8			GTBX	CALc06027				3E-39			
24137	ENU07932	ANI61C6570:951..739			GTBX	CALc06157				1.4E-65			
24138	ENU07933	ANI61C6579:931..141			GTBX	"AFUc02825, AFUc16044"				"9.5e-21, 9.7e-09"			
24139	ENU07934	ANI61C5852:88..835			GTBX	CALc05688				3.7E-57			
24140	ENU07935	ANI61C5852:2281..1223			GTBX	"AFUc07544, AFUc08833"				"7.4e-09, 2.7e-29"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24141	ENU07936	ANI61C5853:1007..1811			GTBX	"AFUc10318, AFUc15156"				"4.9e-73, 1.7e-72"			
24142	ENU07937	ANI61C6585:892..1140			GTBX	"AFUc05311, AFUc05311"				"1.7e-47, 1.7e-73"			
24143	ENU07938	ANI61C6588:1804..14			GTBX	"AFUc08190, AFUc11152, AFUc15526, FGRc05298"				"1.2e-09, 2.1e-62, 3.6e-10, 1.1e-08"			
24144	ENU07939	ANI61C5865:538..89			GTBX	FGRc10441				1.7E-47			
24145	ENU07940	ANI61C6598:1573..2608			GTBX	"AFUc01830, FGRc04488"				"2.3e-50, 9.2e-32"			
24146	ENU07941	ANI61S8:287..42			GTBX	AFUc04879				2.1E-32			
24147	ENU07942	ANI61C5885:361..1250			GTBX	AFUc15363				3.4E-94			
24148	ENU07943	ANI61C5886:756..40			GTBX	AFUc19850				9.8E-58			
24149	ENU07944	ANI61C5888:643..1866			GTBX	FGRc11984				1.5E-95			
24150	ENU07945	ANI61S2026:43..360			GTBX	AFUc10511				2.8E-36			
24151	ENU07946	ANI61S1309:546..16			GTBX	AFUc06122				3.2E-88			
24152	ENU07947	ANI61C2202:737..1023			GTBX	"AFUc10677, Y13136"				"1.8e-20, 3.0e-102"			
24153	ENU07948	ANI61C2209:1288..64			GTBX	"AFUc17374, AFUc20460"				"1.1e-59, 9.1e-31"			
24154	ENU07949	ANI61C1100:0:8262..9041			GTBX	AFUc14297				3.3E-45			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24155	ENU07950	ANI61C1100 4:1954..1302			GTBX	AFUc14982				1E-161			
24156	ENU07951	ANI61C2214: 1695..1099			GTBX	AFUc10709				1.3E-47			
24157	ENU07952	ANI61C2216: 54..1022			GTBX	Z71256				9.0e-15			
24158	ENU07953	ANI61C1101 0:1243..2169			GTBX	"AFUc14408, FGRc07288"				"4.0e-33, 2.4e-38"			
24159	ENU07954	ANI61C2220: 29..773			GTBX	AFUc02313				8.5E-22			
24160	ENU07955	ANI61C1102 3:79..1083			GTBX	"AFUc06153, AFUc21355, FGRc08305"				"3.7e-61, 9.8e-54, 4.2e-07"			
24161	ENU07956	ANI61C2235: 1966..1466			GTBX	AFUc06983				6.5E-57			
24162	ENU07957	ANI61C1103 0:300..2243			GTBX	"AFUc15517, AFUc20784, FGRc15017"				"2.6e-20, 4.8e-15, 3.1e-29"			
24163	ENU07958	ANI61C1103 0:8409..9713			GTBX	"AFUc06388, FGRc05792"				"1.0e-22, 8.0e-25"			
24164	ENU07959	ANI61C1103 1:1655..2023			GTBX	AFUc13932				2.9E-51			
24165	ENU07960	ANI61C1103 2:497..48			GTBX	AFUc11402				2.7E-50			
24166	ENU07961	ANI61C1030 4:273..800			GTBX	AFUc15094				5.6E-72			
24167	ENU07962	ANI61C1030 6:613..14			GTBX	AFUc13032				4.4E-37			
24168	ENU07963	ANI61C1103 7:5775..6531			GTBX	AFUc07195				7E-57			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24169	ENU07964	ANI61C1103 8:14225..1277 0			GTBX	"AFUc09489, FGRc09616"				"9.0e-26, 3.6e-17"			
24170	ENU07965	ANI61S1346: 92..435			GTBX	AFUc02348				1.4E-44			
24171	ENU07966	ANI61C1511: 378..1139			GTBX	U00094				5.2e-38			
24172	ENU07967	ANI61C2242: 2406..1912			GTBX	AFUc03452				8.1E-49			
24173	ENU07968	ANI61C1514: 220..815			GTBX	AFUc15554				1.7E-79			
24174	ENU07969	ANI61C1518: 1333..817			GTBX	"AFUc13493, FGRc25564"				"6.5e-23, 4.9e-25"			
24175	ENU07970	ANI61C2249: 68..817			GTBX	AFUc08878				3.5E-79			
24176	ENU07971	ANI61C1031 0:1335..71			GTBX	AFUc09721				3.6E-27			
24177	ENU07972	ANI61C1104 0:2002..2735			GTBX	AFUc09896				3.5E-52			
24178	ENU07973	ANI61C1104 1:851..1973			GTBX	AFUc10517				2.5E-94			
24179	ENU07974	ANI61C1031 3:385..29			GTBX	FGRc07645				1.9E-21			
24180	ENU07975	ANI61C1104 5:39..677			GTBX	U00094				6.2e-38			
24181	ENU07976	ANI61C1104 6:529..740			GTBX	AFUc10641				6.5E-39			
24182	ENU07977	ANI61C1521: 3457..2237			GTBX	AFUc12939				2.7E-101			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvtg	Description
24183	ENU07978	ANI61C1525: 1163..813			GTBX	FGRc04252				2.1E-23			
24184	ENU07979	ANI61C2256: 1738..606			GTBX	"AFUc03478, AFUc06959, FGRc11102"				"5.3e-61, 1.4e-13, 1.6e-68"			
24185	ENU07980	ANI61C1032 4:1456..2640			GTBX	AFUc06432				5.6E-40			
24186	ENU07981	ANI61C1032 4:6683..7378			GTBX	AFUc03858				1.8E-26			
24187	ENU07982	ANI61C1105 7:854..3			GTBX	AFUc15404				1.2E-104			
24188	ENU07983	ANI61C1105 8:1235..3139			GTBX	"AFUc10292, CALc04898"				"1.7e- 140, 3.7e-15"			
24189	ENU07984	ANI61C2264: 819..487			GTBX	AFUc14213				4.3E-22			
24190	ENU07985	ANI61C2266: 678..1117			GTBX	AFUc09002				2.9E-60			
24191	ENU07986	ANI61C1538: 1527..2143			GTBX	FGRc13890				2.3E-55			
24192	ENU07987	ANI61C1106 5:1308..25			GTBX	"AFUc01902, CALc06224"				"2.0e-49, 2.4e-36"			
24193	ENU07988	ANI61C1033 8:1068..1298			GTBX	AFUc15802				5.7E-81			
24194	ENU07989	ANI61C2274: 104..352			GTBX	FGRc17081				5.7E-24			
24195	ENU07990	ANI61C2279: 947..35			GTBX	AFUc12999				3.7E-57			
24196	ENU07991	ANI61C1107 3:10825..9952			GTBX	AFUc08864				1.6E-40			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24197	ENU07992	ANI61C1034 6:148..474			GTBX	AFUc15190				5.2E-32			
24198	ENU07993	ANI61C1107 6:735..40			GTBX	FGRc11607				9.9E-62			
24199	ENU07994	ANI61C2280: 1521..418			GTBX	"AFUc22243, Z71256"				"1.1e-80, 3.3e-65"			
24200	ENU07995	ANI61C1554: 1454..495			GTBX	"AFUc15791, CALc05767"				"1.1e-89, 9.6e-28"			
24201	ENU07996	ANI61C1556: 505..2120			GTBX	"FGRc16102, U00091"				"3.0e-18, 6.1e-13"			
24202	ENU07997	ANI61C1557: 8377..8816			GTBX	"AFUc10195, Y13137"				"2.6e-29, 3.3e-19"			
24203	ENU07998	ANI61C2286: 63..469			GTBX	AFUc19350				1.8E-29			
24204	ENU07999	ANI61C2287: 3657..2752			GTBX	AFUc21287				1.7E-22			
24205	ENU08000	ANI61C1558: 241..1075			GTBX	AFUc07571				1.8E-111			
24206	ENU08001	ANI61C1108 2:2..355			GTBX	AFUc11431				7.8E-49			
24207	ENU08002	ANI61S1390: 27..413			GTBX	AFUc00871				4.2E-54			
24208	ENU08003	ANI61C1035 4:586..266			GTBX	AFUc14370				1E-38			
24209	ENU08004	ANI61C1561: 633..1091			GTBX	"FGRc12428, FGRc23250"				"6.2e-17, 1.3e-26"			
24210	ENU08005	ANI61C1563: 759..984			GTBX	AFUc12486				1.4E-59			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24211	ENU08006	ANI61C1564:425..1061			GTBX	"AFUc03100, AFUc08293"				"1.6e-71, 1.0e-71"			
24212	ENU08007	ANI61C1566:1921..1217			GTBX	AFUc06344				1.5E-31			
24213	ENU08008	ANI61C1036:2:706..1638			GTBX	AFUc05986				2.1E-64			
24214	ENU08009	ANI61C1036:3:84..749			GTBX	AFUc14403				5.9E-76			
24215	ENU08010	ANI61C1109:3:666..283			GTBX	AFUc02155				7.1E-43			
24216	ENU08011	ANI61C1109:8:5774..6408			GTBX	"AFUc02174, AFUc07223"				"3.6e-30, 1.4e-64"			
24217	ENU08012	ANI61C1571:1373..765			GTBX	AFUc09738				2.6E-96			
24218	ENU08013	ANI61C1572:1..528			GTBX	AFUc12035				6.1E-42			
24219	ENU08014	ANI61C1575:538..1212			GTBX	AFUc17343				5.4E-29			
24220	ENU08015	ANI61C404:2:381..3391			GTBX	AFUc10663				1.6E-86			
24221	ENU08016	ANI61C404:5:543..4664			GTBX	AFUc05891				3.5E-65			
24222	ENU08017	ANI61C409:1:650..41			GTBX	"AFUc07919, AFUc13887, AFUc14801, AFUc20578"				"3.7e-46, 4.4e-36, 1.0e-15, 2.9e-59"			
24223	ENU08018	ANI61C1580:532..1125			GTBX	AFUc13632				1.9E-52			
24224	ENU08019	ANI61C1582:909..3			GTBX	Z71257				2.9E-22			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24225	ENU08020	ANI61C1586:787..1352			GTBX	AFUc13343				3.2E-39			
24226	ENU08021	ANI61C1038 0:3189..3954			GTBX	AFUc16966				4.2E-32			
24227	ENU08022	ANI61C419:2 8..469			GTBX	FGRc26357				1.1E-49			
24228	ENU08023	ANI61C1038 4:682..2			GTBX	AFUc15000				8.7E-94			
24229	ENU08024	ANI61C1038 6:428..6			GTBX	AFUc14146				1.9E-37			
24230	ENU08025	ANI61C1038 7:3270..4847			GTBX	"AFUc04379, AFUc12739"				"1.9e-45, 5.7e-53"			
24231	ENU08026	ANI61C1598:479..11			GTBX	AFUc16619				4.3E-35			
24232	ENU08027	ANI61C1039 7:1214..133			GTBX	"AFUc06152, AFUc17696, CALc05205"				"1.1e-28, 2.2e-12, 1.3e-46"			
24233	ENU08028	ANI61C438:2 608..906			GTBX	"AFUc07197, AFUc11134, AFUc11728, AFUc12186"				"5.1e-14, 1.1e-15, 1.4e-14, 1.3e-105"			
24234	ENU08029	ANI61C439:9 124..9705			GTBX	AFUc01048				6E-60			
24235	ENU08030	ANI61C8000:994..2			GTBX	"AFUc02858, U00092"				"2.8e-11, 6.6e-93"			
24236	ENU08031	ANI61C8004:608..3			GTBX	AFUc19180				8.2E-24			
24237	ENU08032	ANI61C8006:514..1077			GTBX	AFUc13623				5.3E-40			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24238	ENU08033	ANI61C440:3 446..3919			GTBX	AFUc17537				3.9E-64			
24239	ENU08034	ANI61C442:5 56..131			GTBX	AFUc21017				6.4E-22			
24240	ENU08035	ANI61C445:7 16..1232			GTBX	GY13139				5.9e-57			
24241	ENU08036	ANI61C449:2 66..1975			GTBX	AFUc15617				1.4E-206			
24242	ENU08037	ANI61C8012: 1970..190			GTBX	AFUc15379				5.1E-111			
24243	ENU08038	ANI61C8013: 1851..3360			GTBX	"AFUc07084, AFUc22432, CALc06078, Y13135"				"4.8e-66, 2.1e-41, 1.1e-54, 5.7e-37" 2.5E-36			
24244	ENU08039	ANI61C8020: 5..382			GTBX	AFUc13797				6.6E-63			
24245	ENU08040	ANI61C8021: 3545..2350			GTBX	AFUc13604							
24246	ENU08041	ANI61C8026: 38..1772			GTBX	"AFUc15772, AFUc21150, FGRc16885"				"4.9e- 143, 2.0e-13, 2.5e-11" 1.3E-47			
24247	ENU08042	ANI61C8029: 16..570			GTBX	AFUc21824							
24248	ENU08043	ANI61C467:5 371..6057			GTBX	AFUc04398				1.6E-38			
24249	ENU08044	ANI61C8031: 823..117			GTBX	AFUc11877				2.7E-59			
24250	ENU08045	ANI61C7308: 36..415			GTBX	AFUc00888				4.1E-24			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
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24252	ENU08047	ANI61C7311: 163..582			GTBX	"AFUc04986, AFUc09264"				"5.4e-16, 5.2e-55"			
24253	ENU08048	ANI61C8044: 326..1058			GTBX	AFUc14880				5E-46			
24254	ENU08049	ANI61C7315: 1841..3604			GTBX	"AFUc12313, AFUc19899"				"2.1e-43, 2.9e-37"			
24255	ENU08050	ANI61C7317: 1666..56			GTBX	"AFUc11411, CALc06214, Y13135"				"8.6e- 115, 1.2e-67, 1.3e-42"			
24256	ENU08051	ANI61C8047: 5242..4733			GTBX	AFUc15695				5.4E-21			
24257	ENU08052	ANI61C7318: 655..1047			GTBX	"AFUc18123, Y13139"				"6.8e-21, 1.2e-09"			
24258	ENU08053	ANI61C489:4 57..3			GTBX	AFUc13648				1.9E-80			
24259	ENU08054	ANI61C8051: 1747..518			GTBX	"CALc04459, CALc04459"				"1.4e-61, 3.0e-62"			
24260	ENU08055	ANI61C7323: 785..241			GTBX	AFUc19691				7E-56			
24261	ENU08056	ANI61C8052: 733..2502			GTBX	"AFUc00069, AFUc16115, CALc04031"				"2.8e-71, 6.0e-34, 7.0e-55"			
24262	ENU08057	ANI61C8053: 610..182			GTBX	AFUc10161				1.7E-21			
24263	ENU08058	ANI61C8055: 2135..174			GTBX	"AFUc11740, AFUc12687, AFUc14731, FGRc23552"				"5.7e-57, 4.0e-21, 5.0e-19, 6.6e-14"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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24265	ENU08060	ANI61C7329: 594..1704			GTBX	"AFUc01746, AFUc02096"				"1.2e-27, 3.5e-52"			
24266	ENU08061	ANI61C492:5 7..884			GTBX	AFUc13259				3.6E-135			
24267	ENU08062	ANI61C499:1 160..732			GTBX	AFUc09357				1.1E-68			
24268	ENU08063	ANI61C7330: 143..2372			GTBX	"AFUc13887, AFUc14801, FGRC09062, FGRC10889, FGRC21319"				"2.5e-43, 1.3e-13, 1.6e-45, 5.2e-99, 1.5e-10"			
24269	ENU08064	ANI61C7330: 3367..4124			GTBX	"AFUc05528, FGRC11979"				"6.7e-27, 3.8e-13"			
24270	ENU08065	ANI61C7331: 4011..2258			GTBX	"AFUc03996, AFUc06614, AFUc15699, AFUc15879"				"1.6e-21, 3.9e-15, 3.4e-19, 1.6e-43"			
24271	ENU08066	ANI61C6607: 1409..2016			GTBX	"AFUc10110, AFUc19217"				"5.5e-22, 1.4e-48"			
24272	ENU08067	ANI61C8066: 866..1393			GTBX	"AFUc11731, CALc05890"				"6.5e-121, 3.7e-112"			
24273	ENU08068	ANI61C7340: 450..7			GTBX	Y13134				9.1e-28			
24274	ENU08069	ANI61C6611: 98..870			GTBX	AFUc07093				4.5E-60			
24275	ENU08070	ANI61C8071: 516..13			GTBX	AFUc09728				1.8E-53			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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24277	ENU08072	ANI61C8074: 5126..4678			GTBX	AFUc12456				2.7E-29			
24278	ENU08073	ANI61C6616: 377..1089			GTBX	"AFUc05353, AFUc19936"				"1.7e-54, 4.0e-12"			
24279	ENU08074	ANI61C6617: 4827..5366			GTBX	Z47047				1.0e-125			
24280	ENU08075	ANI61C7350: 2489..1882			GTBX	FGRc09585				1.6E-22			
24281	ENU08076	ANI61C8082: 1136..2144			GTBX	AFUc15770				3.9E-135			
24282	ENU08077	ANI61C6626: 6507..7319			GTBX	AFUc10550				2.5E-151			
24283	ENU08078	ANI61C6627: 585..838			GTBX	AFUc03450				3.9E-50			
24284	ENU08079	ANI61C7356: 2072..2291			GTBX	"CALc06084, Y13137"				"4.6e-49, 8.3e-235"			
24285	ENU08080	ANI61C8087: 2424..1939			GTBX	AFUc07211				4.7E-51			
24286	ENU08081	ANI61C5902: 1004..261			GTBX	AFUc12988				3.5E-72			
24287	ENU08082	ANI61C8090: 5575..6094			GTBX	FGRc12352				1E-36			
24288	ENU08083	ANI61C7361: 1567..2745			GTBX	AFUc09895				6.4E-117			
24289	ENU08084	ANI61C5903: 811..368			GTBX	AFUc15950				2.6E-157			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24290	ENU08085	ANI61C5904: 765..25			GTBX	"AFUc00773, AFUc11153"				"7.1e-16, 1.9e-29"			
24291	ENU08086	ANI61C6635: 944..282			GTBX	AFUc02614				5.8E-36			
24292	ENU08087	ANI61C7364: 1168..2132			GTBX	"AFUc01872, FGRc01926"				"1.0e-136, 2.4e-24"			
24293	ENU08088	ANI61C5907: 1099..443			GTBX	AFUc02783				2.1E-34			
24294	ENU08089	ANI61C6639: 306..7			GTBX	AFUc10259				3.7E-24			
24295	ENU08090	ANI61C5910: 5311..6464			GTBX	AFUc09815				2.6E-69			
24296	ENU08091	ANI61C7370: 369..1672			GTBX	AFUc10420				5E-119			
24297	ENU08092	ANI61C5913: 489..1			GTBX	"FGRc02041, U00092"				"6.1e-12, 6.1e-12"			
24298	ENU08093	ANI61C6644: 1478..646			GTBX	"AFUc06809, AFUc15344"				"4.6e-09, 4.4e-98"			
24299	ENU08094	ANI61C5918: 499..18			GTBX	FGRc07459				6E-57			
24300	ENU08095	ANI61C6649: 1057..2094			GTBX	AFUc15961				2.5E-39			
24301	ENU08096	ANI61C7379: 962..28			GTBX	AFUc08907				1.2E-21			
24302	ENU08097	ANI61C5922: 1491..291			GTBX	"CALc06174, FGRc08383"				"4.5e-31, 4.8e-31"			
24303	ENU08098	ANI61C7381: 300..1060			GTBX	"AFUc10566, AFUc10566"				"3.6e-30, 9.6e-41"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
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24305	ENU08100	ANI61C7387: 575..3			GTBX	FGRc10619				4.7E-31			
24306	ENU08101	ANI61C7387: 1279..1652			GTBX	"AFUc15408, AFUc21306"				"5.7e-19, 1.5e-31"			
24307	ENU08102	ANI61C7389: 1326..60			GTBX	CALc05599				4.8E-124			
24308	ENU08103	ANI61C5930: 3876..5599			GTBX	"AFUc13125, AFUc17372"				"4.4e-183, 1.6e-68"			
24309	ENU08104	ANI61C6660: 2123..319			GTBX	"AFUc00228, AFUc00481, AFUc02234"				"5.3e-27, 1.0e-27, 9.8e-33"			
24310	ENU08105	ANI61C7390: 1588..2441			GTBX	Y13139				1.0e-127			
24311	ENU08106	ANI61C6661: 3226..5249			GTBX	"AFUc12095, FGRc15027"				"2.5e-198, 4.1e-29"			
24312	ENU08107	ANI61C6662: 5034..5514			GTBX	AFUc09341				2.9E-28			
24313	ENU08108	ANI61C7393: 703..293			GTBX	AFUc15863				2.6E-52			
24314	ENU08109	ANI61C5938: 198..1256			GTBX	AFUc12786				3.3E-79			
24315	ENU08110	ANI61C6670: 1277..1597			GTBX	AFUc00716				1.4E-36			
24316	ENU08111	ANI61C5943: 623..93			GTBX	AFUc15520				1.4E-45			
24317	ENU08112	ANI61C6675: 830..254			GTBX	CALc04506				7E-39			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24318	ENU08113	ANI61C5946: 384..1079			GTBX	AFUc13556				1.7E-75			
24319	ENU08114	ANI61C5952: 520..28			GTBX	AFUc17155				3.9E-41			
24320	ENU08115	ANI61C5954: 55..1083			GTBX	"AFUc03799, AFUc10276"				"3.7e-57, 7.3e-09"			
24321	ENU08116	ANI61C6685: 43..903			GTBX	"CALc04792, FGRC09020, U00093"				"2.4e-53, 2.0e-32, 7.8e-49"			
24322	ENU08117	ANI61C5957: 1663..1999			GTBX	AFUc02793				2.2E-30			
24323	ENU08118	ANI61C6686: 4251..5701			GTBX	AFUc15881				6.9E-80			
24324	ENU08119	ANI61C5961: 1203..511			GTBX	AFUc01030				1.1E-38			
24325	ENU08120	ANI61C5964: 1000..1293			GTBX	AFUc15826				1.8E-25			
24326	ENU08121	ANI61C5966: 658..980			GTBX	AFUc14716				8.1E-39			
24327	ENU08122	ANI61C5968: 1055..834			GTBX	Z71256				1.4e-23			
24328	ENU08123	ANI61C5975: 178..611			GTBX	AFUc02362				1.6E-60			
24329	ENU08124	ANI61C5976: 1505..86			GTBX	"AFUc15353, CALc06066, FGRC02066"				"8.2e-52, 6.3e-34, 5.0e-73"			
24330	ENU08125	ANI61S211: 116..469			GTBX	FGRC08800				3.9E-32			
24331	ENU08126	ANI61C5984: 211..731			GTBX	AFUc15082				4.1E-55			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24332	ENU08127	ANI61C5988: 1524..225			GTBX	"AFUc15870, AFUc18615"				"1.1e-51, 1.5e-32"			
24333	ENU08128	ANI61C3014: 1868..825			GTBX	AFUc12007				3.5E-33			
24334	ENU08129	ANI61C3015: 384..1558			GTBX	"AFUc06441, AFUc18928, FGRC12021, FGRC13993"				"1.4e-23, 2.4e-39, 1.4e-23, 4.5e-17"			
24335	ENU08130	ANI61C5995: 1002..463			GTBX	"AFUc15651, AFUc15651"				"1.3e-66, 4.5e-89"			
24336	ENU08131	ANI61S2128: 94..537			GTBX	AFUc07714				1.3E-44			
24337	ENU08132	ANI61C3022: 992..720			GTBX	AFUc07125				7E-30			
24338	ENU08133	ANI61S2133: 44..472			GTBX	AFUc22602				1.6E-46			
24339	ENU08134	ANI61C2304: 560..132			GTBX	AFUc07438				1.3E-32			
24340	ENU08135	ANI61C3035: 910..296			GTBX	"AFUc11981, FGRC10039"				"6.2e-40, 1.6e-09"			
24341	ENU08136	ANI61C3037: 579..7			GTBX	AFUc09927				7.5E-56			
24342	ENU08137	ANI61C2309: 974..363			GTBX	"AFUc03406, AFUc05614, AFUc08898, CALc05491"				"2.9e-54, 5.7e-54, 1.4e-19, 8.4e-09"			
24343	ENU08138	ANI61C3039: 68..847			GTBX	CALc04805				2E-93			
24344	ENU08139	ANI61C1110 4:3777..2731			GTBX	AFUc12784				1.3E-86			

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24345	ENU08140	ANI61S2144: 274..16			GTBX	AFUc15701				6.1E-35			
24346	ENU08141	ANI61C1110 8:1698..2135			GTBX	AFUc09253				1.3E-29			
24347	ENU08142	ANI61C2315: 1253..672			GTBX	AFUc12154				1E-49			
24348	ENU08143	ANI61C2318: 473..1164			GTBX	AFUc07159				3.2E-63			
24349	ENU08144	ANI61C3049: 1395..2904			GTBX	FGRc02484				3.6E-39			
24350	ENU08145	ANI61S2150: 378..33			GTBX	AFUc02336				7.9E-61			
24351	ENU08146	ANI61C3050: 625..2162			GTBX	"AFUc12924, FGRc04111"				"9.5e-112, 1.7e-33"			
24352	ENU08147	ANI61C2321: 1194..529			GTBX	AFUc22220				7.8E-50			
24353	ENU08148	ANI61C3053: 2266..185			GTBX	"AFUc00609, AFUc14117, CALc02486"				"3.8e-21, 8.0e-195, 6.4e-24"			
24354	ENU08149	ANI61C3054: 747..2100			GTBX	"AFUc06449, AFUc07501, FGRc07589"				"1.6e-07, 9.4e-11, 1.5e-25"			
24355	ENU08150	ANI61C2325: 747..35			GTBX	AFUc13156				2.7E-24			
24356	ENU08151	ANI61C3057: 21..530			GTBX	Y13139				7.7e-28			
24357	ENU08152	ANI61C1112 0:693..4			GTBX	"AFUc01410, CALc06209"				"9.8e-76, 1.5e-39"			
24358	ENU08153	ANI61C1112 5:508..269			GTBX	CALc06229				9.5E-26			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24359	ENU08154	ANI61C1112 8:3194..4053			GTBX	"AFUc09503, CALc05722"				"1.9e-64, 2.7e-76"			
24360	ENU08155	ANI61S1437: 98..399			GTBX	"AFUc13604, AFUc15296"				"4.7e-25, 3.3e-21"			
24361	ENU08156	ANI61C2330: 2800..3374			GTBX	AFUc15919				1.1E-170			
24362	ENU08157	ANI61C2332: 4378..4578			GTBX	AFUc10180				2.8E-34			
24363	ENU08158	ANI61C3062: 2508..1335			GTBX	Y13134				5.7e-120			
24364	ENU08159	ANI61C1605: 643..1020			GTBX	AFUc10143				5.5E-28			
24365	ENU08160	ANI61C3064: 221..668			GTBX	AFUc13128				8.1E-56			
24366	ENU08161	ANI61C1606: 1693..539			GTBX	"AFUc16378, AFUc21308"				"1.1e-30, 9.5e-19"			
24367	ENU08162	ANI61C1607: 524..31			GTBX	AFUc06472				6.4E-37			
24368	ENU08163	ANI61C2338: 1791..877			GTBX	"AFUc07657, AFUc20776, FGRc03047"				"9.3e-58, 8.4e-27, 7.6e-15"			
24369	ENU08164	ANI61C1040 0:1011..199			GTBX	"AFUc15768, CALc05180"				"1.7e-65, 3.5e-30"			
24370	ENU08165	ANI61C1040 4:1681..456			GTBX	AFUc11156				1.7E-68			
24371	ENU08166	ANI61S2170: 458..150			GTBX	AFUc21244				5.8E-49			
24372	ENU08167	ANI61C2340: 1102..1321			GTBX	AFUc08035				2.2E-21			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24373	ENU08168	ANI61C3071: 303..1850			GTBX	AFUc06001				3.6E-49			
24374	ENU08169	ANI61C3071: 2656..2201			GTBX	AFUc11320				9.2E-37			
24375	ENU08170	ANI61C2342: 2..1100			GTBX	AFUc15644				3E-54			
24376	ENU08171	ANI61C2343: 385..998			GTBX	AFUc14858				1.2E-21			
24377	ENU08172	ANI61C1614: 1641..69			GTBX	"AFUc15021, FGRC09385"				"7.2e-79, 6.5e-61"			
24378	ENU08173	ANI61C2344: 772..1143			GTBX	AFUc15170				2.4E-32			
24379	ENU08174	ANI61C1616: 635..183			GTBX	AFUc13750				1.9E-41			
24380	ENU08175	ANI61C1618: 784..110			GTBX	AFUc10659				3.1E-61			
24381	ENU08176	ANI61C1619: 2385..1431			GTBX	"AFUc05005, AFUc10889, AFUc21670"				"2.2e-16, 2.4e-24, 2.0e-20"			
24382	ENU08177	ANI61C1041 2:1921..1718			GTBX	AFUc15311				2.9E-43			
24383	ENU08178	ANI61C1114 1:700..41			GTBX	AFUc09651				4.4E-31			
24384	ENU08179	ANI61C1041 5:1713..2470			GTBX	"AFUc08021, AFUc08021"				"1.5e-89, 2.0e-57"			
24385	ENU08180	ANI61C1041 6:448..26			GTBX	AFUc09679				3.7E-37			
24386	ENU08181	ANI61C1114 5:425..91			GTBX	CALc04731				4.5E-30			

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24387	ENU08182	ANI61C1114 7:186..1347			GTBX	AFUc16242				1.8E-72			
24388	ENU08183	ANI61C3082: 496..1046			GTBX	AFUc05157				2.9E-38			
24389	ENU08184	ANI61C3085: 184..915			GTBX	"AFUc14050, AFUc20977"				"2.2e-50, 1.7e-18"			
24390	ENU08185	ANI61C3086: 61..600			GTBX	"AFUc21878, FGRc17423"				"3.0e-42, 2.4e-44"			
24391	ENU08186	ANI61C1042 0:3236..3461			GTBX	AFUc17331				9.8E-26			
24392	ENU08187	ANI61C1630: 739..967			GTBX	AFUc12693				2.2E-25			
24393	ENU08188	ANI61C3090: 4281..4003			GTBX	AFUc09749				8.6E-36			
24394	ENU08189	ANI61C1632: 3..711			GTBX	AFUc13580				4E-80			
24395	ENU08190	ANI61C1633: 895..350			GTBX	AFUc03062				2.2E-33			
24396	ENU08191	ANI61C3094: 77..861			GTBX	AFUc07151				1.3E-47			
24397	ENU08192	ANI61C1637: 500..782			GTBX	AFUc10559				5.6E-53			
24398	ENU08193	ANI61C2367: 2270..1947			GTBX	AFUc02537				7.4E-47			
24399	ENU08194	ANI61C2368: 1548..425			GTBX	AFUc15814				3.5E-57			
24400	ENU08195	ANI61C3097: 135..716			GTBX	"AFUc15533, AFUc15533"				"2.0e-70, 3.3e-35"			

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24402	ENU08197	ANI61C1043 0:732..430			GTBX	"AFUc04312, AFUc04312"				"2.4e-38, 5.3e-50"			
24403	ENU08198	ANI61C1043 2:1380..543			GTBX	"AFUc09009, FGRe21606"				"9.8e-32, 5.5e-37"			
24404	ENU08199	ANI61C1116 3:615..1731			GTBX	Y13134				1.7e-84			
24405	ENU08200	ANI61C1116 7:1389..1628			GTBX	AFUc10437				8.1E-110			
24406	ENU08201	ANI61C1116 8:637..1234			GTBX	"AFUc05778, Y13139"				"9.9e-11, 4.5e-69"			
24407	ENU08202	ANI61C1646: 1677..1930			GTBX	AFUc14823				5.8E-91			
24408	ENU08203	ANI61C2376: 607..1538			GTBX	AFUc10283				2.4E-117			
24409	ENU08204	ANI61C1648: 1309..924			GTBX	AFUc15899				4.3E-26			
24410	ENU08205	ANI61C1117 2:3..540			GTBX	AFUc10300				2.3E-35			
24411	ENU08206	ANI61C1044 6:3962..6140			GTBX	"AFUc08784, AFUc20323, CALc05827, Y13136"				"3.0e-40, 4.1e-64, 1.3e-71, 2.4e-61"			
24412	ENU08207	ANI61C1117 7:38..1146			GTBX	"AFUc17428, AFUc22468"				"2.6e-29, 1.2e-69"			
24413	ENU08208	ANI61C1117 8:26..420			GTBX	FGRe03277				5.9E-21			
24414	ENU08209	ANI61C1654: 963..33			GTBX	CALc05018				1.1E-73			

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24416	ENU08211	ANI61C2386: 1473..1077			GTBX	AFUc05516				2.4E-35			
24417	ENU08212	ANI61C1657: 36..718			GTBX	AFUc01220				3.3E-30			
24418	ENU08213	ANI61C2387: 419..792			GTBX	"AFUc08391, U00093"				"1.1e-29, 1.5e-28"			
24419	ENU08214	ANI61C1045 2:2736..3671			GTBX	"AFUc01446, AFUc03449"				"3.6e-49, 5.3e-62"			
24420	ENU08215	ANI61C1045 5:10291..6040			GTBX	"AFUc02402, AFUc13896, AFUc15794, FGRc10936, FGRc19244"				"7.6e-13, 4.1e-90, 9.2e-59, 4.8e-08, 2.7e-24"			
24421	ENU08216	ANI61C1118 4:2930..1174			GTBX	"AFUc12122, AFUc19794"				"8.4e-30, 3.5e-11"			
24422	ENU08217	ANI61C1118 5:724..365			GTBX	AFUc17013				5.9E-43			
24423	ENU08218	ANI61C1118 6:6652..6341			GTBX	AFUc15274				7.9E-30			
24424	ENU08219	ANI61C1118 7:5255..6412			GTBX	AFUc11057				2.3E-165			
24425	ENU08220	ANI61C1118 8:3786..1817			GTBX	"AFUc03500, FGRc12085"				"3.9e-11, 1.6e-27"			
24426	ENU08221	ANI61C1118 9:437..772			GTBX	AFUc05827				2.1E-56			
24427	ENU08222	ANI61C2396: 4105..3424			GTBX	AFUc20773				1.9E-45			

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24428	ENU08223	ANI61C1667:458..2025			GTBX	"AFUc01694, AFUc03534, AFUc09885"				"5.0e-13, 3.7e-37, 1.5e-68"			
24429	ENU08224	ANI61C1046 0:2527..3230			GTBX	"AFUc10414, FGRc04734"				"3.0e-47, 4.3e-09"			
24430	ENU08225	ANI61C1119 1:776..79			GTBX	AFUc15108				3.8E-31			
24431	ENU08226	ANI61C1046 5:2467..4478			GTBX	"AFUc12339, AFUc12339"				"2.1e-67, 2.9e-31"			
24432	ENU08227	ANI61C1046 8:4997..5533			GTBX	AFUc08587				8.5E-68			
24433	ENU08228	ANI61C1119 9:60..490			GTBX	AFUc14731				1.9E-24			
24434	ENU08229	ANI61C1672:893..597			GTBX	AFUc14113				6.4E-90			
24435	ENU08230	ANI61C500:284..899			GTBX	AFUc12648				1.6E-30			
24436	ENU08231	ANI61C504:720..1087			GTBX	FGRc12152				1.8E-64			
24437	ENU08232	ANI61C508:3282..3902			GTBX	AFUc04843				3.5E-38			
24438	ENU08233	ANI61C1047 7:1761..819			GTBX	"FGRc06621, FGRc19870, FGRc21283"				"2.5e-17, 1.7e-14, 8.5e-50"			
24439	ENU08234	ANI61C1683:611..1742			GTBX	"AFUc01385, AFUc06858, CALc02967"				"5.7e-25, 1.9e-46, 7.0e-43"			
24440	ENU08235	ANI61C513:415..729			GTBX	FGRc09331				4.8E-67			
24441	ENU08236	ANI61C1690:414..704			GTBX	AFUc04365				1.2E-36			

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24442	ENU08237	ANI61C524:1 24..354			GTBX	AFUc15671				8.4E-83			
24443	ENU08238	ANI61C525:7 223..2333			GTBX	"AFUc09623, AFUc15525, FGRc16821, Z12576, Y13138"				"1.0e-131, 8.9e-312, 4.1e-18, 0.0, 6.5e-82" "4.7e-64, 3.9e-188"			
24444	ENU08239	ANI61C1049 0:5643..6771			GTBX	"AFUc05896, CALc06013"				1.1E-65			
24445	ENU08240	ANI61C528:4 831..4175			GTBX	AFUc13014				1.8E-63			
24446	ENU08241	ANI61C528:7 449..8035			GTBX	AFUc10735				"4.7e-32, 1.0e-98"			
24447	ENU08242	ANI61C1049 2:1047..2721			GTBX	"AFUc09485, AFUc15798"				"9.3e-63, 1.7e-11"			
24448	ENU08243	ANI61C1049 2:3842..4935			GTBX	"AFUc04378, AFUc07681"				2.3E-52			
24449	ENU08244	ANI61C529:4 2..431			GTBX	AFUc11443				"6.4e-92, 9.2e-131, 1.3e-193, 6.0e-37"			
24450	ENU08245	ANI61C1049 5:3717..6173			GTBX	"AFUc05971, AFUc11732, CALc05629, CALc05629"				3.2E-56			
24451	ENU08246	ANI61C534:4 533..5332			GTBX	AFUc08068				"3.5e-33, 1.7e-10, 3.2e-25"			
24452	ENU08247	ANI61C534:7 739..6453			GTBX	"AFUc19364, FGRc04608, FGRc14414"							

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24453	ENU08248	ANI61C536:7 47..385			GTBX	AFUc09242				1.2E-32			
24454	ENU08249	ANI61C540:1 115..107			GTBX	"AFUc15779, FGRc15231, X59720"				"4.4e-109, 3.4e-42, 4.8e-08"			
24455	ENU08250	ANI61C543:5 4..1726			GTBX	"AFUc10780, CALc05902, Z71257"				"1.1e-30, 5.7e-131, 1.0e-59"			
24456	ENU08251	ANI61C8110: 2590..5977			GTBX	"AFUc15540, FGRc10976, FGRc25479"				"2.6e-137, 2.1e-79, 2.2e-11"			
24457	ENU08252	ANI61C8111: 1800..544			GTBX	AFUc11194				2E-70			
24458	ENU08253	ANI61C8113: 1223..2311			GTBX	CALc04732				2.2E-61			
24459	ENU08254	ANI61C8115: 2748..3329			GTBX	AFUc13681				6.9E-26			
24460	ENU08255	ANI61C8118: 2544..2122			GTBX	AFUc00564				4.7E-45			
24461	ENU08256	ANI61C556:1 452..2621			GTBX	AFUc08057				6.9E-42			
24462	ENU08257	ANI61C556:3 609..3139			GTBX	AFUc05897				8.2E-34			
24463	ENU08258	ANI61C8121: 828..109			GTBX	"AFUc11352, FGRc00210, Y13138"				"2.0e-55, 1.5e-25, 1.6e-29"			
24464	ENU08259	ANI61C8123: 2579..1657			GTBX	AFUc12416				2.2E-38			
24465	ENU08260	ANI61C8127: 1150..2			GTBX	"AFUc05079, AFUc05496"				"1.8e-26, 1.6e-23"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24466	ENU08261	ANI61C565:3 474..5173			GTBX	Z71257				1.0e-107			
24467	ENU08262	ANI61C7402: 111..1536			GTBX	"AFUc06900, AFUc14568"				"2.3e-30, 5.9e-31"			
24468	ENU08263	ANI61C7406: 1092..374			GTBX	"AFUc04078, CALc05482"				"8.6e-47, 1.0e-69"			
24469	ENU08264	ANI61C8136: 3774..4745			GTBX	AFUc13396				2.2E-98			
24470	ENU08265	ANI61C8139: 4306..4841			GTBX	FGRc04774				3.1E-35			
24471	ENU08266	ANI61C576:4 55..90			GTBX	AFUc09285				5.9E-43			
24472	ENU08267	ANI61C8142: 2033..3024			GTBX	AFUc14097				3.3E-35			
24473	ENU08268	ANI61C7414: 299..789			GTBX	AFUc11487				4.3E-59			
24474	ENU08269	ANI61C8146: 340..23			GTBX	Y13138				1.6e-32			
24475	ENU08270	ANI61C8149: 1236..58			GTBX	AFUc15484				4.1E-88			
24476	ENU08271	ANI61C8154: 611..13			GTBX	AFUc01706				2.4E-23			
24477	ENU08272	ANI61C7427: 712..74			GTBX	Y13139				4.6e-19			
24478	ENU08273	ANI61C8158: 2634..1709			GTBX	AFUc12228				5.1E-25			
24479	ENU08274	ANI61C591:6 59..21			GTBX	AFUc10307				4.4E-69			

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24480	ENU08275	ANI61C6703: 3206..4413			GTBX	"AFUc15895, FGRc12402"				"3.6e-40, 6.1e-31"			
24481	ENU08276	ANI61C6705: 4844..5990			GTBX	"AFUc13044, AFUc15912"				"2.2e-106, 3.6e-90"			
24482	ENU08277	ANI61C6710: 1220..1609			GTBX	AFUc01691				1.9E-27			
24483	ENU08278	ANI61C8171: 347..1607			GTBX	"AFUc08832, AFUc09980, FGRc01231"				"4.7e-50, 9.0e-34, 4.2e-51"			
24484	ENU08279	ANI61C8173: 440..2176			GTBX	"AFUc05587, AFUc07211, AFUc08234, AFUc21621"				"1.4e-107, 1.1e-65, 4.8e-95, 2.2e-46"			
24485	ENU08280	ANI61C6719: 484..128			GTBX	AFUc15031				1.6E-36			
24486	ENU08281	ANI61C6720: 349..919			GTBX	AFUc13243				2.8E-68			
24487	ENU08282	ANI61C7451: 1751..2032			GTBX	AFUc01939				1.1E-51			
24488	ENU08283	ANI61C8185: 431..1227			GTBX	"AFUc00988, CALc06038"				"3.3e-60, 2.8e-38"			
24489	ENU08284	ANI61C7457: 434..208			GTBX	AFUc15970				4.2E-78			
24490	ENU08285	ANI61C6728: 612..949			GTBX	AFUc08768				1.8E-44			
24491	ENU08286	ANI61C8188: 3201..1912			GTBX	"AFUc01114, AFUc18282, AFUc20635"				"1.3e-35, 1.4e-22, 8.8e-10"			
24492	ENU08287	ANI61C7459: 697..41			GTBX	AFUc04086				4E-82			

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24493	ENU08288	ANI61C6730: 156..509			GTBX	AFUc03916				1.4E-26			
24494	ENU08289	ANI61C8191: 1018..156			GTBX	AFUc09445				3.2E-100			
24495	ENU08290	ANI61C6734: 5607..6701			GTBX	"AFUc21317, Z71257"				"6.1e-07, 1.4e-32"			
24496	ENU08291	ANI61C7465: 1954..2550			GTBX	AFUc14734				3E-161			
24497	ENU08292	ANI61C8194: 2076..2470			GTBX	Y13137				8.2e-186			
24498	ENU08293	ANI61C6738: 5489..4467			GTBX	"AFUc01683, CALc04817, FGRc00806"				"1.6e-45, 3.1e-21, 1.6e-32"			
24499	ENU08294	ANI61C7475: 1427..483			GTBX	"AFUc17643, FGRc05979"				"1.2e-08, 1.2e-45"			
24500	ENU08295	ANI61C7476: 28..1165			GTBX	"AFUc02079, AFUc09659"				"3.0e-52, 7.5e-07"			
24501	ENU08296	ANI61C7479: 864..121			GTBX	AFUc04883				1.9E-88			
24502	ENU08297	ANI61C6750: 1592..800			GTBX	AFUc02986				4.9E-36			
24503	ENU08298	ANI61C7483: 5160..6015			GTBX	"AFUc12789, Y13134"				"3.0e-68, 1.5e-12"			
24504	ENU08299	ANI61C7486: 1350..379			GTBX	"AFUc02949, AFUc04582, FGRc10932"				"7.7e-71, 5.6e-39, 2.7e-18"			
24505	ENU08300	ANI61C6759: 2649..1266			GTBX	"AFUc10464, CALc06073"				"2.9e-71, 4.8e-98"			
24506	ENU08301	ANI61C7491: 481..1258			GTBX	AFUc15766				3.3E-67			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24507	ENU08302	ANI61C6763: 845..1658			GTBX	"AFUc13390, AFUc13390"				"2.5e-45, 3.8e-77"			
24508	ENU08303	ANI61C7493: 1854..41			GTBX	AFUc15810				1.4E-236			
24509	ENU08304	ANI61C7499: 1893..2258			GTBX	AFUc09120				5.7E-46			
24510	ENU08305	ANI61C6771: 955..77			GTBX	"FGRc02670, Y13139"				"4.1e-40, 8.9e-18"			
24511	ENU08306	ANI61C6780: 1542..1913			GTBX	"AFUc17233, FGRc05382"				"7.2e-52, 1.2e-14"			
24512	ENU08307	ANI61C6782: 138..1073			GTBX	AFUc12300				9.2E-80			
24513	ENU08308	ANI61C6786: 269..868			GTBX	"AFUc03905, CALc03405"				"6.3e-25, 3.1e-20"			
24514	ENU08309	ANI61C6789: 1667..164			GTBX	AFUc12649				3E-156			
24515	ENU08310	ANI61S448:4 50..153			GTBX	FGRc24169				2.3E-21			
24516	ENU08311	ANI61C6792: 700..1644			GTBX	"AFUc06967, FGRc12581"				"7.2e-93, 6.8e-27"			
24517	ENU08312	ANI61C6797: 1035..50			GTBX	Y13135				1.3e-48			
24518	ENU08313	ANI61S2206: 326..28			GTBX	AFUc12261				2E-33			
24519	ENU08314	ANI61C3111: 393..719			GTBX	AFUc15581				2.3E-67			
24520	ENU08315	ANI61C3114: 2..476			GTBX	AFUc10952				1E-22			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24521	ENU08316	ANI61C3120: 317..649			GTBX	AFUc14123				8.4E-42			
24522	ENU08317	ANI61C3122: 3..329			GTBX	"AFUc15397, AFUc15397"				"2.9e-45, 3.3e-72"			
24523	ENU08318	ANI61C3133: 776..1003			GTBX	AI001370				6.5e-14			
24524	ENU08319	ANI61C2406: 34..768			GTBX	"AFUc10109, FGRC24183"				"7.3e-07, 5.1e-25"			
24525	ENU08320	ANI61C3138: 1800..2489			GTBX	AFUc09498				1.4E-33			
24526	ENU08321	ANI61C2409: 23..820			GTBX	AFUc10750				2E-71			
24527	ENU08322	ANI61C1120 5:842..1238			GTBX	AFUc21643				1.3E-32			
24528	ENU08323	ANI61C1120 5:7773..7272			GTBX	AFUc06894				6.5E-33			
24529	ENU08324	ANI61C1120 5:10041..10386			GTBX	Z71256				1.6e-24			
24530	ENU08325	ANI61C1120 5:11046..11351			GTBX	AFUc12485				6.5E-33			
24531	ENU08326	ANI61S1516: 546..243			GTBX	AFUc01209				3.3E-46			
24532	ENU08327	ANI61C2411: 175..744			GTBX	"AFUc06238, AFUc21228"				"1.6e-65, 6.8e-08"			
24533	ENU08328	ANI61C2411: 2361..1216			GTBX	"AFUc03672, CALc04359, Y13139"				"1.9e-38, 1.1e-41, 1.9e-46"			
24534	ENU08329	ANI61C3145: 4077..2208			GTBX	"AFUc03167, AFUc13827"				"9.6e-59, 1.2e-88"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24535	ENU08330	ANI61C3148: 230..1073			GTBX	CALc04288				1.6E-87			
24536	ENU08331	ANI61C1121 0:954..656			GTBX	AFUc14655				3.6E-46			
24537	ENU08332	ANI61C1121 1:1639..690			GTBX	"AFUc05869, AFUc10580, CALc05396"				"1.3e-83, 6.3e-32, 2.3e-89"			
24538	ENU08333	ANI61C1121 4:784..401			GTBX	AFUc15114				1.7E-60			
24539	ENU08334	ANI61C1121 5:541..134			GTBX	AFUc16004				3.7E-24			
24540	ENU08335	ANI61C2420: 2226..2459			GTBX	AFUc03940				6.5E-27			
24541	ENU08336	ANI61C2421: 1057..1414			GTBX	AFUc14756				6.7E-28			
24542	ENU08337	ANI61C2422: 257..1093			GTBX	"AFUc03549, AFUc13726, AFUc13726"				"5.5e-44, 1.6e-28, 2.0e-32"			
24543	ENU08338	ANI61C3152: 439..3434			GTBX	"AFUc11188, U000093"				"1.5e-114, 4.5e-202"			
24544	ENU08339	ANI61C3157: 40..494			GTBX	AFUc21873				2.7E-28			
24545	ENU08340	ANI61C3158: 3582..2955			GTBX	AFUc07435				1.2E-47			
24546	ENU08341	ANI61C1122 3:2614..2006			GTBX	CALc05628				2.8E-47			
24547	ENU08342	ANI61C1122 9:5179..6489			GTBX	"AFUc11755, Y13135"				"2.0e-63, 5.7e-100"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24548	ENU08343	ANI61C2431: 976..59			GTBX	"AFUc01570, AFUc08276"				"4.3e-28, 4.5e-32"			
24549	ENU08344	ANI61C1705: 4995..6299			GTBX	"AFUc00996, Y13134"				"2.1e-19, 9.6e-50"			
24550	ENU08345	ANI61C3165: 211..726			GTBX	CALc05020				4.8E-24			
24551	ENU08346	ANI61C3166: 752..138			GTBX	AFUc13944				2.1E-53			
24552	ENU08347	ANI61C2437: 2200..3538			GTBX	"AFUc01000, AFUc04109, FGRc04331"				"1.2e-28, 2.5e-53, 1.1e-51"			
24553	ENU08348	ANI61C1123 0:3214..1952			GTBX	"AFUc14997, AFUc14997"				"6.3e-80, 6.5e-66"			
24554	ENU08349	ANI61C1050 1:6263..7127			GTBX	Y13138				0.0			
24555	ENU08350	ANI61C1050 6:2..538			GTBX	CALc06073				3.1E-47			
24556	ENU08351	ANI61C1050 8:522..79			GTBX	AFUc13411				3.9E-26			
24557	ENU08352	ANI61C3170: 1199..657			GTBX	AFUc14288				1.1E-73			
24558	ENU08353	ANI61C1713: 2645..1891			GTBX	AFUc03044				4.3E-26			
24559	ENU08354	ANI61C2446: 844..49			GTBX	"AFUc12955, AFUc12955"				"4.9e-32, 9.8e-62"			
24560	ENU08355	ANI61C3177: 3..1536			GTBX	AFUc14427				6.3E-206			
24561	ENU08356	ANI61C2449: 872..402			GTBX	AFUc08082				2.2E-37			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24562	ENU08357	ANI61C1051 0:802..64			GTBX	"AFUc07339, CALc05205"				"1.5e-12, 3.1e-65"			
24563	ENU08358	ANI61C1124 4:331..774			GTBX	FGRc11233				3.4E-30			
24564	ENU08359	ANI61C1124 7:390..923			GTBX	"AFUc18726, AFUc19650"				"1.9e-34, 3.1e-43"			
24565	ENU08360	ANI61C1124 8:23..337			GTBX	AFUc11164				8.1E-22			
24566	ENU08361	ANI61C1720: 1126..146			GTBX	CALc06237				1.6E-27			
24567	ENU08362	ANI61C2450: 1275..88			GTBX	"AFUc09645, FGRc11399, Z4707"				"4.6e-38, 1.9e-11, 2.9e-26"			
24568	ENU08363	ANI61C2455: 1089..1600			GTBX	AFUc06803				4.7E-46			
24569	ENU08364	ANI61C1726: 3193..2059			GTBX	AFUc12449				6.8E-58			
24570	ENU08365	ANI61C3187: 2309..2737			GTBX	AFUc10771				1.6E-42			
24571	ENU08366	ANI61C2459: 3630..4313			GTBX	AFUc04986				8.6E-77			
24572	ENU08367	ANI61C1052 6:98..790			GTBX	"AFUc03097, AFUc07509"				"5.2e-13, 2.5e-67"			
24573	ENU08368	ANI61C1125 7:320..47			GTBX	AFUc08915				7.9E-28			
24574	ENU08369	ANI61C1052 8:381..724			GTBX	AFUc04981				3E-23			
24575	ENU08370	ANI61C1052 9:1858..763			GTBX	AFUc01784				2.8E-27			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24576	ENU08371	ANI61C2461: 2065..212			GTBX	AFUc10369				8.3E-53			
24577	ENU08372	ANI61C2465: 698..3702			GTBX	"AFUc07667, AFUc12566, AFUc13531, AFUc14327, AFUc14338, AFUc15132, FGRc00835, FGRc17112"				"4.3e-12, 1.1e-38, 3.3e-23, 2.0e-42, 2.0e-63, 2.5e-52, 6.0e-27, 1.2e-08"			
24578	ENU08373	ANI61C3199: 1590..2454			GTBX	"AFUc05935, AFUc15519"				"1.3e-10, 1.3e-45"			
24579	ENU08374	ANI61C1126 0:326..605			GTBX	"AFUc15094, AFUc15094, Y13134"				"2.3e-14, 4.6e-17, 2.0e-24"			
24580	ENU08375	ANI61C1126 3:305..27			GTBX	AFUc09950				3.4E-34			
24581	ENU08376	ANI61C1053 4:344..592			GTBX	AFUc13512				2.2E-56			
24582	ENU08377	ANI61C1053 5:4543..3779			GTBX	AFUc14535				1.7E-97			
24583	ENU08378	ANI61C1126 4:350..51			GTBX	AFUc09251				2.3E-41			
24584	ENU08379	ANI61C1126 8:188..526			GTBX	AFUc09884				2.5E-21			
24585	ENU08380	ANI61C1743: 412..1446			GTBX	"AFUc07667, AFUc08168, AFUc08900, AFUc14327"				"3.8e-15, 7.4e-50, 4.1e-11, 5.1e-48"			
24586	ENU08381	ANI61C2475: 1147..548			GTBX	AFUc02096				1.4E-43			
24587	ENU08382	ANI61C2479: 1298..1026			GTBX	AFUc06657				1.2E-22			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24588	ENU08383	ANI61C1054 1:2168..395			GTBX	"AFUc04995, AFUc12046, Y13140"				"2.7e-54, 6.8e-95, 3.0e-130"			
24589	ENU08384	ANI61C1054 5:959..741			GTBX	AFUc15910				4.5E-34			
24590	ENU08385	ANI61C1127 7:180..648			GTBX	"AFUc03512, AFUc08783, FGRc19235"				"7.0e-22, 1.4e-10, 7.8e-21"			
24591	ENU08386	ANI61C1127 8:3084..2773			GTBX	AFUc15452				2.4E-40			
24592	ENU08387	ANI61S1589: 24..506			GTBX	AFUc05281				1E-39			
24593	ENU08388	ANI61C2482: 122..700			GTBX	AFUc16564				6.8E-50			
24594	ENU08389	ANI61C1757: 2400..2857			GTBX	AFUc09694				1.4E-62			
24595	ENU08390	ANI61C1758: 6614..5099			GTBX	"AFUc11939, FGRc23525"				"9.7e-68, 3.5e-10"			
24596	ENU08391	ANI61C1128 0:736..2349			GTBX	"AFUc01284, AFUc02695, AFUc04437"				"3.0e-33, 1.2e-16, 7.2e-15"			
24597	ENU08392	ANI61C1055 5:4688..5219			GTBX	U00094				0.0			
24598	ENU08393	ANI61C1055 9:1572..2414			GTBX	"AFUc03219, AFUc12227"				"3.1e-57, 1.3e-19"			
24599	ENU08394	ANI61C1761: 2281..3753			GTBX	"AFUc09407, FGRc11267, FGRc11267"				"5.6e-36, 1.0e-18, 2.1e-19"			
24600	ENU08395	ANI61C2491: 1150..365			GTBX	"AFUc21763, FGRc25482"				"1.6e-63, 8.0e-19"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24601	ENU08396	ANI61C1765: 3849..4804			GTBX	AFUc08160				2.4E-108			
24602	ENU08397	ANI61C1768: 1071..245			GTBX	"CALc05020, FGRc07538, Y13134"				"2.8e-133, 2.6e-107, 2.6e-107"			
24603	ENU08398	ANI61C1769: 630..424			GTBX	AFUc15659				1.1E-24			
24604	ENU08399	ANI61C1056 0:379..587			GTBX	FGRc10510				1.5E-36			
24605	ENU08400	ANI61C1129 1:680..3			GTBX	"AFUc01382, AFUc06747"				"2.4e-16, 2.3e-108"			
24606	ENU08401	ANI61C1129 2:992..1827			GTBX	"AFUc01815, AFUc19145"				"4.1e-10, 5.5e-40"			
24607	ENU08402	ANI61C1129 3:1130..708			GTBX	"AFUc09000, Y13134"				"3.5e-81, 4.3e-40"			
24608	ENU08403	ANI61C1129 4:28..565			GTBX	AFUc04474				6E-68			
24609	ENU08404	ANI61C1129 8:975..145			GTBX	"CALc04432, FGRc05226"				"8.9e-80, 2.7e-19"			
24610	ENU08405	ANI61C1129 9:1350..1568			GTBX	CALc03902				7E-40			
24611	ENU08406	ANI61C1774: 450..851			GTBX	AFUc11966				5.9E-46			
24612	ENU08407	ANI61C1779: 391..849			GTBX	AFUc12781				9.6E-30			
24613	ENU08408	ANI61C1057 4:957..691			GTBX	AFUc09666				2.4E-38			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24614	ENU08409	ANI61C1781:5..532			GTBX	"AFUc09001, CALc06053"				"3.6e-17, 7.5e-30"			
24615	ENU08410	ANI61C614:81..879			GTBX	AFUc21798				8.5E-31			
24616	ENU08411	ANI61C617:790..344			GTBX	AFUc01603				8.4E-73			
24617	ENU08412	ANI61C10587:125..1577			GTBX	"AFUc13537, AFUc15937, AFUc16854, AFUc18057"				"6.1e-43, 9.1e-33, 5.3e-07, 7.5e-60"			
24618	ENU08413	ANI61C10589:4717..6120			GTBX	AFUc16933				8.6E-28			
24619	ENU08414	ANI61C621:988..27			GTBX	AFUc13969				3.8E-62			
24620	ENU08415	ANI61C629:1426..1674			GTBX	AFUc10182				2.2E-44			
24621	ENU08416	ANI61C632:2615..2967			GTBX	AFUc13337				2.6E-69			
24622	ENU08417	ANI61C638:1513..642			GTBX	AFUc13559				1.7E-119			
24623	ENU08418	ANI61C8202:2327..2693			GTBX	AFUc09447				1.7E-72			
24624	ENU08419	ANI61C8205:1..564			GTBX	AFUc11001				1.7E-28			
24625	ENU08420	ANI61C8211:438..914			GTBX	AFUc10534				3.7E-117			
24626	ENU08421	ANI61C8212:1480..1118			GTBX	AFUc15391				3.5E-112			
24627	ENU08422	ANI61C8220:4..444			GTBX	AFUc05936				2.8E-55			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24628	ENU08423	ANI61C8225:1437..173			GTBX	"AFUc05414, CALc04219"				"7.7e-59, 4.0e-44"			
24629	ENU08424	ANI61C661:391..8			GTBX	AFUc07993				4.6E-33			
24630	ENU08425	ANI61C7502:2085..4478			GTBX	"AFUc11007, Y13135"				"2.0e-65, 1.3e-154"			
24631	ENU08426	ANI61C7503:2046..2255			GTBX	Y13134				3.1e-237			
24632	ENU08427	ANI61C8233:608..326			GTBX	"AFUc15337, AFUc15337"				"3.3e-113, 4.3e-123"			
24633	ENU08428	ANI61C8235:1473..2074			GTBX	"AFUc12073, CALc06007"				"3.1e-32, 1.9e-83"			
24634	ENU08429	ANI61C8236:542..1400			GTBX	AFUc00714				6.8E-52			
24635	ENU08430	ANI61C8238:950..1813			GTBX	AFUc20930				2.6E-32			
24636	ENU08431	ANI61C670:364..585			GTBX	AFUc13626				6.8E-35			
24637	ENU08432	ANI61C671:112..549			GTBX	"AFUc15558, AFUc15558"				"2.0e-65, 4.8e-61"			
24638	ENU08433	ANI61C678:814..30			GTBX	AFUc13964				1.5E-29			
24639	ENU08434	ANI61C8245:1570..437			GTBX	"AFUc14341, FGRc04315"				"1.6e-105, 5.4e-36"			
24640	ENU08435	ANI61C682:2213..1222			GTBX	AFUc15961				1.5E-25			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24641	ENU08436	ANI61C86:5 347..6396			GTBX	"AFUc10299, AFUc13858, AFUc17463"				"5.8e-31, 4.5e-20, 1.1e-57"			
24642	ENU08437	ANI61C86:7 598..6771			GTBX	AFUc04010				1.6E-37			
24643	ENU08438	ANI61C8251: 42..2483			GTBX	"AFUc09565, AFUc20070"				"1.2e-104, 1.6e-30"			
24644	ENU08439	ANI61C7527: 1671..5042			GTBX	"AFUc10374, AFUc13490, AFUc18055"				"9.3e-166, 7.1e-130, 2.1e-26"			
24645	ENU08440	ANI61C8257: 5189..6135			GTBX	"AFUc03480, AFUc13151"				"4.8e-40, 6.3e-85"			
24646	ENU08441	ANI61C699:7 57..494			GTBX	FGRc01809				2.4E-42			
24647	ENU08442	ANI61C6802: 616..2355			GTBX	"AFUc00490, FGRc08907, FGRc25065"				"4.3e-13, 1.1e-44, 1.9e-32"			
24648	ENU08443	ANI61C6803: 300..656			GTBX	AFUc10335				5.4E-24			
24649	ENU08444	ANI61C6804: 1450..522			GTBX	"AFUc02585, AFUc16083, AFUc18105"				"2.3e-28, 5.8e-13, 2.4e-10"			
24650	ENU08445	ANI61C6805: 531..136			GTBX	AFUc13932				4.2E-39			
24651	ENU08446	ANI61C7536: 1..513			GTBX	AFUc15302				9.7E-24			
24652	ENU08447	ANI61C7537: 1238..2244			GTBX	AFUc06075				1.5E-85			
24653	ENU08448	ANI61C6809: 146..427			GTBX	AFUc11377				2.2E-23			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24654	ENU08449	ANI61C8269: 46..569			GTBX	AFUc07452				1.1E-34			
24655	ENU08450	ANI61C6810: 5679..6098			GTBX	AFUc19773				1.5E-29			
24656	ENU08451	ANI61C8270: 427..31			GTBX	"AFUc04808, AFUc04808"				"2.1e-45, 7.2e-47"			
24657	ENU08452	ANI61C8271: 986..34			GTBX	AFUc15466				1.5E-46			
24658	ENU08453	ANI61C7542: 122..989			GTBX	"AFUc11101, AFUc11101"				"4.8e-38, 8.3e-26"			
24659	ENU08454	ANI61C7543: 1033..176			GTBX	"AFUc15495, FGRc16134"				"8.0e-47, 4.6e-07"			
24660	ENU08455	ANI61C8272: 1151..1600			GTBX	AFUc14280				1.7E-82			
24661	ENU08456	ANI61C6815: 1176..454			GTBX	FGRc10208				5.2E-54			
24662	ENU08457	ANI61C7549: 1848..425			GTBX	"AFUc04568, FGRc00446"				"2.7e-28, 8.6e-14"			
24663	ENU08458	ANI61C8279: 1068..691			GTBX	FGRc20509				1.3E-23			
24664	ENU08459	ANI61C6820: 1111..501			GTBX	AFUc03505				1.6E-49			
24665	ENU08460	ANI61C8286: 479..137			GTBX	AFUc15334				1.6E-21			
24666	ENU08461	ANI61C8286: 839..1285			GTBX	AFUc14069				9.5E-45			
24667	ENU08462	ANI61C6829: 1840..166			GTBX	"CALc03297, Y13139"				"1.2e-17, 3.4e-56"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24668	ENU08463	ANI61C8288: 1325..501			GTBX	AFUc05810				2.6E-31			
24669	ENU08464	ANI61C6831: 148..1585			GTBX	"AFUc04998, FGRc01824"				"5.7e-56, 3.5e-16"			
24670	ENU08465	ANI61C6834: 357..867			GTBX	"AFUc12667, AFUc15842"				"8.8e-56, 2.3e-15"			
24671	ENU08466	ANI61C7563: 1403..972			GTBX	AFUc06136				1.6E-52			
24672	ENU08467	ANI61C6835: 679..1407			GTBX	AFUc03378				6.6E-21			
24673	ENU08468	ANI61C8295: 336..1098			GTBX	"FGRc00692, FGRc11948"				"3.8e-30, 3.3e-22"			
24674	ENU08469	ANI61C7566: 1430..741			GTBX	AFUc19723				3.7E-27			
24675	ENU08470	ANI61C6839: 5869..5612			GTBX	"AFUc04055, AFUc05745"				"3.1e-13, 8.0e-61"			
24676	ENU08471	ANI61C8299: 716..3012			GTBX	"AFUc09176, AFUc09176, FGRc09522"				"1.3e-165, 2.6e-63, 7.0e-09"			
24677	ENU08472	ANI61C7570: 583..1210			GTBX	FGRc00007				2.2E-68			
24678	ENU08473	ANI61C7571: 608..210			GTBX	AFUc10686				1E-25			
24679	ENU08474	ANI61C7577: 78..566			GTBX	AFUc00513				8.2E-23			
24680	ENU08475	ANI61C7578: 2539..2834			GTBX	AFUc02252				3.3E-31			
24681	ENU08476	ANI61C7587: 2348..2067			GTBX	FGRc12388				3E-31			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24682	ENU08477	ANI61C7588: 1381..602			GTBX	"AFUc06763, AFUc07411, FGRc21800"				"2.5e-71, 1.4e-13, 2.1e-20"			
24683	ENU08478	ANI61S519:2..592			GTBX	"FGRc07962, FGRc16898"				"1.1e-09, 1.8e-29"			
24684	ENU08479	ANI61C7591: 1015..1599			GTBX	AFUc12136				2.1E-78			
24685	ENU08480	ANI61C6863: 1573..1244			GTBX	AFUc10542				7.8E-26			
24686	ENU08481	ANI61C6864: 2992..4626			GTBX	"AFUc07814, CALc01848, Z17256"				"2.5e-77, 6.1e-27, 2.2e-30"			
24687	ENU08482	ANI61C6870: 949..73			GTBX	"AFUc09260, CALc05985"				"1.4e-91, 4.6e-57"			
24688	ENU08483	ANI61C6874: 509..30			GTBX	AFUc15201				8.3E-117			
24689	ENU08484	ANI61C6875: 478..1035			GTBX	"AFUc15186, AFUc15186"				"2.1e-45, 9.8e-52"			
24690	ENU08485	ANI61C6883: 6..281			GTBX	AFUc08480				2.3E-27			
24691	ENU08486	ANI61C6883: 1538..1254			GTBX	AFUc08221				6.7E-38			
24692	ENU08487	ANI61C6888: 2405..2970			GTBX	AFUc11742				1.8E-66			
24693	ENU08488	ANI61C6890: 1004..189			GTBX	AFUc08698				4E-54			
24694	ENU08489	ANI61C6890: 1898..2209			GTBX	AFUc09533				2.4E-56			
24695	ENU08490	ANI61C6891: 1691..1221			GTBX	AFUc03109				5.6E-25			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24696	ENU08491	ANI61C6896: 960..191			GTBX	AFUc14439				6.5E-64			
24697	ENU08492	ANI61C6897: 9..776			GTBX	AFUc12120				2E-37			
24698	ENU08493	ANI61S2306: 399..4			GTBX	"AFUc13642, Y13138"				"4.5e-52, 4.1e-09"			
24699	ENU08494	ANI61C3208: 1447..1953			GTBX	AFUc10936				5.8E-66			
24700	ENU08495	ANI61C3209: 956..2284			GTBX	AFUc15271				8.2E-44			
24701	ENU08496	ANI61S2314: 70..548			GTBX	CALc06228				2.1E-21			
24702	ENU08497	ANI61S3044: 78..524			GTBX	CALc05604				6E-28			
24703	ENU08498	ANI61C3211: 1102..2301			GTBX	"AFUc19019, FGRC18454, Y13138"				"1.4e-48, 1.4e-29, 5.3e-105"			
24704	ENU08499	ANI61C3214: 567..1777			GTBX	"AFUc19711, AFUc21339"				"8.6e-54, 5.8e-35"			
24705	ENU08500	ANI61C3215: 3946..5307			GTBX	"AFUc12382, AFUc15610"				"2.2e-89, 6.9e-46"			
24706	ENU08501	ANI61C3217: 1504..2206			GTBX	"AFUc13189, AFUc21901"				"9.0e-158, 9.1e-10"			
24707	ENU08502	ANI61S2328: 554..315			GTBX	"AFUc10225, Z71257"				"1.5e-14, 7.1e-55"			
24708	ENU08503	ANI61C3226: 785..93			GTBX	"AFUc08295, AFUc08295"				"1.9e-41, 7.2e-37"			
24709	ENU08504	ANI61C2503: 1119..1520			GTBX	"FGRC05378, FGRC11560"				"8.0e-32, 7.5e-31"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24710	ENU08505	ANI61C3235: 59..1675			GTBX	"AFUc01811, AFUc13887, CALc04895, FGRC00754, FGRC05142"				"1.3e-75, 1.1e-16, 3.0e-61, 1.2e-51, 2.5e-23"			
24711	ENU08506	ANI61C3236: 1660..614			GTBX	AFUc10571				4.8E-29			
24712	ENU08507	ANI61C2507: 1225..200			GTBX	"AFUc02726, AFUc04017"				"1.0e-27, 3.9e-66"			
24713	ENU08508	ANI61C2508: 906..65			GTBX	AFUc04584				3.6E-41			
24714	ENU08509	ANI61C2509: 1495..683			GTBX	AFUc14282				1.2E-102			
24715	ENU08510	ANI61C3238: 2274..3441			GTBX	CALc05093				5E-33			
24716	ENU08511	ANI61C1130 0:1611..872			GTBX	Z71257				2.2e-76			
24717	ENU08512	ANI61C1130 1:137..2796			GTBX	"AFUc05446, AFUc08551, AFUc16108, AFUc20988, CALc01643"				"7.2e-11, 2.8e-38, 3.1e-61, 2.3e-43, 1.5e-17"			
24718	ENU08513	ANI61C2510: 555..49			GTBX	CALc05636				3.6E-63			
24719	ENU08514	ANI61C2511: 1515..260			GTBX	CALc05278				6.4E-124			
24720	ENU08515	ANI61C2512: 41..685			GTBX	AFUc14444				3.6E-48			
24721	ENU08516	ANI61C3245: 2214..196			GTBX	"AFUc15224, FGRC07913"				"4.4e-65, 7.4e-51"			
24722	ENU08517	ANI61C1131 7:109..887			GTBX	AFUc06140				1.4E-48			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
24723	ENU08518	ANI61S3085: 1..474			GTBX	AFUc10385				6E-34			
24724	ENU08519	ANI61C3251: 2782..3157			GTBX	AFUc13043				4.6E-49			
24725	ENU08520	ANI61C3255: 2764..2980			GTBX	Y13140				9.5e-39			
24726	ENU08521	ANI61C1132 5:653..41			GTBX	AFUc10893				2.6E-39			
24727	ENU08522	ANI61C1132 8:1793..19			GTBX	"AFUc02484, AFUc04329, AFUc14153"				"2.1e-21, 2.0e-53, 2.9e-174"			
24728	ENU08523	ANI61C3261: 2760..3156			GTBX	AFUc15767				1.4E-271			
24729	ENU08524	ANI61C3262: 516..42			GTBX	AFUc16517				6.2E-38			
24730	ENU08525	ANI61C3264: 1738..2478			GTBX	"AFUc02688, AFUc15728, AFUc15728"				"1.7e-46, 2.2e-30, 6.4e-109"			
24731	ENU08526	ANI61C2538: 16..453			GTBX	"AFUc14903, AFUc15880"				"9.3e-25, 8.8e-07"			
24732	ENU08527	ANI61C1060 1:1012..2306			GTBX	"CALc06147, FGRc12101"				"2.7e-25, 6.2e-23"			
24733	ENU08528	ANI61C1060 2:1474..542			GTBX	"AFUc03068, FGRc11923"				"1.3e-91, 7.4e-43"			
24734	ENU08529	ANI61C1133 2:469..3			GTBX	FGRc25342				8.3E-21			
24735	ENU08530	ANI61C1133 3:419..3			GTBX	AFUc07909				4.1E-39			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24736	ENU08531	ANI61C1060 5:763..5			GTBX	"AFUc09745, CALc06186"				"7.8e-56, 1.0e-55"			
24737	ENU08532	ANI61C1133 6:88..652			GTBX	AFUc15671				1.8E-77			
24738	ENU08533	ANI61C2540: 53..867			GTBX	"AFUc14945, AFUc22252"				"2.1e-11, 1.6e-31"			
24739	ENU08534	ANI61C1811: 216..464			GTBX	FGRc11239				2.3E-23			
24740	ENU08535	ANI61C2541: 386..1450			GTBX	"AFUc03214, FGRc12435"				"2.1e-101, 6.5e-10"			
24741	ENU08536	ANI61C3271: 618..4			GTBX	AFUc10952				2.1E-36			
24742	ENU08537	ANI61C2544: 1425..331			GTBX	"AFUc10649, AFUc12123"				"3.1e-51, 4.0e-17"			
24743	ENU08538	ANI61C3274: 2373..2881			GTBX	AFUc02920				4.4E-81			
24744	ENU08539	ANI61C3279: 1619..1183			GTBX	AFUc14951				8E-175			
24745	ENU08540	ANI61C1134 3:331..1459			GTBX	"AFUc09854, AFUc09854"				"2.4e-113, 2.9e-87"			
24746	ENU08541	ANI61C1061 5:1232..399			GTBX	"AFUc18846, FGRc03863"				"5.5e-67, 4.5e-27"			
24747	ENU08542	ANI61C1134 5:1952..1431			GTBX	AFUc14213				4.3E-49			
24748	ENU08543	ANI61C1134 6:1470..487			GTBX	"AFUc00459, AFUc17980, AFUc18124, FGRc01734"				"1.5e-13, 1.6e-21, 3.9e-31, 1.8e-40"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24749	ENU08544	ANI61C1061 7:2430..444			GTBX	"AFUc02314, AFUc19482, CALc06208"				"4.9e-60, 1.5e-95, 2.7e-61"			
24750	ENU08545	ANI61C1134 8:2809..3127			GTBX	"AFUc13004, AFUc13004"				"1.3e-41, 2.7e-27"			
24751	ENU08546	ANI61C1134 9:670..1324			GTBX	AFUc14220				3.6E-114			
24752	ENU08547	ANI61C2550: 1720..2019			GTBX	AFUc11380				6.6E-52			
24753	ENU08548	ANI61C1823: 4..1605			GTBX	"AFUc09877, AFUc09877"				"2.5e-95, 8.9e-174"			
24754	ENU08549	ANI61C2554: 768..16			GTBX	AFUc12616				1.9E-72			
24755	ENU08550	ANI61C2556: 66..404			GTBX	AFUc14572				6E-30			
24756	ENU08551	ANI61C1062 0:736..361			GTBX	AFUc03637				2E-45			
24757	ENU08552	ANI61C1135 2:1895..3234			GTBX	"AFUc03502, AFUc07772"				"3.4e-59, 3.2e-91"			
24758	ENU08553	ANI61S1661: 445..2			GTBX	AFUc02010				2.3E-40			
24759	ENU08554	ANI61C1062 6:4810..5096			GTBX	"AFUc05250, CALc06081"				"2.6e-49, 2.4e-21"			
24760	ENU08555	ANI61C1135 6:346..1950			GTBX	AFUc15510				9.1E-121			
24761	ENU08556	ANI61C1830: 318..882			GTBX	AFUc10397				2.1E-122			
24762	ENU08557	ANI61C2562: 1530..2081			GTBX	"CALc05470, CALc05792"				"2.5e-32, 1.7e-37"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24763	ENU08558	ANI61C2568: 24..638			GTBX	AFUc05821				1.1E-28			
24764	ENU08559	ANI61C1839: 330..1127			GTBX	"AFUc09025, AFUc11515"				"6.1e-41, 5.2e-77"			
24765	ENU08560	ANI61C1063 0:465..32			GTBX	AFUc05997				6.4E-30			
24766	ENU08561	ANI61C1063 1:186..1843			GTBX	"AFUc01713, AFUc05435, AFUc05435"				"1.3e-63, 6.4e-41, 6.5e-55"			
24767	ENU08562	ANI61C1840: 1346..639			GTBX	AFUc18505				1.1E-37			
24768	ENU08563	ANI61C1843: 115..501			GTBX	FGRc11281				8.9E-46			
24769	ENU08564	ANI61C1846: 284..1741			GTBX	"FGRc02282, FGRc05940, FGRc11631"				"2.6e-23, 1.4e-13, 1.3e-09"			
24770	ENU08565	ANI61C2577: 199..920			GTBX	"CALc05069, FGRc17612"				"2.7e-41, 6.0e-44"			
24771	ENU08566	ANI61C1064 1:1707..3655			GTBX	"AFUc11683, Y13135"				"3.3e- 190, 5.1e- 119"			
24772	ENU08567	ANI61C1137 2:74..894			GTBX	AFUc17844				3.7E-26			
24773	ENU08568	ANI61C1064 5:47..619			GTBX	AFUc21723				2E-68			
24774	ENU08569	ANI61C2582: 5424..5048			GTBX	AFUc01594				1.5E-28			
24775	ENU08570	ANI61C1856: 658..141			GTBX	AFUc16536				3.5E-26			
24776	ENU08571	ANI61C2588: 754..22			GTBX	"AFUc08407, FGRc10457"				"4.6e-49, 6.6e-60"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24777	ENU08572	ANI61C2589: 186..1330			GTBX	AFUc13209				8.9E-77			
24778	ENU08573	ANI61C1138 1:1081..1457			GTBX	AFUc17037				5.9E-32			
24779	ENU08574	ANI61C1138 3:624..383			GTBX	FGRC08856				4.6E-27			
24780	ENU08575	ANI61C1065 4:7892..8920			GTBX	Y13135				3.8e-149			
24781	ENU08576	ANI61C1065 5:912..54			GTBX	CALc06050				4.2E-84			
24782	ENU08577	ANI61C1065 7:6666..6094			GTBX	AFUc03173				6.6E-39			
24783	ENU08578	ANI61C1138 8:62..701			GTBX	AFUc15731				4.1E-47			
24784	ENU08579	ANI61C1861: 1870..524			GTBX	AFUc14963				3E-180			
24785	ENU08580	ANI61C2592: 1363..3			GTBX	"AFUc17647, FGRC25036"				"9.1e-29, 1.8e-53"			
24786	ENU08581	ANI61C1865: 1589..2224			GTBX	AFUc06633				1.4E-63			
24787	ENU08582	ANI61C2594: 5002..1392			GTBX	"AFUc09935, Y13140"				"3.6e-55, 0.0"			
24788	ENU08583	ANI61C1866: 1568..1080			GTBX	AFUc10713				4.1E-44			
24789	ENU08584	ANI61C2599: 460..72			GTBX	Y13135				2.6e-62			
24790	ENU08585	ANI61C1066 5:664..406			GTBX	AFUc02315				5.3E-23			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24791	ENU08586	ANI61C1139 5:3021..2575			GTBX	AFUc22562				1.1E-28			
24792	ENU08587	ANI61C1871: 260..54			GTBX	"AFUc01385, AFUc09613"				"3.1e-34, 1.1e-19"			
24793	ENU08588	ANI61C1067 3:922..1413			GTBX	CALc03969				3.2E-57			
24794	ENU08589	ANI61C1067 5:2719..1441			GTBX	"AFUc15461, AFUc15461"				"1.2e-96, 2.3e-121"			
24795	ENU08590	ANI61C1067 5:3404..3889			GTBX	AFUc10889				2.7E-50			
24796	ENU08591	ANI61C1067 8:1080..600			GTBX	AFUc11094				8.3E-27			
24797	ENU08592	ANI61C9002: 1846..878			GTBX	AFUc11192				3.2E-94			
24798	ENU08593	ANI61C9004: 3235..3965			GTBX	"AFUc11110, Y13138"				"5.7e-30, 1.2e-14"			
24799	ENU08594	ANI61C9008: 314..861			GTBX	AFUc12481				2.4E-63			
24800	ENU08595	ANI61C1880: 72..1179			GTBX	"AFUc04431, AFUc16451"				"1.6e-82, 2.8e-14"			
24801	ENU08596	ANI61C1883: 546..19			GTBX	AFUc21307				3.5E-30			
24802	ENU08597	ANI61C1885: 1021..95			GTBX	AFUc10552				1.1E-64			
24803	ENU08598	ANI61C710:2 805..1017			GTBX	"AFUc11549, AFUc15367, AFUc17813"				"1.5e-81, 1.0e-41, 4.1e-53"			
24804	ENU08599	ANI61C713:1 670..74			GTBX	"AFUc05242, AFUc10990"				"6.0e-55, 2.5e-114"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24805	ENU08600	ANI61C1068 3:1487..1242			GTBX	AFUc13939				1.4E-22			
24806	ENU08601	ANI61C1068 9:1065..390			GTBX	"AFUc13250, FGRc13107"				"6.4e-93, 1.4e-10"			
24807	ENU08602	ANI61C9015: 405..1			GTBX	AFUc12921				3.1E-56			
24808	ENU08603	ANI61C1895: 23..652			GTBX	AFUc10988				1.4E-60			
24809	ENU08604	ANI61C720:1 602..685			GTBX	CALc06106				3.6E-78			
24810	ENU08605	ANI61C1069 5:865..252			GTBX	AFUc10487				9.9E-50			
24811	ENU08606	ANI61C9025: 463..194			GTBX	AFUc00949				5.1E-49			
24812	ENU08607	ANI61C8300: 800..189			GTBX	"AFUc08390, AFUc13837"				"3.3e-41, 6.5e-22"			
24813	ENU08608	ANI61C9030: 1085..11			GTBX	"AFUc06221, CALc06213, Y13134"				"8.3e-40, 2.3e-13, 4.6e-13"			
24814	ENU08609	ANI61C9039: 5769..6530			GTBX	"AFUc00570, FGRc14945"				"3.4e-28, 2.5e-08"			
24815	ENU08610	ANI61C8310: 465..181			GTBX	FGRc10180				3.2E-24			
24816	ENU08611	ANI61C8314: 2724..2023			GTBX	AFUc21917				5.4E-31			
24817	ENU08612	ANI61C9048: 61..1497			GTBX	"AFUc14050, FGRc03000"				"1.3e-98, 3.4e-28"			
24818	ENU08613	ANI61C751:4 20..749			GTBX	AFUc06278				1.4E-42			

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24819	ENU08614	ANI61C758:4 029..103			GTBX	"AFUc05783, AFUc05961, AFUc12204, AFUc12677, CALc06075, FGRc11436, FGRc17690"				"2.5e-72, 1.5e-27, 6.6e-196, 7.1e-126, 8.6e-128, 3.7e-75, 2.9e-35"			
24820	ENU08615	ANI61C8322: 1663..1077			GTBX	"AFUc04172, FGRc02654"							
24821	ENU08616	ANI61C8325: 79..477			GTBX	AFUc12859					3.5E-37		
24822	ENU08617	ANI61C8326: 860..1122			GTBX	AFUc09750				1.8E-25			
24823	ENU08618	ANI61C8330: 1999..807			GTBX	"AFUc02770, AFUc09905"				"8.7e-69, 1.6e-54"			
24824	ENU08619	ANI61C7605: 1939..1517			GTBX	AFUc09154				4.4E-30			
24825	ENU08620	ANI61C9063: 6060..4119			GTBX	"AFUc13510, AFUc14636, FGRc04398"				"1.4e-81, 1.8e-100, 1.1e-08"			
24826	ENU08621	ANI61C7606: 185..886			GTBX	AFUc09586				1.7E-35			
24827	ENU08622	ANI61C9067: 4043..1889			GTBX	"AFUc09078, AFUc18318, FGRc07495, FGRc07643"				"1.5e-11, 4.3e-09, 6.4e-29, 1.4e-29"			
24828	ENU08623	ANI61C770:7 83..35			GTBX	AFUc01959				1.1E-58			
24829	ENU08624	ANI61C775:4 81..1025			GTBX	"AFUc04122, Y13139"				"7.8e-21, 5.9e-61"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24830	ENU08625	ANI61C8340: 600..1358			GTBX	"AFUc09848, FGRC00517"				"2.6e-41, 1.0e-27"			
24831	ENU08626	ANI61C7615: 53..558			GTBX	AFUc01625				3.5E-52			
24832	ENU08627	ANI61C7616: 3166..2391			GTBX	"AFUc00961, FGRC05631"				"1.7e-25, 5.5e-16"			
24833	ENU08628	ANI61C7617: 1020..82			GTBX	"AFUc13516, CALc04464"				"1.8e-84, 9.5e-47"			
24834	ENU08629	ANI61C7618: 449..192			GTBX	AFUc12936				6.3E-53			
24835	ENU08630	ANI61C9077: 618..241			GTBX	AFUc02355				2.6E-33			
24836	ENU08631	ANI61C8348: 1562..2188			GTBX	AFUc06232				1.9E-58			
24837	ENU08632	ANI61C9078: 2867..1238			GTBX	"CALc05373, FGRC09215, FGRC14791, Y13140"				"1.3e-93, 1.3e-21, 1.1e-43, 9.9e-187"			
24838	ENU08633	ANI61C780:4 46..1			GTBX	"AFUc13983, Y13137"				"2.6e-42, 4.3e-33"			
24839	ENU08634	ANI61C781:6 3..979			GTBX	AFUc10848				5.4E-43			
24840	ENU08635	ANI61C789:4 022..2710			GTBX	"AFUc16570, AFUc17384"				"1.9e-52, 1.0e-67"			
24841	ENU08636	ANI61C8350: 2742..4517			GTBX	CALc06237				2.9E-46			
24842	ENU08637	ANI61C9080: 2749..969			GTBX	"AFUc07425, AFUc19355"				"3.7e-17, 1.2e-21"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24843	ENU08638	ANI61C9082: 251..958			GTBX	AFUc15938				7.9E-64			
24844	ENU08639	ANI61C8354: 1395..895			GTBX	"AFUc12206, Y13140"				"3.9e-65, 1.1e-30"			
24845	ENU08640	ANI61C8355: 551..2115			GTBX	"AFUc01781, AFUc01807, AFUc08308"				"1.4e-08, 1.3e-11, 1.6e-22"			
24846	ENU08641	ANI61C7628: 3..290			GTBX	CALc06163				2.5E-28			
24847	ENU08642	ANI61C792:6 85..317			GTBX	AFUc20257				1.8E-38			
24848	ENU08643	ANI61C794:1 079..852			GTBX	AFUc15667				5.6E-29			
24849	ENU08644	ANI61C797:1 521..2941			GTBX	"AFUc12939, AFUc14002"				"3.4e-18, 2.0e-68"			
24850	ENU08645	ANI61C798:5 48..14			GTBX	"AFUc10758, AFUc10988"				"2.2e-36, 9.8e-13"			
24851	ENU08646	ANI61C7633: 311..964			GTBX	AFUc01337				1.1E-46			
24852	ENU08647	ANI61C8363: 497..1386			GTBX	"AFUc15806, AFUc22456, FGRc02315, Y13136"				"5.9e-50, 3.4e-47, 1.0e-46, 3.3e-44"			
24853	ENU08648	ANI61C9092: 198..1162			GTBX	"AFUc15550, U00092"				"7.9e-30, 1.3e-62"			
24854	ENU08649	ANI61C6908: 658..381			GTBX	AFUc11236				2E-80			
24855	ENU08650	ANI61C6910: 1381..152			GTBX	AFUc11952				5E-68			
24856	ENU08651	ANI61C8372: 870..1638			GTBX	"AFUc09758, CALc05309"				"3.5e-77, 2.4e-13"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24857	ENU08652	ANI61C8375: 3081..370			GTBX	"AFUc05629, AFUc21466"				"2.3e-91, 1.3e-40"			
24858	ENU08653	ANI61C6919: 239..529			GTBX	AFUc14464				3.6E-35			
24859	ENU08654	ANI61C7649: 949..566			GTBX	AFUc18416				3.9E-25			
24860	ENU08655	ANI61C7651: 786..70			GTBX	CALc05557				1.5E-24			
24861	ENU08656	ANI61C6925: 1425..2330			GTBX	"AFUc04661, AFUc22181"				"2.6e-31, 2.0e-36"			
24862	ENU08657	ANI61C6926: 692..1049			GTBX	AFUc01242				1.3E-46			
24863	ENU08658	ANI61C6927: 3535..2135			GTBX	"AFUc03128, AFUc07465"				"1.8e-65, 5.3e-67"			
24864	ENU08659	ANI61C8385: 3004..3390			GTBX	AFUc09509				3.1E-59			
24865	ENU08660	ANI61C6930: 909..328			GTBX	AFUc07723				3.6E-44			
24866	ENU08661	ANI61C6931: 1816..796			GTBX	AFUc03234				1.2E-51			
24867	ENU08662	ANI61C7661: 1..306			GTBX	AFUc08515				5.1E-41			
24868	ENU08663	ANI61C8391: 1166..822			GTBX	"AFUc02256, AFUc08836"				"2.0e-43, 1.1e-20"			
24869	ENU08664	ANI61C7663: 1683..29			GTBX	"AFUc07074, AFUc11027"				"7.7e-34, 4.4e-29"			
24870	ENU08665	ANI61C7664: 620..1668			GTBX	"CALc05819, FGRc11819, FGRc11819"				"2.1e-66, 1.2e-50, 4.0e-37"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24871	ENU08666	ANI61C7665: 1405..1690			GTBX	"AFUc20344, FGRc25908"				"3.0e-52, 9.4e-22"			
24872	ENU08667	ANI61C7667: 217..764			GTBX	AFUc15868				2.8E-59			
24873	ENU08668	ANI61C7668: 546..21			GTBX	AFUc19926				1.1E-48			
24874	ENU08669	ANI61C7669: 1362..145			GTBX	"AFUc16122, AFUc18675, CALc06209"				"6.4e-69, 4.8e-37, 4.3e-96"			
24875	ENU08670	ANI61C8398: 1256..1657			GTBX	"CALc03932, FGRc14057, FGRc23953"				"4.4e-108, 2.3e-24, 2.2e-44"			
24876	ENU08671	ANI61C6941: 2770..1688			GTBX	CALc06022				4E-79			
24877	ENU08672	ANI61C6942: 1015..337			GTBX	"AFUc09643, FGRc10423"				"9.0e-22, 6.3e-13"			
24878	ENU08673	ANI61C7672: 4149..5074			GTBX	AFUc15338				2.1E-67			
24879	ENU08674	ANI61C7673: 2706..3490			GTBX	U00094				4.6e-253			
24880	ENU08675	ANI61C7675: 7588..6036			GTBX	"AFUc09612, AFUc18486"				"8.0e-40, 1.4e-39"			
24881	ENU08676	ANI61C6948: 514..290			GTBX	AFUc14750				2.7E-34			
24882	ENU08677	ANI61C7689: 2240..860			GTBX	AFUc07888				4.6E-109			
24883	ENU08678	ANI61C10:13 51..46			GTBX	AFUc04257				9.9E-80			
24884	ENU08679	ANI61C18:28 ..740			GTBX	AFUc06457				1.5E-24			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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24886	ENU08681	ANI61C7695: 1205..3			GTBX	"AFUc14143, FGRc21455"				"2.4e-80, 1.1e-26"			
24887	ENU08682	ANI61C6967: 687..361			GTBX	"AFUc15762, AFUc15762"				"1.8e-68, 3.0e-170"			
24888	ENU08683	ANI61C6968: 222..943			GTBX	"AFUc08123, CALc05688"				"6.6e-24, 5.1e-87"			
24889	ENU08684	ANI61C6969: 1497..1			GTBX	AFUc08629				1.1E-84			
24890	ENU08685	ANI61C21:10 21..690			GTBX	"FGRc05811, U00094"				"1.1e-51, 1.2e-97"			
24891	ENU08686	ANI61C24:13 02..541			GTBX	AFUc10888				2.2E-38			
24892	ENU08687	ANI61C27:13 60..1941			GTBX	CALc04049				5.6E-149			
24893	ENU08688	ANI61C29:12 40..77			GTBX	U00094				2.0e-29			
24894	ENU08689	ANI61C6974: 1512..1835			GTBX	"AFUc12767, FGRc04567"				"1.8e-09, 1.4e-32"			
24895	ENU08690	ANI61C6976: 780..11			GTBX	AFUc20643				5.4E-33			
24896	ENU08691	ANI61C6978: 936..477			GTBX	FGRc17293				5E-24			
24897	ENU08692	ANI61C6979: 2007..2660			GTBX	AFUc14080				3.3E-22			
24898	ENU08693	ANI61C4002: 1132..302			GTBX	AFUc10817				4.7E-59			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24899	ENU08694	ANI61C34:77 8..2349			GTBX	"AFUc10260, FGRc02884, FGRc12117, FGRc19667"				"3.5e-56, 6.5e-48, 5.2e-50, 1.7e-24" 4.6E-33			
24900	ENU08695	ANI61C36:77 ..634			GTBX	AFUc00656							
24901	ENU08696	ANI61C6980: 363..1007			GTBX	Y13135				1.2e-31			
24902	ENU08697	ANI61C6985: 625..5			GTBX	"FGRc11412, FGRc17886"				"4.7e-19, 2.8e-36"			
24903	ENU08698	ANI61C6986: 1531..763			GTBX	AFUc12892				1.2E-52			
24904	ENU08699	ANI61C40:84 1..1771			GTBX	AFUc15961				1.2E-45			
24905	ENU08700	ANI61C46:92 8..116			GTBX	AFUc15151				1.5E-77			
24906	ENU08701	ANI61S645:4 1..428			GTBX	AFUc13524				3.1E-39			
24907	ENU08702	ANI61C6999: 887..135			GTBX	AFUc15217				8E-28			
24908	ENU08703	ANI61C4021: 1037..14			GTBX	AFUc00826				1.7E-28			
24909	ENU08704	ANI61C55:10 16..1329			GTBX	AFUc09449				1.8E-23			
24910	ENU08705	ANI61C61:65 60..4412			GTBX	"AFUc07978, FGRc00983, FGRc23299"				"9.0e-24, 2.0e-21, 2.6e-23"			
24911	ENU08706	ANI61C61:96 64..8595			GTBX	AFUc12810				6.1E-33			
24912	ENU08707	ANI61C4034: 490..254			GTBX	FGRc12892				3.8E-40			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24913	ENU08708	ANI61C3307: 997..1236			GTBX	AFUc14556				7.7E-33			
24914	ENU08709	ANI61C3309: 3590..1383			GTBX	"AFUc19897, CALc05545, FGRc10593"				"3.7e-34, 9.3e-107, 6.2e-41" 3.8e-13			
24915	ENU08710	ANI61S3148: 132..339			GTBX	U00094							
24916	ENU08711	ANI61C70:15 4..1477			GTBX	AFUc13679				3.1E-42			
24917	ENU08712	ANI61C74:20 41..1277			GTBX	"FGRc02814, FGRc10359, FGRc18356"				"6.6e-59, 2.0e-50, 1.3e-07" 6.4E-117			
24918	ENU08713	ANI61C3315: 1021..1941			GTBX	AFUc14821							
24919	ENU08714	ANI61C3317: 4317..4820			GTBX	AFUc11811				1E-69			
24920	ENU08715	ANI61C4046: 944..2324			GTBX	AFUc09421				3.9E-37			
24921	ENU08716	ANI61C4047: 816..382			GTBX	AFUc02478				2.6E-45			
24922	ENU08717	ANI61C81:39 81..2518			GTBX	AFUc10625				3E-101			
24923	ENU08718	ANI61C3322: 447..49			GTBX	AFUc19143				1.4E-21			
24924	ENU08719	ANI61C3323: 5065..4721			GTBX	AFUc13265				1.3E-49			
24925	ENU08720	ANI61C84:12 67..794			GTBX	CALc05272				2.5E-47			
24926	ENU08721	ANI61C3328: 10..492			GTBX	Y13136				2.9e-49			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24927	ENU08722	ANI61C3329: 2681..3493			GTBX	"AFUc16245, AFUc18755"				"1.4e-08, 3.6e-21"			
24928	ENU08723	ANI61C2600: 1242..340			GTBX	"AFUc06261, FGRcl2448"				"1.0e-73, 4.7e-46"			
24929	ENU08724	ANI61C3330: 816..12			GTBX	AFUc11045				6.1E-47			
24930	ENU08725	ANI61C4065: 192..470			GTBX	FGRcl2294				2.6E-23			
24931	ENU08726	ANI61C3337: 2136..49			GTBX	"AFUc06141, AFUc08576, Y13134"				"1.1e-28, 7.3e-84, 1.6e-61"			
24932	ENU08727	ANI61C3338: 1298..395			GTBX	AFUc09204				1.7E-36			
24933	ENU08728	ANI61C2609: 955..215			GTBX	AFUc10760				4.8E-38			
24934	ENU08729	ANI61C98:15 62..599			GTBX	"AFUc07359, AFUc07383, AFUc15393"				"2.9e-35, 2.8e-60, 1.4e-55"			
24935	ENU08730	ANI61C1140 0:738..1813			GTBX	AFUc15950				2.7E-91			
24936	ENU08731	ANI61C1140 4:4363..3848			GTBX	"AFUc05972, AFUc08582"				"4.6e-27, 3.5e-14"			
24937	ENU08732	ANI61S1712: 90..437			GTBX	"AFUc05166, CALc01912"				"7.1e-13, 1.4e-38"			
24938	ENU08733	ANI61S1715: 46..375			GTBX	AFUc07612				6E-30			
24939	ENU08734	ANI61C3342: 3..452			GTBX	AFUc05841				6.7E-35			
24940	ENU08735	ANI61C3342: 1691..763			GTBX	"AFUc18170, Z71256"				"1.4e-15, 5.6e-14"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24941	ENU08736	ANI61C4072: 1036..572			GTBX	AFUc03577				8.2E-78			
24942	ENU08737	ANI61C2615: 427..2074			GTBX	"AFUc19837, Y13138"				"2.6e-44, 1.4e-41"			
24943	ENU08738	ANI61C3344: 172..816			GTBX	FGRc02406				5.1E-25			
24944	ENU08739	ANI61C2616: 820..2283			GTBX	"AFUc05687, AFUc08664, CALc05800, CALc06229"				"1.7e-49, 7.9e-07, 1.9e-35, 8.4e-26"			
24945	ENU08740	ANI61C4074: 249..872			GTBX	"FGRc11944, U00092"				"4.4e-70, 4.4e-36"			
24946	ENU08741	ANI61C4076: 30..557			GTBX	"AFUc13132, FGRc02840"				"6.1e-32, 2.0e-09"			
24947	ENU08742	ANI61C1141 5:2205..964			GTBX	"AFUc09709, AFUc12435"				"1.5e-66, 6.1e-81"			
24948	ENU08743	ANI61C4080: 37..961			GTBX	AFUc07865				6.1E-73			
24949	ENU08744	ANI61C4082: 632..399			GTBX	AFUc11950				1.1E-26			
24950	ENU08745	ANI61C3355: 619..1088			GTBX	AFUc10222				1.5E-54			
24951	ENU08746	ANI61C3356: 976..367			GTBX	AFUc12958				1.1E-81			
24952	ENU08747	ANI61C3358: 4765..6066			GTBX	AFUc15520				3.1E-70			
24953	ENU08748	ANI61C3359: 1074..440			GTBX	AFUc13793				4.5E-78			
24954	ENU08749	ANI61C1142 2:674..66			GTBX	AFUc07909				2.1E-36			

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24955	ENU08750	ANI61C1142 3:748..1			GTBX	AFUc05597				1.8E-83			
24956	ENU08751	ANI61C1142 7:3870..2475			GTBX	"AFUc08441, FGRc23451, Y13140"				"6.1e-07, 4.6e-12, 4.6e-41"			
24957	ENU08752	ANI61C1142 9:1930..573			GTBX	AFUc06257				1.6E-22			
24958	ENU08753	ANI61C2630: 541..105			GTBX	AFUc08424				3.4E-59			
24959	ENU08754	ANI61C2633: 2625..2233			GTBX	AFUc05841				3.1E-54			
24960	ENU08755	ANI61C4093: 333..85			GTBX	AFUc04043				3.8E-27			
24961	ENU08756	ANI61C2636: 1040..489			GTBX	AFUc11267				4.1E-79			
24962	ENU08757	ANI61C1909: 1..484			GTBX	AFUc13018				2.2E-63			
24963	ENU08758	ANI61C4098: 1484..2175			GTBX	"AFUc12633, AFUc13482, CALc05318"				"5.9e-20, 3.8e-68, 1.2e-10"			
24964	ENU08759	ANI61C1070 0:5786..6253			GTBX	AFUc10021				2.9E-39			
24965	ENU08760	ANI61C1143 0:499..1727			GTBX	AFUc11277				1.9E-64			
24966	ENU08761	ANI61C1143 2:3308..3949			GTBX	"AFUc16152, AFUc16297"				"7.7e-15, 4.1e-26"			
24967	ENU08762	ANI61C1070 4:90..2062			GTBX	"AFUc03602, AFUc18530"				"2.2e-36, 4.7e-60"			
24968	ENU08763	ANI61C1143 5:345..1916			GTBX	"AFUc05782, AFUc15229, FGRc13683"				"1.4e- 122, 2.6e-09, 2.4e-37"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
24969	ENU08764	ANI61C1070 6:9612..11235			GTBX	"AFUc07945, AFUc12767, FGRc10695"				"2.3e-24, 5.9e-12, 5.7e-66"			
24970	ENU08765	ANI61C1143 6:8706..8281			GTBX	FGRc12034				1.2E-21			
24971	ENU08766	ANI61C1070 7:948..1825			GTBX	"AFUc11321, AFUc14716, Y13135"				"6.5e-95, 1.7e-40, 5.5e-09"			
24972	ENU08767	ANI61C1070 9:111..425			GTBX	AFUc09791				5.5E-28			
24973	ENU08768	ANI61C1910: 407..1			GTBX	AFUc15581				8.3E-33			
24974	ENU08769	ANI61C1912: 1407..133			GTBX	"AFUc08239, FGRc26694"				"1.1e-64, 1.4e-38"			
24975	ENU08770	ANI61C3371: 1098..181			GTBX	AFUc05453				4.4E-22			
24976	ENU08771	ANI61C1913: 2846..474			GTBX	"CALc05504, U00094"				"1.5e-77, 1.8e-11"			
24977	ENU08772	ANI61C3372: 682..993			GTBX	AFUc14289				7.5E-43			
24978	ENU08773	ANI61C1915: 2216..2827			GTBX	AFUc16313				1.2E-50			
24979	ENU08774	ANI61C3376: 1445..891			GTBX	AFUc12472				3.7E-45			
24980	ENU08775	ANI61C2647: 36..452			GTBX	AFUc00608				6.1E-35			
24981	ENU08776	ANI61C1919: 773..19			GTBX	U00094				1.3e-87			
24982	ENU08777	ANI61C3378: 1216..2			GTBX	AFUc10430				2.9E-166			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
24983	ENU08778	ANI61C1071 3:1728..3141			GTBX	"AFUc05029, FGRc10887"				"1.9e-28, 1.0e-24"			
24984	ENU08779	ANI61C1144 4:4343..5216			GTBX	"AFUc08298, AFUc22104"				"3.9e-17, 1.2e-23"			
24985	ENU08780	ANI61C1071 6:3219..1252			GTBX	"AFUc09877, AFUc11768, FGRc03217"				"6.4e-52, 4.4e-81, 3.6e-26"			
24986	ENU08781	ANI61C2651: 1167..676			GTBX	AFUc06429				1.4E-47			
24987	ENU08782	ANI61C2653: 670..338			GTBX	FGRc07112				4.2E-45			
24988	ENU08783	ANI61C2654: 823..1444			GTBX	Y13138				2.9e-38			
24989	ENU08784	ANI61C2656: 2061..2360			GTBX	FGRc02646				6.5E-25			
24990	ENU08785	ANI61C1928: 1654..734			GTBX	AFUc12945				5.9E-109			
24991	ENU08786	ANI61C3388: 954..17			GTBX	AFUc08509				2.9E-47			
24992	ENU08787	ANI61C1072 0:565..84			GTBX	AFUc06323				6.2E-26			
24993	ENU08788	ANI61C1072 1:2272..1494			GTBX	AFUc12398				7.6E-75			
24994	ENU08789	ANI61C1072 2:562..1611			GTBX	"AFUc15498, AFUc18421"				"4.6e- 113, 7.1e-50"			
24995	ENU08790	ANI61S1767: 76..593			GTBX	AFUc10191				9.3E-93			
24996	ENU08791	ANI61C1930: 1036..686			GTBX	CALc06119				1.1E-69			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25011	ENU08806	ANI61C1074 0:919..22			GTBX	"AFUc10091, FGRc03364"				"2.7e-56, 2.1e-23"			
25012	ENU08807	ANI61C1074 1:1607..918			GTBX	AFUc14682				1.9E-80			
25013	ENU08808	ANI61C1147 1:2164..1046			GTBX	AFUc03516				1E-25			
25014	ENU08809	ANI61C1074 2:1908..2430			GTBX	AFUc06521				1.9E-43			
25015	ENU08810	ANI61C1147 8:1292..2764			GTBX	AFUc14969				6.3E-198			
25016	ENU08811	ANI61C1952: 2185..3687			GTBX	"AFUc14718, FGRc15556"				"4.9e- 131, 9.1e-41" 8.4E-87			
25017	ENU08812	ANI61C1957: 1467..1747			GTBX	AFUc14883				1E-44			
25018	ENU08813	ANI61C1075 0:1589..2369			GTBX	AFUc14574				4.6E-32			
25019	ENU08814	ANI61C1148 1:482..35			GTBX	AFUc11691				1.5E-24			
25020	ENU08815	ANI61C1075 3:141..476			GTBX	AFUc15229				1.8E-26			
25021	ENU08816	ANI61C1960: 1871..1443			GTBX	AFUc04303				2.8E-128			
25022	ENU08817	ANI61C2692: 3428..2316			GTBX	AFUc09746				1.8E-45			
25023	ENU08818	ANI61C2693: 449..95			GTBX	AFUc13804				"6.5e-27, 4.2e-61"			
25024	ENU08819	ANI61C2698: 745..259			GTBX	"AFUc07690, AFUc12854"							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	% Description
25025	ENU08820	ANI61C2698:1594..988			GTBX	"AFUc09690, AFUc12854, FGRc07517"				"2.8e-25, 4.2e-61, 1.6e-18"			
25026	ENU08821	ANI61C1076 4:709..109			GTBX	"CALc05408, FGRc05636"				"2.6e-24, 2.2e-25"			
25027	ENU08822	ANI61C1076 7:2475..3500			GTBX	AFUc11524				3.5E-85			
25028	ENU08823	ANI61C1972:1158..691			GTBX	Z47047				8.1e-21			
25029	ENU08824	ANI61C1973:128..544			GTBX	AFUc15874				8.6E-34			
25030	ENU08825	ANI61C1974:196..552			GTBX	AFUc14463				2.7E-47			
25031	ENU08826	ANI61C1975:2720..6			GTBX	"AFUc11768, AFUc14088, AFUc14691, FGRc19856"				"1.2e-72, 7.4e-92, 9.9e-72, 1.3e-13"			
25032	ENU08827	ANI61C807:104..363			GTBX	FGRc08860				1.3E-23			
25033	ENU08828	ANI61C809:397..740			GTBX	AFUc15761				9.8E-56			
25034	ENU08829	ANI61C1077 6:4764..5669			GTBX	AFUc14848				2.3E-87			
25035	ENU08830	ANI61C9100:1569..543			GTBX	AFUc10383				4.6E-54			
25036	ENU08831	ANI61C9104:5043..5687			GTBX	"AFUc03688, FGRc07492"				"9.0e-27, 1.5e-26"			
25037	ENU08832	ANI61C9105:1952..601			GTBX	AFUc05381				3.2E-57			
25038	ENU08833	ANI61C9107:3660..5664			GTBX	"AFUc13126, FGRc07962"				"5.8e-55, 5.9e-42"			

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25039	ENU08834	ANI61C818:3 256..2912			GTBX	FGRc24873				4.6E-41			
25040	ENU08835	ANI61C1078 8:1519..49			GTBX	FGRc09740				3.1E-28			
25041	ENU08836	ANI61C1078 9:1896..1027			GTBX	AFUc13090				3.1E-114			
25042	ENU08837	ANI61C9112: 2215..3174			GTBX	AFUc05724				7.5E-81			
25043	ENU08838	ANI61C9112: 4794..3825			GTBX	AFUc12748				1.9E-60			
25044	ENU08839	ANI61C9117: 4650..5342			GTBX	AFUc22177				4.9E-54			
25045	ENU08840	ANI61C9118: 2481..4081			GTBX	"AFUc05152, AFUc06401"				"3.3e-67, 4.0e-15"			
25046	ENU08841	ANI61C822:9 78..138			GTBX	AFUc05328				2.1E-37			
25047	ENU08842	ANI61C826:4 55..1470			GTBX	"AFUc06686, AFUc11073"				"1.3e-44, 1.5e-19"			
25048	ENU08843	ANI61C827:1 030..74			GTBX	"AFUc12162, AFUc19854"				"2.2e-62, 5.0e-45"			
25049	ENU08844	ANI61C828:2 324..2715			GTBX	AFUc02177				1.4E-38			
25050	ENU08845	ANI61C1079 2:295..726			GTBX	"AFUc03882, FGRc06121"				"1.9e-40, 7.0e-35"			
25051	ENU08846	ANI61C1079 6:1764..38			GTBX	"AFUc04821, Y13138"				"4.2e- 100, 7.6e- 120"			
25052	ENU08847	ANI61C9125: 1139..627			GTBX	AFUc12750				2E-36			

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25053	ENU08848	ANI61C836:8 95..335			GTBX	"AFUc14883, AFUc14883"				"5.8e-46, 7.5e-53"			
25054	ENU08849	ANI61C837:4 1..566			GTBX	AFUc20588				3.6E-38			
25055	ENU08850	ANI61C8403: 2265..1942			GTBX	AFUc08360				7.3E-22			
25056	ENU08851	ANI61C8406: 3383..1653			GTBX	"AFUc12104, AFUc15297, Y13135"				"4.0e-62, 3.7e-23, 3.0e-46"			
25057	ENU08852	ANI61C9136: 666..908			GTBX	AFUc13948				5.9E-32			
25058	ENU08853	ANI61C8407: 2066..705			GTBX	"AFUc13751, AFUc13751"				"3.4e- 186, 6.1e- 210"			
25059	ENU08854	ANI61C848:1 328..2315			GTBX	AFUc08609				1.7E-86			
25060	ENU08855	ANI61C8411: 739..2328			GTBX	"CALc05880, D50617"				"3.4e-96, 2.2e-48"			
25061	ENU08856	ANI61C8413: 1811..1191			GTBX	"AFUc07925, Y13139"				"1.6e- 105, 2.0e-95"			
25062	ENU08857	ANI61C8414: 79..1278			GTBX	"AFUc01427, FGRc11796"				"1.1e-07, 3.1e-73"			
25063	ENU08858	ANI61C8418: 1559..1860			GTBX	AFUc13723				3.3E-33			
25064	ENU08859	ANI61C8419: 1451..2381			GTBX	"AFUc08249, FGRc12401"				"2.7e- 159, 1.8e-23"			
25065	ENU08860	ANI61C9149: 2758..2324			GTBX	AFUc02271				1.4E-50			

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25067	ENU08862	ANI61C853:7 64..1566			GTBX	AFUc12396				9.4E-77			
25068	ENU08863	ANI61C855:7 0..519			GTBX	"AFUc12828, FGRc08325"				"2.8e-34, 1.4e-22"			
25069	ENU08864	ANI61C857:2 364..1240			GTBX	AFUc21112				4.9E-55			
25070	ENU08865	ANI61C9154: 1083..30			GTBX	AFUc10496				1.8E-45			
25071	ENU08866	ANI61C8429: 1639..1370			GTBX	AFUc09889				1.4E-68			
25072	ENU08867	ANI61C867:9 93..1			GTBX	Y13135				2.2e-20			
25073	ENU08868	ANI61C7703: 1506..530			GTBX	"AFUc11864, AFUc13604, AFUc15296"				"4.3e-21, 7.0e-54, 4.0e-20"			
25074	ENU08869	ANI61C7704: 1011..306			GTBX	FGRc20146				3.6E-34			
25075	ENU08870	ANI61C8433: 3..374			GTBX	AFUc14422				1.3E-50			
25076	ENU08871	ANI61C8436: 1397..1989			GTBX	AFUc12944				1.3E-83			
25077	ENU08872	ANI61C7709: 812..115			GTBX	FGRc12224				1.6E-70			
25078	ENU08873	ANI61C875:2 057..1446			GTBX	Y13135				6.9e-17			
25079	ENU08874	ANI61C8441: 1416..541			GTBX	FGRc12904				2.8E-24			

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25080	ENU08875	ANI61C7714:1136..2228			GTBX	"FGRc06342, FGRc14811"				"8.4e-13, 6.0e-22"			
25081	ENU08876	ANI61C8446:620..29			GTBX	"AFUc11909, FGRc12199"				"3.5e-19, 7.9e-38"			
25082	ENU08877	ANI61C7717:1113..1711			GTBX	AFUc07025				3.2E-41			
25083	ENU08878	ANI61C7717:5981..5119			GTBX	"AFUc16351, FGRc04611"				"4.4e-23, 7.7e-20"			
25084	ENU08879	ANI61C9179:3890..5546			GTBX	"AFUc13046, AFUc22205"				"7.7e-96, 9.1e-37"			
25085	ENU08880	ANI61C886:5224..3674			GTBX	"AFUc04165, AFUc14221"				"5.2e-09, 9.9e-39"			
25086	ENU08881	ANI61C888:4222..3713			GTBX	AFUc20805				2.2E-28			
25087	ENU08882	ANI61C7721:563..1320			GTBX	"AFUc12977, AFUc14414"				"6.6e-33, 6.6e-17"			
25088	ENU08883	ANI61C7724:45..794			GTBX	AFUc10173				3.6E-116			
25089	ENU08884	ANI61C8456:2127..40			GTBX	"AFUc09795, Z71256"				"7.6e-59, 6.7e-212"			
25090	ENU08885	ANI61C9189:1464..940			GTBX	AFUc00837				8.5E-38			
25091	ENU08886	ANI61C894:1514..653			GTBX	AFUc15628				4.7E-69			
25092	ENU08887	ANI61C9190:1512..525			GTBX	"FGRc00983, FGRc26079"				"3.9e-44, 5.8e-18"			
25093	ENU08888	ANI61C8463:815..1153			GTBX	AFUc11295				5.4E-117			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
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25096	ENU08891	ANI61C9196: 509..1774			GTBX	"AFUc05790, AFUc13990, FGRc15154"				"2.0e-29, 1.8e-29, 3.4e-25"			
25097	ENU08892	ANI61C7739: 947..600			GTBX	FGRc14654				2.7E-22			
25098	ENU08893	ANI61C9198: 816..496			GTBX	AFUc09614				2.3E-27			
25099	ENU08894	ANI61C8469: 1100..398			GTBX	"AFUc18110, FGRc17629"				"3.2e-58, 3.5e-11"			
25100	ENU08895	ANI61C8470: 1108..629			GTBX	AFUc02394				1.1E-22			
25101	ENU08896	ANI61C7741: 2522..4541			GTBX	"AFUc13489, AFUc17708, CALc05924"				"1.9e-19, 1.5e-38, 6.9e-239"			
25102	ENU08897	ANI61C8475: 731..1763			GTBX	AFUc21062				3.5E-43			
25103	ENU08898	ANI61C7756: 1266..573			GTBX	"CALc05253, FGRc26927"				"7.8e-60, 1.4e-15"			
25104	ENU08899	ANI61C8486: 2739..3881			GTBX	"AFUc12062, AFUc14671"				"1.9e-102, 3.9e-98"			
25105	ENU08900	ANI61C8487: 2372..427			GTBX	AFUc15656				1.1E-244			
25106	ENU08901	ANI61C7759: 141..404			GTBX	CALc04035				1.6E-33			

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25107	ENU08902	ANI61C8490:171..1778			GTBX	"CALc05635, FGRc06214, FGRc20613"				"9.5e-66, 4.0e-20, 9.4e-68"			
25108	ENU08903	ANI61C7762:584..1			GTBX	AFUc10277				6E-91			
25109	ENU08904	ANI61C7765:763..57			GTBX	Z71256				7.6e-26			
25110	ENU08905	ANI61C7766:86..706			GTBX	AFUc02641				2.8E-22			
25111	ENU08906	ANI61C7767:4855..4230			GTBX	AFUc21500				2.9E-46			
25112	ENU08907	ANI61C7768:3372..3915			GTBX	AFUc15315				1.9E-112			
25113	ENU08908	ANI61C7770:989..79			GTBX	AFUc03608				4.9E-58			
25114	ENU08909	ANI61S14:618..264			GTBX	"FGRc00672, FGRc09713"				"9.2e-07, 2.9e-37"			
25115	ENU08910	ANI61C7771:4802..3214			GTBX	"AFUc01209, AFUc05079"				"4.0e-28, 3.9e-16"			
25116	ENU08911	ANI61C7773:503..1698			GTBX	"AFUc02171, FGRc00650"				"3.1e-32, 3.4e-14"			
25117	ENU08912	ANI61C7774:3657..2305			GTBX	AFUc01162				5.6E-121			
25118	ENU08913	ANI61C7777:1063..1767			GTBX	"AFUc05844, FGRc12412"				"8.7e-74, 4.4e-30"			
25119	ENU08914	ANI61C7786:232..921			GTBX	AFUc05158				3.6E-50			
25120	ENU08915	ANI61C7789:735..1117			GTBX	AFUc14811				7.1E-29			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25121	ENU08916	ANI61S7194 58..168			GTBX	AFUc05321				1E-29			
25122	ENU08917	ANI61C7792: 207..1448			GTBX	"AFUc15949, FGRc07097"				"3.3e-38, 7.1e-24"			
25123	ENU08918	ANI61C4102: 1585..1031			GTBX	AFUc14601				9.8E-63			
25124	ENU08919	ANI61C4103: 891..301			GTBX	"AFUc02035, AFUc18244, FGRc16341"				"6.8e-16, 6.3e-49, 1.0e-12"			
25125	ENU08920	ANI61C4106: 888..1172			GTBX	AFUc12497				6.4E-29			
25126	ENU08921	ANI61C4107: 3073..4246			GTBX	"AFUc03644, AFUc03949, AFUc07144"				"2.3e-51, 1.8e-29, 3.7e-22"			
25127	ENU08922	ANI61C4107: 6848..4563			GTBX	"AFUc10284, AFUc16568, FGRc23371"				"3.4e- 124, 1.8e-25, 4.3e-10"			
25128	ENU08923	ANI61C4108: 1056..2837			GTBX	"AFUc05077, AFUc15554, FGRc08841"				"2.6e-43, 5.2e- 121, 4.0e-59"			
25129	ENU08924	ANI61S51:11. .352			GTBX	AFUc09974				4.7E-50			
25130	ENU08925	ANI61C4116: 565..195			GTBX	"AFUc14805, AFUc20877"				"6.4e-36, 4.6e-38"			
25131	ENU08926	ANI61C4119: 741..313			GTBX	AFUc06070				1E-39			
25132	ENU08927	ANI61C4124: 2482..2991			GTBX	AFUc11634				4.7E-39			

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25133	ENU08928	ANI61C4126: 978..3417			GTBX	"AFUc14940, FGRc02042, U00094"				"3.5e-270, 7.0e-28, 3.2e-273"			
25134	ENU08929	ANI61S75:57 8..25			GTBX	AFUc15050				3.2E-59			
25135	ENU08930	ANI61C3400: 994..518			GTBX	AFUc08654				7.8E-23			
25136	ENU08931	ANI61C3402: 1027..517			GTBX	"CALc06080, CALc06080"				"1.5e-56, 2.4e-60"			
25137	ENU08932	ANI61C4132: 2782..3311			GTBX	"AFUc19418, FGRc07284"				"1.5e-37, 1.6e-95"			
25138	ENU08933	ANI61C4134: 495..1116			GTBX	AFUc04164				1.2E-68			
25139	ENU08934	ANI61C3406: 2435..654			GTBX	"AFUc01839, AFUc16911, AFUc22154, FGRc12232"				"1.2e-26, 2.2e-14, 4.4e-21, 6.2e-23"			
25140	ENU08935	ANI61C3409: 255..582			GTBX	AFUc20668				5.5E-26			
25141	ENU08936	ANI61C4139: 1078..24			GTBX	AFUc11116				3.5E-33			
25142	ENU08937	ANI61C4143: 51..749			GTBX	"AFUc21598, FGRc22967"				"4.1e-10, 3.8e-30"			
25143	ENU08938	ANI61C4145: 47..552			GTBX	AFUc15424				7.6E-67			
25144	ENU08939	ANI61C3416: 1545..1820			GTBX	AFUc05316				2E-23			
25145	ENU08940	ANI61S772:2 79..49			GTBX	AFUc04175				6.6E-32			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25146	ENU08941	ANI61C4154: 750..427			GTBX	FGRc08165				5.1E-38			
25147	ENU08942	ANI61C3426: 799..1035			GTBX	AFUc14425				1.2E-32			
25148	ENU08943	ANI61C4156: 811..158			GTBX	AFUc01911				2.8E-33			
25149	ENU08944	ANI61C4164: 1102..2126			GTBX	"AFUc07502, CALc06043"				"2.2e-72, 2.1e-26"			
25150	ENU08945	ANI61C4165: 2879..2147			GTBX	AFUc05660				5.7E-114			
25151	ENU08946	ANI61C3439: 1918..547			GTBX	AFUc08088				3.6E-86			
25152	ENU08947	ANI61S798:2..358			GTBX	AFUc06449				3.1E-21			
25153	ENU08948	ANI61S3272: 1..396			GTBX	AFUc06662				1.4E-68			
25154	ENU08949	ANI61C3442: 978..2365			GTBX	"AFUc15654, AFUc15654"				"3.4e-148, 5.7e-208"			
25155	ENU08950	ANI61C3444: 1126..196			GTBX	AFUc04760				3.1E-33			
25156	ENU08951	ANI61C4177: 622..1022			GTBX	AFUc06724				4.5E-52			
25157	ENU08952	ANI61C2723: 2..913			GTBX	AFUc15132				8.6E-70			
25158	ENU08953	ANI61C2724: 875..213			GTBX	AFUc15688				7.1E-95			
25159	ENU08954	ANI61C2726: 574..30			GTBX	CALc05920				1.4E-46			

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25160	ENU08955	ANI61C4187: 379..1145			GTBX	AFUc14608				1.2E-83			
25161	ENU08956	ANI61C3458: 1001..567			GTBX	AFUc10128				4.9E-42			
25162	ENU08957	ANI61C3459: 669..199			GTBX	AFUc12576				4.2E-60			
25163	ENU08958	ANI61S1831: 532..19			GTBX	FGRc00578				1.1E-29			
25164	ENU08959	ANI61S1834: 390..665			GTBX	AFUc11038				1.9E-63			
25165	ENU08960	ANI61S2569: 41..484			GTBX	FGRc24279				2.8E-35			
25166	ENU08961	ANI61C3460: 1017..1299			GTBX	AFUc13761				2E-109			
25167	ENU08962	ANI61C3461: 849..64			GTBX	"AFUc00703, AFUc13932"				"1.6e-11, 2.8e-64"			
25168	ENU08963	ANI61C4191: 1298..198			GTBX	AFUc07701				6.1E-56			
25169	ENU08964	ANI61C4195: 1387..1874			GTBX	AFUc11252				5.6E-91			
25170	ENU08965	ANI61C2738: 853..278			GTBX	"FGRc06990, Z71257"				"6.1e-15, 1.5e-33"			
25171	ENU08966	ANI61C4198: 582..151			GTBX	AFUc01658				6.5E-35			
25172	ENU08967	ANI61C1080 6:191..656			GTBX	"AFUc07431, AFUc13621"				"9.6e-15, 1.4e-57"			
25173	ENU08968	ANI61C1080 7:5457..6306			GTBX	"AFUc01138, CALc03518"				"3.6e-08, 3.8e-33"			

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25174	ENU08969	ANI61C3470: 1388..1606			GTBX	AFUc07764				9.6E-105			
25175	ENU08970	ANI61C3473: 772..392			GTBX	AFUc18497				6.7E-24			
25176	ENU08971	ANI61C3475: 3209..3995			GTBX	AFUc05872				9.5E-50			
25177	ENU08972	ANI61C2747: 43..471			GTBX	AFUc14390				2.1E-34			
25178	ENU08973	ANI61C1081 2:1544..3776			GTBX	"AFUc13531, AFUc14233, AFUc14327, AFUc14338"				"3.9e-29, 2.4e-31, 9.0e-57, 3.8e-50"			
25179	ENU08974	ANI61C1081 4:545..141			GTBX	"AFUc09407, FGRc11267"				"3.5e-23, 4.1e-07"			
25180	ENU08975	ANI61S1855: 51..573			GTBX	AFUc14395				7.2E-32			
25181	ENU08976	ANI61C2753: 713..1036			GTBX	AFUc12177				4.6E-28			
25182	ENU08977	ANI61C3482: 1159..1505			GTBX	"AFUc08947, Y13137"				"3.6e-76, 2.1e-44"			
25183	ENU08978	ANI61C2754: 1..520			GTBX	AFUc11200				1.1E-29			
25184	ENU08979	ANI61C3487: 334..1136			GTBX	AFUc21091				1.2E-22			
25185	ENU08980	ANI61C2758: 96..608			GTBX	FGRc12220				7.4E-48			
25186	ENU08981	ANI61C2763: 1297..582			GTBX	"AFUc13692, AFUc13754"				"5.8e-77, 4.6e-43"			
25187	ENU08982	ANI61C3497: 38..559			GTBX	FGRc10471				6.1E-74			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25188	ENU08983	ANI61C1083 6:2079..834			GTBX	"AFUc14311, AFUc22325"				"1.8e-106, 1.3e-30"			
25189	ENU08984	ANI61C2777: 249..27			GTBX	AFUc09165				8.8E-23			
25190	ENU08985	ANI61C1084 2:263..21			GTBX	AFUc15294				1.5E-26			
25191	ENU08986	ANI61C1084 6:2234..3543			GTBX	"AFUc14245, CALc05322, Y13140"				"9.0e-161, 5.3e-60, 5.3e-108"			
25192	ENU08987	ANI61C1084 8:416..3			GTBX	"AFUc21087, CALc06090"				"8.3e-21, 1.3e-24"			
25193	ENU08988	ANI61C1084 9:3548..4105			GTBX	AFUc10042				4.5E-54			
25194	ENU08989	ANI61C2783: 1271..2181			GTBX	AFUc08854				1.3E-97			
25195	ENU08990	ANI61C2791: 906..498			GTBX	AFUc14237				2.6E-38			
25196	ENU08991	ANI61C2792: 876..36			GTBX	AFUc16118				1.2E-34			
25197	ENU08992	ANI61C2794: 1584..1084			GTBX	AFUc13519				5.2E-35			
25198	ENU08993	ANI61C2799: 1320..1669			GTBX	AFUc14105				2.7E-43			
25199	ENU08994	ANI61C1086 2:1103..489			GTBX	AFUc13456				5.7E-82			
25200	ENU08995	ANI61C1086 9:1089..200			GTBX	"AFUc12779, AFUc12779"				"1.0e-29, 1.0e-37"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25201	ENU08996	ANI61C1087 2:2004..2818			GTBX	"CALc05217, Y13138"				"1.9e-159, 5.5e-211"			
25202	ENU08997	ANI61C1087 3:1155..2865			GTBX	"CALc03654, X59720"				"1.5e-46, 2.0e-50"			
25203	ENU08998	ANI61C1087 4:3565..4204			GTBX	AFUc15811				1.1E-83			
25204	ENU08999	ANI61C1087 5:82..2501			GTBX	"AFUc04817, AFUc21485, FGRc09205"				"1.9e-69, 7.3e-13, 3.3e-22"			
25205	ENU09000	ANI61C9200: 1423..2081			GTBX	AFUc15632				1.4E-33			
25206	ENU09001	ANI61C9201: 617..383			GTBX	AFUc08928				7.5E-42			
25207	ENU09002	ANI61C9203: 4520..63			GTBX	"AFUc09601, AFUc13531, AFUc15132, AFUc19875"				"1.1e-32, 4.6e-40, 5.1e-48, 1.4e-22"			
25208	ENU09003	ANI61C9206: 770..81			GTBX	AFUc08110				1E-27			
25209	ENU09004	ANI61C9207: 3570..1397			GTBX	"AFUc15140, AFUc15140, AFUc19221"				"1.7e-141, 2.8e-29, 4.6e-48"			
25210	ENU09005	ANI61C914:4 504..3529			GTBX	"AFUc09101, CALc01241, FGRc07803"				"9.2e-51, 2.8e-29, 2.3e-25"			
25211	ENU09006	ANI61C918:1 53..1052			GTBX	AFUc11011				6.2E-58			
25212	ENU09007	ANI61C9211: 2395..3456			GTBX	"AFUc14615, AFUc22530"				"3.1e-51, 9.2e-42"			
25213	ENU09008	ANI61C9215: 1494..1788			GTBX	AFUc00720				9.1E-26			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25214	ENU09009	ANI61C9216:2755..1219			GTBX	"AFUc14313, AFUc14313"				"1.1e-160, 1.6e-157"			
25215	ENU09010	ANI61C923:685..239			GTBX	FGRc06929				5.2E-27			
25216	ENU09011	ANI61C10892:2598..1435			GTBX	"AFUc03032, AFUc05892, Y13140"				"4.4e-43, 5.3e-16, 5.4e-18"			
25217	ENU09012	ANI61C9227:49..1215			GTBX	"AFUc09616, FGRc06065"				"3.1e-106, 5.0e-45"			
25218	ENU09013	ANI61C9229:44..629			GTBX	AFUc20770				1.3E-32			
25219	ENU09014	ANI61C931:4332..1795			GTBX	"AFUc06172, AFUc06611"				"6.7e-29, 3.0e-41"			
25220	ENU09015	ANI61C8503:4176..4553			GTBX	FGRc01667				2.7E-21			
25221	ENU09016	ANI61C8508:1008..2044			GTBX	"AFUc11315, CALc04402"				"7.7e-85, 4.4e-53"			
25222	ENU09017	ANI61C9237:282..2495			GTBX	Y13134				8.0e-80			
25223	ENU09018	ANI61C948:106..598			GTBX	AFUc19097				3.3E-34			
25224	ENU09019	ANI61C9240:1748..61			GTBX	"AFUc15932, AFUc15932"				"2.9e-38, 3.7e-47"			
25225	ENU09020	ANI61C8511:892..413			GTBX	AFUc13528				8E-52			
25226	ENU09021	ANI61C8517:556..35			GTBX	FGRc00709				6.1E-30			
25227	ENU09022	ANI61C9247:2593..1793			GTBX	AFUc01187				2.4E-29			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25228	ENU09023	ANI61C8519:1036..209			GTBX	AFUc11611				6E-54			
25229	ENU09024	ANI61C953:912..1			GTBX	AFUc13929				4.2E-68			
25230	ENU09025	ANI61C957:22..627			GTBX	AFUc14610				1.8E-80			
25231	ENU09026	ANI61C8522:2171..1635			GTBX	AFUc02919				2.5E-49			
25232	ENU09027	ANI61C9253:2222..3333			GTBX	"AFUc05780, FGRC20446"				"1.4e-15, 3.6e-23"			
25233	ENU09028	ANI61C8526:841..65			GTBX	"AFUc09020, Y13136"				"2.0e-41, 7.5e-31"			
25234	ENU09029	ANI61C8526:4617..5334			GTBX	"AFUc21180, CALc04630"				"4.4e-40, 8.5e-22"			
25235	ENU09030	ANI61C9257:1241..480			GTBX	CALc05995				1.4E-53			
25236	ENU09031	ANI61C8531:3577..3233			GTBX	AFUc07659				2.6E-27			
25237	ENU09032	ANI61C8533:2549..1044			GTBX	AFUc06933				8.6E-41			
25238	ENU09033	ANI61C9265:8351..8701			GTBX	AFUc13733				2.4E-119			
25239	ENU09034	ANI61C7807:752..321			GTBX	AFUc15441				2.4E-34			
25240	ENU09035	ANI61C973:607..278			GTBX	FGRC18829				6.4E-22			
25241	ENU09036	ANI61C975:70..423			GTBX	AFUc04456				3.4E-33			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25242	ENU09037	ANI61C976:5 01..755			GTBX	"AFUc08733, AFUc10087"				"1.9e-31, 1.3e-67"			
25243	ENU09038	ANI61C978:7 61..18			GTBX	"AFUc02805, AFUc21089"				"3.5e-45, 8.0e-26"			
25244	ENU09039	ANI61C8542: 2..313			GTBX	AFUc16158				7.5E-31			
25245	ENU09040	ANI61C7814: 2279..2073			GTBX	U00092				2.9e-11			
25246	ENU09041	ANI61C8544: 6230..7238			GTBX	"AFUc02018, AFUc15483, AFUc15778"				"7.4e-51, 9.7e-18, 3.9e-26"			
25247	ENU09042	ANI61C7817: 2093..38			GTBX	"AFUc12368, AFUc15695, AFUc15695"				"2.6e-82, 1.1e-30, 3.1e-12"			
25248	ENU09043	ANI61C8547: 2244..2879			GTBX	"AFUc03289, AFUc12872"				"1.2e-08, 1.9e-31"			
25249	ENU09044	ANI61C7825: 1907..493			GTBX	"AFUc07632, AFUc16753, CALc05461"				"2.4e-80, 3.7e-25, 5.1e-25"			
25250	ENU09045	ANI61C7827: 166..912			GTBX	AFUc15752				3.3E-134			
25251	ENU09046	ANI61C992:2 850..3833			GTBX	"AFUc08206, AFUc13826"				"2.1e-21, 4.5e-77"			
25252	ENU09047	ANI61C8562: 871..199			GTBX	AFUc13633				5E-74			
25253	ENU09048	ANI61C8565: 637..1002			GTBX	FGRc02523				4.8E-30			
25254	ENU09049	ANI61C9295: 1450..440			GTBX	"AFUc08217, FGRc09703"				"1.7e-83, 6.6e-23"			
25255	ENU09050	ANI61C8566: 770..39			GTBX	"AFUc15765, CALc05653"				"8.4e-56, 4.2e-83"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25256	ENU09051	ANI61C8568: 1119..68			GTBX	AFUc03216				4.1E-61			
25257	ENU09052	ANI61C9298: 815..18			GTBX	"AFUc14355, AFUc22510"				"5.1e-25, 5.2e-74"			
25258	ENU09053	ANI61C9299: 657..1844			GTBX	"AFUc00708, AFUc09276"				"3.5e-38, 3.5e-49"			
25259	ENU09054	ANI61C7844: 946..392			GTBX	AFUc15765				3.5E-112			
25260	ENU09055	ANI61C8574: 1601..2681			GTBX	"AFUc06883, FGRc14811"				"3.7e-79, 6.3e-13"			
25261	ENU09056	ANI61C7847: 931..2031			GTBX	"AFUc10607, U00094"				"1.6e-61, 1.1e-32"			
25262	ENU09057	ANI61C7849: 4332..4955			GTBX	"AFUc03724, FGRc24839"				"5.3e-29, 1.9e-21"			
25263	ENU09058	ANI61C8580: 10232..10627			GTBX	AFUc06423				8.9E-30			
25264	ENU09059	ANI61C8584: 101..535			GTBX	Y13140				2.3e-12			
25265	ENU09060	ANI61C7855: 2920..4065			GTBX	AFUc12170				1.4E-123			
25266	ENU09061	ANI61C7855: 6507..4837			GTBX	AFUc19366				5.1E-49			
25267	ENU09062	ANI61C7857: 488..1039			GTBX	AFUc02328				5.9E-22			
25268	ENU09063	ANI61C7864: 3045..3936			GTBX	"AFUc03531, AFUc12810"				"3.9e-21, 3.2e-20"			
25269	ENU09064	ANI61C8596: 2092..2			GTBX	"AFUc03147, CALc06221, Z71257"				"1.4e-13, 8.8e-21, 2.0e-143"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25270	ENU09065	ANI61S4000: 472..6			GTBX	"AFUc15463, Y13135"				"4.6e-32, 9.3e-25"			
25271	ENU09066	ANI61C7872: 891..147			GTBX	AFUc15367				1.3E-32			
25272	ENU09067	ANI61C7875: 4433..500			GTBX	"AFUc05240, AFUc12411, FGRc05490, FGRc06942, FGRc06942, FGRc21802"				"1.8e-11, 8.3e-53, 1.1e-98, 1.5e-15, 2.0e-14, 1.8e-39"			
25273	ENU09068	ANI61C7878: 277..566			GTBX	FGRc14988				1.5E-32			
25274	ENU09069	ANI61C7879: 719..118			GTBX	FGRc09098				1.6E-29			
25275	ENU09070	ANI61C7886: 5..805			GTBX	"AFUc04118, AFUc11270"				"1.6e-44, 2.6e-34"			
25276	ENU09071	ANI61C7892: 1342..1082			GTBX	AFUc02446				1.9E-36			
25277	ENU09072	ANI61C7896: 2170..2465			GTBX	CALc05565				2E-23			
25278	ENU09073	ANI61C7899: 5873..5220			GTBX	CALc02982				1.2E-79			
25279	ENU09074	ANI61C4200: 725..149			GTBX	FGRc08664				5.3E-52			
25280	ENU09075	ANI61C4203: 1767..622			GTBX	"AFUc01235, AFUc07012"				"1.0e-61, 9.5e-19"			
25281	ENU09076	ANI61C4208: 344..15			GTBX	AFUc14843				1.1E-38			
25282	ENU09077	ANI61C4212: 601..8			GTBX	FGRc13621				2.6E-48			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25283	ENU09078	ANI61C4212:1134..2468			GTBX	Y13134				2.1e-68			
25284	ENU09079	ANI61C4216:4911..5121			GTBX	AFUc03988				2.2E-35			
25285	ENU09080	ANI61C4219:2071..864			GTBX	AFUc13992				2.4E-190			
25286	ENU09081	ANI61C4223:1637..692			GTBX	AFUc14306				1.8E-91			
25287	ENU09082	ANI61C4224:191..1741			GTBX	"CALc03890, Y13135"				"4.2e-60, 1.9e-76"			
25288	ENU09083	ANI61C4233:3113..4950			GTBX	"AFUc01615, AFUc12868, AFUc20678, AFUc22517"				"1.0e-31, 2.9e-24, 4.2e-56, 2.5e-13"			
25289	ENU09084	ANI61C4234:1331..1654			GTBX	AFUc03297				2.1E-31			
25290	ENU09085	ANI61C3508:817..356			GTBX	FGRc06621				2.9E-35			
25291	ENU09086	ANI61C3509:1575..16			GTBX	CALc04641				4.5E-178			
25292	ENU09087	ANI61S2616:50..511			GTBX	AFUc06531				6.2E-27			
25293	ENU09088	ANI61C3511:798..19			GTBX	"AFUc06952, AFUc11209, AFUc13557"				"3.5e-13, 2.2e-18, 8.2e-54"			
25294	ENU09089	ANI61S878:19..522			GTBX	FGRc06247				2.1E-46			
25295	ENU09090	ANI61C4254:841..526			GTBX	AFUc14249				2.6E-57			
25296	ENU09091	ANI61C3528:308..516			GTBX	CALc04521				9.2E-30			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25297	ENU09092	ANI61C4258: 2516..1242			GTBX	"AFUc12040, CALc05713"				"2.7e-192, 7.8e-37"			
25298	ENU09093	ANI61C4260: 1739..6			GTBX	"AFUc03360, FGRc19992"				"6.2e-57, 1.2e-13"			
25299	ENU09094	ANI61C2802: 1479..234			GTBX	U00094				4.1e-78			
25300	ENU09095	ANI61C3532: 49..627			GTBX	AFUc05925				8.1E-31			
25301	ENU09096	ANI61C2803: 568..68			GTBX	FGRc09627				1E-65			
25302	ENU09097	ANI61C3534: 2422..1935			GTBX	CALc03078				1.9E-32			
25303	ENU09098	ANI61C2806: 969..1276			GTBX	AFUc12155				5.3E-37			
25304	ENU09099	ANI61S898:1 63..579			GTBX	AFUc09587				2.8E-60			
25305	ENU09100	ANI61C3540: 514..302			GTBX	FGRc16169				3.5E-24			
25306	ENU09101	ANI61C4278: 2298..1835			GTBX	FGRc24333				3E-34			
25307	ENU09102	ANI61C4278: 2825..4111			GTBX	"AFUc06051, FGRc18955"				"2.3e-08, 8.1e-33"			
25308	ENU09103	ANI61C4280: 1451..765			GTBX	"AFUc13963, FGRc19878"				"6.5e-20, 1.4e-35"			
25309	ENU09104	ANI61C2825: 1042..103			GTBX	AFUc09268				1.8E-72			
25310	ENU09105	ANI61C4283: 2142..2672			GTBX	AFUc12329				4.3E-48			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25311	ENU09106	ANI61C4285: 2704..4107			GTBX	AFUc07246				3.2E-153			
25312	ENU09107	ANI61C3557: 107..924			GTBX	AFUc13932				2.7E-33			
25313	ENU09108	ANI61C3558: 1507..913			GTBX	"FGRc09765, Y13135"				"7.1e-33, 3.2e-53"			
25314	ENU09109	ANI61C2834: 1324..253			GTBX	"AFUc14023, AFUc18413, FGRc11244"				"2.3e-36, 1.6e-52, 8.8e-07"			
25315	ENU09110	ANI61C3565: 80..1109			GTBX	"AFUc12638, AFUc14019"				"3.6e-94, 1.7e-19"			
25316	ENU09111	ANI61C2836: 842..1150			GTBX	AFUc09693				3.9E-47			
25317	ENU09112	ANI61C4295: 526..2590			GTBX	"AFUc14660, AFUc15941, AFUc15941"				"2.9e-12, 4.1e-55, 6.5e-45"			
25318	ENU09113	ANI61C3569: 22..474			GTBX	AFUc01238				1.1E-22			
25319	ENU09114	ANI61C1090 0:246..490			GTBX	FGRc11747				9.5E-32			
25320	ENU09115	ANI61C1090 1:24..497			GTBX	AFUc13935				3.6E-65			
25321	ENU09116	ANI61C3570: 607..1650			GTBX	"CALc05316, U00094"				"2.9e-10, 1.1e-41"			
25322	ENU09117	ANI61C3578: 68..364			GTBX	AFUc04929				9.7E-23			
25323	ENU09118	ANI61C1091 2:864..129			GTBX	AFUc15752				1.8E-26			
25324	ENU09119	ANI61C1091 6:1704..605			GTBX	AFUc14099				1.1E-29			

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25325	ENU09120	ANI61C2852:1722..1			GTBX	"AFUc10454, AFUc14364, CALc03886"				"3.9e-33, 3.7e-94, 6.7e-58"			
25326	ENU09121	ANI61C3582:1760..305			GTBX	AFUc09771				6.3E-23			
25327	ENU09122	ANI61C2856:623..366			GTBX	CALc06129				1.1E-37			
25328	ENU09123	ANI61C3587:576..272			GTBX	AFUc17615				1.5E-30			
25329	ENU09124	ANI61C10927:603..24			GTBX	AFUc14337				8.9E-30			
25330	ENU09125	ANI61S2694:358..12			GTBX	FGRc08083				1.3E-39			
25331	ENU09126	ANI61C2860:743..120			GTBX	FGRc01600				7.9E-57			
25332	ENU09127	ANI61C3590:2212..1250			GTBX	AFUc01539				5.3E-59			
25333	ENU09128	ANI61C2864:234..450			GTBX	FGRc05834				1.2E-23			
25334	ENU09129	ANI61C2866:400..2			GTBX	AFUc06319				6.3E-54			
25335	ENU09130	ANI61C3596:508..8			GTBX	AFUc09790				4.4E-62			
25336	ENU09131	ANI61C10931:1458..1075			GTBX	AFUc09609				1.7E-30			
25337	ENU09132	ANI61C10932:2674..1592			GTBX	"AFUc16521, AFUc16612"				"1.2e-23, 2.8e-09"			
25338	ENU09133	ANI61C10934:2128..413			GTBX	"AFUc16639, FGRc02861, FGRc09286, FGRc11948"				"1.1e-81, 1.6e-60, 1.3e-56, 6.3e-08"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25339	ENU09134	ANI61C1093 7:1836..2395			GTBX	AFUc04964				1.3E-86			
25340	ENU09135	ANI61C1094 6:1623..629			GTBX	"AFUc07110, AFUc18195"				"6.0e-77, 1.6e-11"			
25341	ENU09136	ANI61C2889; 806..204			GTBX	AFUc12218				5.6E-93			
25342	ENU09137	ANI61C1095 4:2579..3314			GTBX	Y13139				1.7e-39			
25343	ENU09138	ANI61C1095 5:532..42			GTBX	AFUc18408				3.1E-33			
25344	ENU09139	ANI61C1095 5:777..2889			GTBX	AFUc13607				5.8E-159			
25345	ENU09140	ANI61C2891: 102..356			GTBX	AFUc07028				4.3E-80			
25346	ENU09141	ANI61C1096 4:14..1231			GTBX	"AFUc11060, AFUc15343"				"3.8e-59, 5.7e-32"			
25347	ENU09142	ANI61C1097 0:2035..312			GTBX	"AFUc12156, AFUc15465, AFUc15465, FGRc00470"				"4.9e-55, 1.5e-10, 2.5e-45, 5.6e-11" 4.3E-55			
25348	ENU09143	ANI61C1097 4:2482..3605			GTBX	AFUc13816				1.6E-108			
25349	ENU09144	ANI61C1097 4:9381..10970			GTBX	CALc05781				6.4E-29			
25350	ENU09145	ANI61C1097 5:827..1721			GTBX	AFUc16580				6.3E-41			
25351	ENU09146	ANI61C1097 5:7763..8178			GTBX	FGRc01084				8E-37			
25352	ENU09147	ANI61C1097 8:1139..422			GTBX	AFUc10468							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25353	ENU09148	ANI61C9302:1377..310			GTBX	"AFUc10685, AFUc15487"				"1.6e-66, 2.6e-15"			
25354	ENU09149	ANI61C9308:3085..3645			GTBX	"AFUc01566, AFUc02071"				"7.9e-38, 2.7e-18"			
25355	ENU09150	ANI61C1098:0:35..700			GTBX	AFUc04598				2.2E-28			
25356	ENU09151	ANI61C1098:1:7354..7898			GTBX	AFUc08664				2.4E-33			
25357	ENU09152	ANI61C1098:9:720..515			GTBX	AFUc12150				4.4E-39			
25358	ENU09153	ANI61C9317:662..250			GTBX	AFUc13330				1.5E-33			
25359	ENU09154	ANI61C9317:1109..2233			GTBX	"AFUc00802, AFUc20080, CALc06223"				"3.7e-48, 4.2e-14, 4.0e-19"			
25360	ENU09155	ANI61C9318:4746..5269			GTBX	"AFUc07003, AFUc07003, AFUc10141"				"6.6e-111, 7.7e-89, 6.1e-135"			
25361	ENU09156	ANI61C1099:1:621..883			GTBX	U00094				2.1e-49			
25362	ENU09157	ANI61C1099:7:8203..9278			GTBX	"AFUc12472, AFUc14082"				"2.4e-45, 3.0e-56"			
25363	ENU09158	ANI61C1099:9:4895..5915			GTBX	FGRe21400				1.6E-28			
25364	ENU09159	ANI61C9322:484..1044			GTBX	AFUc15756				6.7E-26			
25365	ENU09160	ANI61C9325:1369..280			GTBX	"AFUc11534, AFUc18844, CALc03970"				"8.0e-103, 1.6e-37, 5.1e-62"			

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25366	ENU09161	ANI61C8601: 282..17			GTBX	AFUc08235				4.1E-30			
25367	ENU09162	ANI61C9331: 1071..388			GTBX	AFUc13604				2.3E-35			
25368	ENU09163	ANI61C9332: 444..5			GTBX	"AFUc10065, FGRc19031"				"1.5e-30, 2.9e-12"			
25369	ENU09164	ANI61C8605: 420..208			GTBX	AFUc06416				5.3E-44			
25370	ENU09165	ANI61C9338: 2923..37			GTBX	"AFUc09246, AFUc11804, CALc06165, FGRc18522"				"3.8e-35, 2.2e-225, 2.0e-183, 6.1e-37"			
25371	ENU09166	ANI61C8612: 16..372			GTBX	AFUc09632				1.1E-45			
25372	ENU09167	ANI61C8612: 2351..879			GTBX	"AFUc06058, AFUc09335"				"7.6e-07, 3.0e-80"			
25373	ENU09168	ANI61C9342: 2713..2181			GTBX	AFUc08063				5.5E-104			
25374	ENU09169	ANI61C8614: 2981..15			GTBX	"AFUc15297, FGRc05338, FGRc25875"				"3.0e-73, 7.9e-24, 7.7e-11"			
25375	ENU09170	ANI61C9344: 4379..4882			GTBX	AFUc11946				4.1E-23			
25376	ENU09171	ANI61C8619: 3798..2506			GTBX	AFUc12001				8.5E-46			
25377	ENU09172	ANI61C8620: 1357..303			GTBX	"AFUc12034, CALc05986"				"2.6e-24, 3.2e-86"			
25378	ENU09173	ANI61C8620: 5794..6098			GTBX	AFUc14066				1.3E-110			

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25379	ENU09174	ANI61C9355: 1253..680			GTBX	AFUc15687				9.2E-108			
25380	ENU09175	ANI61C8628: 36..656			GTBX	AFUc06137				2.8E-77			
25381	ENU09176	ANI61C9357: 137..1530			GTBX	AFUc09529				2.2E-49			
25382	ENU09177	ANI61C7900: 2532..4277			GTBX	"AFUc08848, AFUc09907, AFUc20452"				"7.5e-39, 2.4e-73, 1.6e-11"			
25383	ENU09178	ANI61C8631: 1103..2171			GTBX	AFUc19468				7.7E-45			
25384	ENU09179	ANI61C8631: 4111..2590			GTBX	"AFUc08405, AFUc16754, FGRc14352, Z71257"				"1.2e-107, 1.3e-33, 1.3e-37, 2.5e-81"			
25385	ENU09180	ANI61C9363: 2758..3087			GTBX	AFUc22414				IE-31			
25386	ENU09181	ANI61C8636: 895..300			GTBX	"AFUc01391, FGRc18380"				"3.0e-11, 2.2e-37"			
25387	ENU09182	ANI61C8638: 1064..405			GTBX	AFUc10092				1.3E-25			
25388	ENU09183	ANI61C9371: 1504..552			GTBX	AFUc12786				5.8E-50			
25389	ENU09184	ANI61C8645: 1124..1467			GTBX	AFUc11981				4.8E-31			
25390	ENU09185	ANI61C7918: 301..11			GTBX	AFUc01678				1.6E-27			
25391	ENU09186	ANI61C7918: 1104..1421			GTBX	AFUc14675				1.4E-28			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25392	ENU09187	ANI61C9377: 493..810			GTBX	"AFUc12614, FGRc18368"				"1.5e-113, 2.6e-07"			
25393	ENU09188	ANI61C9378: 906..1421			GTBX	AFUc11838				1.5E-77			
25394	ENU09189	ANI61C8650: 3512..3901			GTBX	AFUc12134				2.5E-43			
25395	ENU09190	ANI61C7924: 412..8			GTBX	AFUc15732				2.7E-26			
25396	ENU09191	ANI61C8653: 1726..828			GTBX	AFUc13073				1.2E-130			
25397	ENU09192	ANI61C9383: 6530..7124			GTBX	AFUc17773				5.3E-67			
25398	ENU09193	ANI61C8656: 3851..3351			GTBX	AFUc05544				8.9E-73			
25399	ENU09194	ANI61C8657: 133..693			GTBX	AFUc08713				1.9E-58			
25400	ENU09195	ANI61C8659: 2496..3023			GTBX	"AFUc03782, FGRc10049"				"1.0e-18, 4.9e-38"			
25401	ENU09196	ANI61C7930: 659..1267			GTBX	"AFUc05717, AFUc21348"				"6.6e-43, 1.6e-09"			
25402	ENU09197	ANI61C8661: 3313..3669			GTBX	FGRc07994				1.6E-28			
25403	ENU09198	ANI61C8667: 78..575			GTBX	AFUc05732				5.1E-32			
25404	ENU09199	ANI61C9398: 391..77			GTBX	AFUc20294				1.1E-23			
25405	ENU09200	ANI61C7941: 923..25			GTBX	CALc05278				1.2E-32			

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25406	ENU09201	ANI61C8670: 1370..185			GTBX	"FGRc08201, Y13135"				"1.0e-15, 4.4e-33"			
25407	ENU09202	ANI61C8675: 1001..198			GTBX	"AFUc00793, FGRc05104, FGRc16937"				"1.1e-42, 2.9e-13, 1.3e-27"			
25408	ENU09203	ANI61C7953: 1094..460			GTBX	"AFUc10606, AFUc21738"				"8.2e-37, 7.6e-63"			
25409	ENU09204	ANI61C8684: 649..89			GTBX	AFUc05878				5.6E-37			
25410	ENU09205	ANI61C8686: 4315..5067			GTBX	AFUc14227				1.5E-32			
25411	ENU09206	ANI61C8687: 2002..1217			GTBX	"AFUc18036, FGRc00673"				"5.6e-34, 1.9e-46"			
25412	ENU09207	ANI61C8694: 1591..479			GTBX	"AFUc08873, FGRc22249"				"6.3e-98, 1.0e-48"			
25413	ENU09208	ANI61C7976: 322..71			GTBX	AFUc18580				1.7E-30			
25414	ENU09209	ANI61C5001: 1403..1140			GTBX	"AFUc02640, Y13134"				"1.7e-30, 5.7e-119"			
25415	ENU09210	ANI61C5009: 24..377			GTBX	FGRc17279				4.8E-39			
25416	ENU09211	ANI61C7980: 53..1288			GTBX	AFUc11561				4.4E-51			
25417	ENU09212	ANI61C5019: 76..693			GTBX	AFUc08840				9.1E-56			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25418	ENU09213	ANI61C7995:1601..6527			GTBX	"AFUc01564, AFUc05116, AFUc09051, AFUc11907, AFUc11907"				"1.9e-44, 1.1e-118, 1.5e-129, 2.7e-65, 7.2e-77"			
25419	ENU09214	ANI61C4300:1696..1159			GTBX	"AFUc08580, CALc03532"				"5.0e-68, 1.7e-70"			
25420	ENU09215	ANI61C4303:8..436			GTBX	AFUc03796				9.3E-47			
25421	ENU09216	ANI61C5033:40..1000			GTBX	AFUc06232				3.8E-70			
25422	ENU09217	ANI61C5036:600..238			GTBX	"AFUc14677, AFUc15942"				"3.5e-27, 5.0e-08"			
25423	ENU09218	ANI61C4307:1506..298			GTBX	"AFUc03507, AFUc09984, AFUc12002"				"1.9e-46, 2.0e-41, 3.3e-09"			
25424	ENU09219	ANI61C5037:994..581			GTBX	AFUc15029				6.6E-33			
25425	ENU09220	ANI61C4310:1263..517			GTBX	AFUc13413				4.4E-144			
25426	ENU09221	ANI61C4314:115..406			GTBX	AFUc14056				6.6E-29			
25427	ENU09222	ANI61C4317:1103..288			GTBX	AFUc13039				1.8E-48			
25428	ENU09223	ANI61C4320:616..2524			GTBX	AFUc12578				2.4E-249			
25429	ENU09224	ANI61S957:540..1			GTBX	AFUc13345				4.4E-34			
25430	ENU09225	ANI61C3603:5..547			GTBX	AFUc12517				2.2E-39			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25431	ENU09226	ANI61C4336: 728..1			GTBX	AFUc15803				1.4E-40			
25432	ENU09227	ANI61C4337: 952..483			GTBX	"AFUc13626, FGRc03674"				"3.8e-48, 1.2e-40"			
25433	ENU09228	ANI61C4338: 666..96			GTBX	"AFUc13451, AFUc13451"				"1.7e-54, 1.7e-61"			
25434	ENU09229	ANI61C4341: 829..287			GTBX	AFUc01317				3.4E-35			
25435	ENU09230	ANI61C4344: 3049..1141			GTBX	"AFUc12501, CALc06236"				"2.4e-17, 1.1e-94"			
25436	ENU09231	ANI61C3616: 1216..1622			GTBX	AFUc11581				3.2E-33			
25437	ENU09232	ANI61C3617: 1144..657			GTBX	AFUc07024				6.9E-65			
25438	ENU09233	ANI61C3619: 755..48			GTBX	"AFUc12259, Y13138"				"3.9e-58, 1.8e-10"			
25439	ENU09234	ANI61C3621: 68..522			GTBX	CALc03177				3.4E-44			
25440	ENU09235	ANI61C3624: 887..140			GTBX	FGRc06045				4.9E-24			
25441	ENU09236	ANI61C3626: 905..3359			GTBX	"AFUc13163, AFUc13851"				"6.4e-96, 5.4e-119"			
25442	ENU09237	ANI61C5085: 1915..5			GTBX	"AFUc11103, D50617"				"2.3e-108, 1.2e-157"			
25443	ENU09238	ANI61C3627: 7636..8229			GTBX	"AFUc03814, AFUc21290"				"2.0e-37, 1.8e-12"			
25444	ENU09239	ANI61C4357: 3358..4103			GTBX	"AFUc13706, AFUc22334, FGRc07656"				"5.6e-33, 4.7e-38, 2.4e-29"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
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25446	ENU09241	ANI61C4359: 163..1020			GTBX	AFUc08911				1.4E-42			
25447	ENU09242	ANI61C5089: 65..538			GTBX	AFUc00666				1.8E-48			
25448	ENU09243	ANI61S4199: 93..693			GTBX	AFUc15350				8E-41			
25449	ENU09244	ANI61C3636: 6447..7685			GTBX	AFUc20583				1.6E-24			
25450	ENU09245	ANI61C4365: 67..429			GTBX	AFUc10569				2.5E-29			
25451	ENU09246	ANI61C4368: 2709..1873			GTBX	AFUc11858				1.1E-108			
25452	ENU09247	ANI61C5097: 487..44			GTBX	AFUc05222				1.2E-24			
25453	ENU09248	ANI61S3472: 367..44			GTBX	"AFUc18364, CALc04995"				"7.5e-43, 3.5e-19"			
25454	ENU09249	ANI61C3640: 1580..893			GTBX	AFUc15969				3.1E-153			
25455	ENU09250	ANI61C4370: 216..1478			GTBX	"AFUc13516, AFUc14043, AFUc15051, FGRc01953"				"3.6e-42, 8.1e-24, 5.2e-105, 8.5e-21"			
25456	ENU09251	ANI61C2912: 629..16			GTBX	AFUc10688				9E-43			
25457	ENU09252	ANI61C4373: 445..695			GTBX	AFUc09914				9.6E-53			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25458	ENU09253	ANI61C3645: 5320..6232			GTBX	FGRc09513				1.3E-21			
25459	ENU09254	ANI61C4378: 239..1305			GTBX	"AFUc02594, AFUc07825"				"2.6e-23, 4.9e-61"			
25460	ENU09255	ANI61S3489: 113..452			GTBX	CALc04906				9.1E-48			
25461	ENU09256	ANI61C2920: 965..1437			GTBX	Y13140				2.1e-24			
25462	ENU09257	ANI61C3650: 1816..3768			GTBX	AFUc15925				1.7E-151			
25463	ENU09258	ANI61C4382: 39..667			GTBX	AFUc06115				3.9E-28			
25464	ENU09259	ANI61C3655: 5..607			GTBX	"AFUc04082, FGRc03487"				"1.1e-16, 2.7e-26"			
25465	ENU09260	ANI61C2927: 556..311			GTBX	AFUc10442				7.5E-25			
25466	ENU09261	ANI61C2932: 377..873			GTBX	CALc04475				4.6E-79			
25467	ENU09262	ANI61C3661: 613..2			GTBX	"AFUc01462, AFUc19592"				"1.1e-31, 2.0e-18"			
25468	ENU09263	ANI61C4391: 2513..355			GTBX	"AFUc13024, AFUc15301"				"2.3e-68, 7.6e-132"			
25469	ENU09264	ANI61C4391: 5770..4632			GTBX	"AFUc08279, Y13139"				"1.2e-32, 5.3e-65"			
25470	ENU09265	ANI61C2934: 335..1188			GTBX	"AFUc11881, AFUc11881"				"1.7e-77, 2.7e-77"			
25471	ENU09266	ANI61C4392: 918..57			GTBX	AFUc07215				1.1E-54			

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25472	ENU09267	ANI61C4393: 4..780			GTBX	"AFUc13630, Y13134"				"4.6e-34, 2.5e-61"			
25473	ENU09268	ANI61C3665: 744..13			GTBX	"AFUc12550, CALc05628, FGRc10684"				"8.4e-45, 2.3e-41, 1.2e-68"			
25474	ENU09269	ANI61C2936: 3..788			GTBX	"AFUc11814, FGRc11194"				"6.4e-45, 1.3e-77"			
25475	ENU09270	ANI61C3669: 674..4			GTBX	CALc05387				6.1E-60			
25476	ENU09271	ANI61C4398: 167..484			GTBX	AFUc05879				4.1E-42			
25477	ENU09272	ANI61C2942: 599..1304			GTBX	"AFUc06459, AFUc13777"				"3.1e-14, 1.9e-50"			
25478	ENU09273	ANI61C3681: 820..1754			GTBX	"AFUc14966, CALc04781"				"6.1e-140, 9.4e-56"			
25479	ENU09274	ANI61C3692: 649..71			GTBX	"AFUc02774, AFUc02886"				"1.3e-41, 1.0e-06"			
25480	ENU09275	ANI61C3696: 4..633			GTBX	AFUc12839				7.9E-64			
25481	ENU09276	ANI61C2969: 3638..2636			GTBX	"AFUc09259, AFUc09259"				"2.0e-40, 5.6e-58"			
25482	ENU09277	ANI61C2971: 73..501			GTBX	FGRc24981				1.9E-21			
25483	ENU09278	ANI61C2976: 1318..175			GTBX	AFUc04211				5.4E-93			
25484	ENU09279	ANI61C2999: 876..1			GTBX	Z71256				6.5e-84			
25485	ENU09280	ANI61C9402: 2171..856			GTBX	"FGRc03487, FGRc09159, FGRc09159, FGRc23883"				"1.3e-37, 4.4e-29, 8.6e-30, 5.8e-11"			

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25486	ENU09281	ANI61C9439: 80..469			GTBX	AFUc15622				8.9E-30			
25487	ENU09282	ANI61C9440: 779..462			GTBX	AFUc11219				3.3E-61			
25488	ENU09283	ANI61C9440: 3473..3216			GTBX	AFUc08291				8.7E-44			
25489	ENU09284	ANI61C9441: 564..293			GTBX	AFUc08255				8.9E-26			
25490	ENU09285	ANI61C8713: 857..341			GTBX	AFUc05686				3.6E-29			
25491	ENU09286	ANI61C8714: 1347..1968			GTBX	AFUc20415				2E-24			
25492	ENU09287	ANI61C9445: 256..1691			GTBX	AFUc07629				5.2E-69			
25493	ENU09288	ANI61C9446: 221..547			GTBX	AFUc12171				4.8E-35			
25494	ENU09289	ANI61C9451: 4905..5724			GTBX	"AFUc05775, CALc05482"				"7.3e-64, 9.1e-41"			
25495	ENU09290	ANI61C8722: 765..153			GTBX	AFUc03370				5.4E-35			
25496	ENU09291	ANI61C8722: 2606..3753			GTBX	"AFUc03885, AFUc11035"				"1.8e-30, 3.8e-53"			
25497	ENU09292	ANI61C9455: 480..79			GTBX	AFUc18390				2.9E-23			
25498	ENU09293	ANI61C9456: 1440..613			GTBX	AFUc12641				1.1E-86			
25499	ENU09294	ANI61C8727: 4183..3316			GTBX	AFUc09501				1.1E-72			

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25500	ENU09295	ANI61C9459: 759..1691			GTBX	"AFUc18002, AFUc20595"				"3.4e-58, 1.5e-39"		
25501	ENU09296	ANI61C8730: 4397..5083			GTBX	"AFUc07855, FGRc11749"				"1.1e-24, 1.7e-09"		
25502	ENU09297	ANI61C9461: 1997..2263			GTBX	AFUc03878				2.7E-36		
25503	ENU09298	ANI61C9464: 1019..1336			GTBX	AFUc10300				2.6E-29		
25504	ENU09299	ANI61C9465: 2884..3407			GTBX	"AFUc08665, AFUc08665"				"8.6e-122, 9.5e-97"		
25505	ENU09300	ANI61C8737: 1091..741			GTBX	AFUc12153				2.4E-35		
25506	ENU09301	ANI61C9469: 248..1142			GTBX	AFUc11644				8.5E-33		
25507	ENU09302	ANI61C8741: 856..1840			GTBX	AFUc13104				1.4E-61		
25508	ENU09303	ANI61C9470: 774..202			GTBX	AFUc15952				4.4E-72		
25509	ENU09304	ANI61C8743: 4032..4467			GTBX	AFUc15883				8.5E-24		
25510	ENU09305	ANI61C8745: 778..11			GTBX	AFUc07060				4E-35		
25511	ENU09306	ANI61C9477: 2962..3512			GTBX	AFUc09065				2E-58		
25512	ENU09307	ANI61C9479: 1230..7			GTBX	AFUc14503				1.5E-32		
25513	ENU09308	ANI61C8750: 1390..2176			GTBX	CALc06230				1.2E-262		

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25514	ENU09309	ANI61C8751: 2404..14			GTBX	"AFUc04130, AFUc16265"				"1.5e-29, 8.4e-27"			
25515	ENU09310	ANI61C8757: 1640..1332			GTBX	AFUc08891				7.1E-22			
25516	ENU09311	ANI61C8759: 3132..3793			GTBX	FGRc16689				7.5E-21			
25517	ENU09312	ANI61C9491: 2615..1865			GTBX	CALc06160				8E-24			
25518	ENU09313	ANI61C8765: 548..896			GTBX	AFUc09309				1.1E-36			
25519	ENU09314	ANI61C8767: 1869..1250			GTBX	AFUc14377				4.9E-28			
25520	ENU09315	ANI61C9497: 1070..1664			GTBX	"AFUc10902, AFUc10902"				"8.1e-43, 9.7e-22"			
25521	ENU09316	ANI61C8780: 1254..2080			GTBX	"AFUc15659, FGRc19707"				"1.3e-15, 1.2e-29"			
25522	ENU09317	ANI61C8781: 1983..1047			GTBX	"AFUc03553, AFUc07731"				"1.7e-119, 2.6e-30"			
25523	ENU09318	ANI61C8795: 1064..834			GTBX	FGRc02905				2.8E-39			
25524	ENU09319	ANI61C8797: 620..834			GTBX	AFUc13831				3.4E-59			
25525	ENU09320	ANI61C8797: 1467..2151			GTBX	"AFUc03642, AFUc13831"				"2.8e-13, 3.4e-59"			
25526	ENU09321	ANI61C5102: 300..535			GTBX	AFUc19728				2.1E-22			
25527	ENU09322	ANI61C5103: 402..1			GTBX	AFUc14207				9.4E-86			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25528	ENU09323	ANI61C5110: 1141..410			GTBX	"AFUc18303, CALc06183"				"1.2e-34, 1.4e-90"			
25529	ENU09324	ANI61C5111: 912..1773			GTBX	"AFUc05704, AFUc13358"				"1.1e-34, 1.1e-34"			
25530	ENU09325	ANI61C5115: 1345..1022			GTBX	AFUc19450				1.1E-44			
25531	ENU09326	ANI61C5119: 582..14			GTBX	AFUc07458				2.7E-28			
25532	ENU09327	ANI61C5124: 804..1031			GTBX	AFUc07545				5.5E-22			
25533	ENU09328	ANI61C4400: 2306..1797			GTBX	"FGRc08787, FGRc14740"				"7.0e-21, 4.4e-17"			
25534	ENU09329	ANI61C4401: 2345..1654			GTBX	"AFUc05876, FGRc05155"				"4.8e-30, 7.0e-10"			
25535	ENU09330	ANI61C4406: 538..251			GTBX	AFUc07366				1.4E-21			
25536	ENU09331	ANI61C4407: 4154..5342			GTBX	"AFUc01633, AFUc19340"				"6.1e-20, 1.6e-39"			
25537	ENU09332	ANI61C4408: 1390..3			GTBX	AFUc13334				8E-99			
25538	ENU09333	ANI61C5137: 1034..13			GTBX	U00091				3.4e-45			
25539	ENU09334	ANI61C4409: 579..2167			GTBX	"AFUc02131, CALc04637, FGRc10200"				"1.1e-80, 4.6e-17, 7.3e-65"			
25540	ENU09335	ANI61S4243: 78..437			GTBX	Y18138				2.5e-15			
25541	ENU09336	ANI61S3519: 56..256			GTBX	AFUc13413				4E-24			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25542	ENU09337	ANI61C5143: 665..148			GTBX	AFUc22527				2.5E-69			
25543	ENU09338	ANI61C4415: 697..308			GTBX	AFUc08588				8.1E-50			
25544	ENU09339	ANI61C4415: 1944..2984			GTBX	"AFUc14631, Z71256"				"5.7e-117, 4.2e-40"			
25545	ENU09340	ANI61C5153: 400..1153			GTBX	AFUc15665				9.9E-110			
25546	ENU09341	ANI61C4428: 2186..509			GTBX	"AFUc03693, AFUc15500"				"1.3e-09, 4.9e-36"			
25547	ENU09342	ANI61C4429: 456..989			GTBX	AFUc02454				1.9E-48			
25548	ENU09343	ANI61C4430: 590..6			GTBX	"AFUc05777, AFUc11518"				"3.2e-11, 3.9e-35"			
25549	ENU09344	ANI61C4431: 865..1682			GTBX	CALc05985				7.5E-34			
25550	ENU09345	ANI61C4431: 2288..1929			GTBX	AFUc19720				1.9E-32			
25551	ENU09346	ANI61C5161: 6479..8758			GTBX	"AFUc15497, FGRc01538"				"2.1e-195, 1.2e-29"			
25552	ENU09347	ANI61C4435: 44..619			GTBX	AFUc10109				2.3E-49			
25553	ENU09348	ANI61C4436: 562..5			GTBX	"AFUc20304, FGRc08260"				"2.3e-42, 1.2e-10"			
25554	ENU09349	ANI61C4439: 603..957			GTBX	"AFUc15143, AFUc22336"				"4.2e-45, 1.0e-09"			
25555	ENU09350	ANI61C3716: 495..52			GTBX	AFUc17201				8.4E-27			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25556	ENU09351	ANI61C5184: 1185..739			GTBX	FGRc06929				2.5E-27			
25557	ENU09352	ANI61C5184: 1958..2668			GTBX	"AFUc02805, AFUc21089"				"2.8e-37, 4.9e-21"			
25558	ENU09353	ANI61C5189: 1018..77			GTBX	AFUc11900				1.1E-105			
25559	ENU09354	ANI61C3732: 61..673			GTBX	AFUc01401				2.1E-67			
25560	ENU09355	ANI61C3733: 3210..1934			GTBX	"FGRc03487, FGRc09159"				"5.7e-40, 2.8e-32"			
25561	ENU09356	ANI61C5191: 8..424			GTBX	AFUc09001				5.6E-37			
25562	ENU09357	ANI61C3738: 6..715			GTBX	"AFUc03774, AFUc13364"				"8.2e-10, 1.8e-39"			
25563	ENU09358	ANI61C5199: 1578..1127			GTBX	AFUc14538				3.3E-24			
25564	ENU09359	ANI61S2843: 428..10			GTBX	"AFUc14444, FGRc10441"				"8.6e-31, 9.2e-07"			
25565	ENU09360	ANI61C3747: 51..467			GTBX	AFUc14515				1.4E-45			
25566	ENU09361	ANI61S3584: 97..486			GTBX	AFUc10638				2.5E-31			
25567	ENU09362	ANI61C3751: 892..219			GTBX	FGRc00730				4.1E-26			
25568	ENU09363	ANI61C3754: 4387..4890			GTBX	"AFUc02406, CALc04204"				"8.0e-11, 5.7e-83"			
25569	ENU09364	ANI61C4484: 195..646			GTBX	AFUc11050				2.8E-26			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25570	ENU09365	ANI61C4485: 470..1338			GTBX	AFUc11852				2.8E-121			
25571	ENU09366	ANI61C3758: 368..568			GTBX	FGRc26076				1E-32			
25572	ENU09367	ANI61S2863: 456..103			GTBX	AFUc00783				2E-55			
25573	ENU09368	ANI61C4495: 836..438			GTBX	AFUc01513				6.8E-93			
25574	ENU09369	ANI61C4496: 973..1308			GTBX	FGRc10958				4E-67			
25575	ENU09370	ANI61C4497: 1059..277			GTBX	AFUc15397				2.5E-74			
25576	ENU09371	ANI61C3777: 414..651			GTBX	"AFUc21795, FGRc13545"				"1.3e-28, 3.1e-25"			
25577	ENU09372	ANI61C3785: 1070..87			GTBX	"AFUc09448, FGRc15416"				"3.1e-107, 8.7e-28"			
25578	ENU09373	ANI61C3786: 347..670			GTBX	AFUc15598				4.3E-84			
25579	ENU09374	ANI61C9504: 1509..983			GTBX	AFUc15752				6E-62			
25580	ENU09375	ANI61C9505: 6..593			GTBX	FGRc08493				8.8E-24			
25581	ENU09376	ANI61C9508: 1395..319			GTBX	"AFUc02590, AFUc21220"				"1.3e-22, 3.5e-14"			
25582	ENU09377	ANI61C9521: 1526..810			GTBX	"AFUc02035, FGRc16341"				"5.7e-54, 1.2e-07"			
25583	ENU09378	ANI61C9523: 2194..13			GTBX	"AFUc08207, AFUc09870"				"1.8e-65, 7.3e-119"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25584	ENU09379	ANI61C9524: 491..986			GTBX	AFUc15203				2.5E-28			
25585	ENU09380	ANI61C9528: 1204..737			GTBX	AFUc05005				1.1E-24			
25586	ENU09381	ANI61C9529: 368..93			GTBX	AFUc05865				5.5E-26			
25587	ENU09382	ANI61C9531: 724..2			GTBX	AFUc08448				6.3E-38			
25588	ENU09383	ANI61C8803: 60..1376			GTBX	"AFUc06649, AFUc09276, AFUc09645, AFUc15313, FGRc11399"				"8.5e-10, 8.2e-10, 6.1e-38, 3.1e-53, 5.2e-08", 2.6E-64			
25589	ENU09384	ANI61C8808: 3412..4903			GTBX	FGRc04144							
25590	ENU09385	ANI61C8809: 304..1298			GTBX	"AFUc10278, FGRc24365"				"1.3e-76, 1.7e-38"			
25591	ENU09386	ANI61C9539: 1484..1182			GTBX	AFUc03644				3.4E-48			
25592	ENU09387	ANI61C8814: 3867..5544			GTBX	AFUc12826				4.6E-78			
25593	ENU09388	ANI61C9543: 28..687			GTBX	"AFUc05060, AFUc19153"				"5.8e-10, 7.8e-22"			
25594	ENU09389	ANI61C8815: 226..648			GTBX	AFUc22266				2.3E-27			
25595	ENU09390	ANI61C8818: 1872..1054			GTBX	AFUc13384				9.4E-45			
25596	ENU09391	ANI61C9547: 556..56			GTBX	AFUc09688				6.5E-47			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25597	ENU09392	ANI61C9548:1206..482			GTBX	AFUc02615				5E-21			
25598	ENU09393	ANI61C9549:160..864			GTBX	AFUc01363				2.1E-25			
25599	ENU09394	ANI61C8820:2367..49			GTBX	"AFUc00774, AFUc02877, AFUc05794, AFUc15944, AFUc22301"				"8.7e-55, 1.1e-11, 3.2e-60, 6.1e-25, 3.4e-16" 7.2E-44			
25600	ENU09395	ANI61C8821:1333..384			GTBX	AFUc10083							
25601	ENU09396	ANI61C8821:1619..2665			GTBX	"FGRc04178, Z71256"				"5.1e-08, 6.6e-88"			
25602	ENU09397	ANI61C9553:2145..406			GTBX	"AFUc06513, AFUc07337, CALc06139"				"1.2e-55, 9.6e-62, 4.0e-40" 2.8E-61			
25603	ENU09398	ANI61C9556:7313..7830			GTBX	FGRc11417							
25604	ENU09399	ANI61C8827:1639..428			GTBX	FGRc06586				7.5E-35			
25605	ENU09400	ANI61C8831:2299..2823			GTBX	"AFUc01894, CALc05378"				"4.2e-36, 1.8e-38"			
25606	ENU09401	ANI61C9566:2382..1796			GTBX	"AFUc14024, FGRc03629"				"8.2e-20, 5.8e-27"			
25607	ENU09402	ANI61C9567:1721..2586			GTBX	AFUc08775				2.6E-28			
25608	ENU09403	ANI61C9569:1936..900			GTBX	"AFUc11045, FGRc07076"				"1.3e-26, 2.2e-09"			
25609	ENU09404	ANI61C9572:3019..2194			GTBX	CALc05999				4.9E-122			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25610	ENU09405	ANI61C8846: 2.490			GTBX	AFUc09502				2.1E-50			
25611	ENU09406	ANI61C9579: 4150..3347			GTBX	AFUc05155				2.4E-30			
25612	ENU09407	ANI61C9582: 1668..221			GTBX	"AFUc09791, AFUc14294, AFUc15490"				"1.2e-28, 3.4e-45, 5.5e-78"			
25613	ENU09408	ANI61C8854: 633..1820			GTBX	"AFUc03263, AFUc08210"				"1.4e-07, 1.2e-33"			
25614	ENU09409	ANI61C8857: 2334..2536			GTBX	AFUc06435				1.5E-121			
25615	ENU09410	ANI61C9592: 105..520			GTBX	"FGRc09345, FGRc21977"				"6.9e-29, 2.9e-14"			
25616	ENU09411	ANI61C9595: 1129..674			GTBX	AFUc14898				6.6E-58			
25617	ENU09412	ANI61C8867: 803..26			GTBX	"AFUc08398, CALc05816"				"5.9e-24, 1.3e-17"			
25618	ENU09413	ANI61C8873: 8152..7032			GTBX	AFUc12824				2.7E-89			
25619	ENU09414	ANI61C8875: 12..1277			GTBX	AFUc14483				4.9E-162			
25620	ENU09415	ANI61C8878: 44..934			GTBX	AFUc14882				7.3E-46			
25621	ENU09416	ANI61C8879: 1404..2768			GTBX	AFUc14241				1.9E-70			
25622	ENU09417	ANI61C8884: 1067..53			GTBX	AFUc07086				4.5E-95			
25623	ENU09418	ANI61C8888: 1156..1536			GTBX	U00093				1.2e-74			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25624	ENU09419	ANI61C8889: 702..1898			GTBX	"AFUc03016, CALc03652"				"1.4e-55, 2.8e-59"			
25625	ENU09420	ANI61C8892: 1683..192			GTBX	"AFUc13932, FGRc11747, FGRc17309, FGRc26009"				"1.4e-25, 1.3e-10, 5.3e-09, 1.1e-16"			
25626	ENU09421	ANI61C8895: 67..904			GTBX	"AFUc11204, AFUc11814"				"2.5e-34, 1.2e-104"			
25627	ENU09422	ANI61C5207: 316..663			GTBX	AFUc15608				1.5E-46			
25628	ENU09423	ANI61C5207: 1872..793			GTBX	"AFUc03870, AFUc07633, AFUc19031"				"6.3e-16, 1.2e-19, 9.9e-70"			
25629	ENU09424	ANI61C5208: 2536..2216			GTBX	"AFUc06181, Y13138"				"1.5e-32, 9.0e-162"			
25630	ENU09425	ANI61C5209: 1457..2136			GTBX	"AFUc17725, FGRc11373"				"3.9e-27, 7.4e-19"			
25631	ENU09426	ANI61C5210: 2139..105			GTBX	AFUc15196				3.7E-186			
25632	ENU09427	ANI61C5215: 2509..2763			GTBX	AFUc15348				7.2E-121			
25633	ENU09428	ANI61C5222: 2322..719			GTBX	"AFUc07927, FGRc02874"				"7.9e-86, 9.0e-10"			
25634	ENU09429	ANI61C5224: 1472..13			GTBX	CALc05716				1.7E-119			
25635	ENU09430	ANI61C5228: 399..962			GTBX	AFUc14750				1.2E-90			
25636	ENU09431	ANI61S3608: 177..573			GTBX	AFUc22203				1.8E-23			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25637	ENU09432	ANI61C4506: 499..29			GTBX	AFUc15788				9.6E-33			
25638	ENU09433	ANI61C5237: 420..1271			GTBX	AFUc14942				6.9E-104			
25639	ENU09434	ANI61C5247: 4110..4852			GTBX	AFUc13730				1E-97			
25640	ENU09435	ANI61C4519: 2052..587			GTBX	AFUc15419				5.4E-127			
25641	ENU09436	ANI61C5251: 672..47			GTBX	Y13137				4.1e-43			
25642	ENU09437	ANI61C4526: 1413..1054			GTBX	AFUc15744				1.3E-147			
25643	ENU09438	ANI61C5256: 674..26			GTBX	"AFUc06812, AFUc08626"				"1.7e-44, 2.8e-09"			
25644	ENU09439	ANI61C4528: 509..147			GTBX	AFUc15759				1.9E-29			
25645	ENU09440	ANI61S4368: 60..639			GTBX	AFUc07754				2.2E-21			
25646	ENU09441	ANI61C3803: 1096..2			GTBX	"AFUc08591, AFUc13887"				"1.1e-55, 4.4e-75"			
25647	ENU09442	ANI61C3805: 4035..3580			GTBX	AFUc04676				6.3E-45			
25648	ENU09443	ANI61C3808: 743..411			GTBX	Y13138				5.8e-14			
25649	ENU09444	ANI61C5269: 1394..2229			GTBX	"AFUc02280, AFUc22008"				"9.4e-57, 2.0e-43"			
25650	ENU09445	ANI61C3810: 82..437			GTBX	AFUc15201				4E-52			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25651	ENU09446	ANI61C3811: 1376..1654			GTBX	AFUc06467				3.5E-30			
25652	ENU09447	ANI61C4542: 916..574			GTBX	"AFUc02869, AFUc02869"				"1.7e-65, 4.7e-26"			
25653	ENU09448	ANI61C3813: 1846..3158			GTBX	"FGRc12841, FGRc22473, FGRc23239"				"4.6e-26, 7.9e-35, 1.6e-43"			
25654	ENU09449	ANI61C5273: 2..1156			GTBX	"AFUc05117, AFUc11543"				"5.4e-27, 1.6e-92"			
25655	ENU09450	ANI61C3817: 78..1162			GTBX	AFUc12851				2.7E-75			
25656	ENU09451	ANI61C3821: 672..411			GTBX	AFUc15435				4.7E-56			
25657	ENU09452	ANI61C4551: 151..475			GTBX	AFUc18864				3.2E-45			
25658	ENU09453	ANI61C5280: 1840..2502			GTBX	"AFUc04510, AFUc18595"				"1.2e-24, 2.7e-07"			
25659	ENU09454	ANI61C3823: 22..252			GTBX	AFUc12507				7.4E-60			
25660	ENU09455	ANI61C3824: 595..981			GTBX	FGRc23435				2.8E-21			
25661	ENU09456	ANI61C3825: 375..735			GTBX	"AFUc06063, CALc02020, Y13134"				"5.9e-40, 3.0e-16, 6.7e-17"			
25662	ENU09457	ANI61C5283: 954..108			GTBX	AFUc12676				4.8E-36			
25663	ENU09458	ANI61C5286: 531..786			GTBX	"AFUc12628, AFUc12628, FGRc07656"				"5.6e-24, 6.7e-29, 3.4e-13"			
25664	ENU09459	ANI61C4559: 151..684			GTBX	AFUc21004				3.4E-31			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25665	ENU09460	ANI61S4392: 18..500			GTBX	"AFUc01686, Y13138"				"1.1e-43, 2.9e-62"			
25666	ENU09461	ANI61C4561: 27..754			GTBX	"AFUc10269, FGRc22925"				"3.0e-23, 2.5e-28"			
25667	ENU09462	ANI61C3833: 646..232			GTBX	FGRc04710				8.2E-72			
25668	ENU09463	ANI61C3834: 1167..1727			GTBX	AFUc16457				3.3E-29			
25669	ENU09464	ANI61C5294: 1041..654			GTBX	"AFUc15936, FGRc11101"				"1.2e-123, 5.2e-24"			
25670	ENU09465	ANI61S3674: 270..8			GTBX	AFUc10670				8.6E-33			
25671	ENU09466	ANI61C3840: 162..656			GTBX	"AFUc18322, AFUc21010"				"1.7e-19, 2.1e-26"			
25672	ENU09467	ANI61C4570: 2285..3385			GTBX	AFUc17804				1.3E-21			
25673	ENU09468	ANI61C4585: 983..30			GTBX	Y13135				4.5e-64			
25674	ENU09469	ANI61C4589: 727..290			GTBX	AFUc21610				2E-25			
25675	ENU09470	ANI61C3869: 25..390			GTBX	AFUc08072				4.6E-43			
25676	ENU09471	ANI61C4599: 54..440			GTBX	AFUc08426				1.4E-25			
25677	ENU09472	ANI61C3870: 791..270			GTBX	CALc05830				2.9E-34			
25678	ENU09473	ANI61C3877: 1384..1001			GTBX	AFUc01915				1.9E-47			

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25679	ENU09474	ANI61C3878: 1289..596			GTBX	"CALc04339, FGRc02339"				"4.4e-76, 3.3e-84"			
25680	ENU09475	ANI61C3879: 684..79			GTBX	AFUc09507				2.3E-40			
25681	ENU09476	ANI61C3881: 785..207			GTBX	CALc03328				5.8E-44			
25682	ENU09477	ANI61C3888: 813..247			GTBX	AFUc05510				6.2E-28			
25683	ENU09478	ANI61C3889: 1158..606			GTBX	AFUc13973				9.9E-73			
25684	ENU09479	ANI61C3893: 1373..3			GTBX	"AFUc04394, AFUc14651"				"8.1e-41, 2.6e-96"			
25685	ENU09480	ANI61C3895: 540..755			GTBX	AFUc12362				1.1E-54			
25686	ENU09481	ANI61C9601: 7148..7954			GTBX	AFUc17920				5.3E-44			
25687	ENU09482	ANI61C9605: 1032..50			GTBX	AFUc12404				5.5E-76			
25688	ENU09483	ANI61C9609: 1184..573			GTBX	"AFUc12674, AFUc16179, FGRc06836"				"7.5e-22, 5.1e-25, 3.7e-61"			
25689	ENU09484	ANI61C9611: 1087..208			GTBX	CALc04433				2.7E-99			
25690	ENU09485	ANI61C9621: 2017..1559			GTBX	AFUc01710				9.7E-47			
25691	ENU09486	ANI61C9624: 1287..1999			GTBX	"AFUc04270, AFUc04681, AFUc04681"				"2.7e-49, 1.4e-28, 2.4e-35"			
25692	ENU09487	ANI61C8901: 1882..2697			GTBX	AFUc13517				4.7E-78			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25693	ENU09488	ANI61C9632: 65..1007			GTBX	"AFUc20792, FGRc07150"				"5.8e-09, 7.4e-37"			
25694	ENU09489	ANI61C9634: 8369..7788			GTBX	AFUc09350				1.2E-36			
25695	ENU09490	ANI61C9635: 2193..2786			GTBX	AFUc09871				4.3E-66			
25696	ENU09491	ANI61C8908: 2891..3656			GTBX	AFUc15919				1.5E-46			
25697	ENU09492	ANI61C9638: 4270..7025			GTBX	"AFUc01729, FGRc17590"				"1.5e-35, 8.5e-29"			
25698	ENU09493	ANI61C9639: 1425..1036			GTBX	AFUc08511				5.7E-79			
25699	ENU09494	ANI61C9640: 2603..911			GTBX	"AFUc04955, AFUc09378, FGRc08438, FGRc21707"				"6.5e-69, 4.9e-120, 4.2e-12, 1.6e-10"			
25700	ENU09495	ANI61C9642: 2035..1577			GTBX	AFUc08746				3.3E-29			
25701	ENU09496	ANI61C8922: 1295..31			GTBX	"AFUc02649, CALc04199, CALc04199"				"1.3e-35, 3.3e-29, 8.8e-22"			
25702	ENU09497	ANI61C8922: 3530..2993			GTBX	FGRc02534				4E-40			
25703	ENU09498	ANI61C9657: 3865..2196			GTBX	"AFUc04650, CALc04969"				"2.4e-13, 2.3e-140"			
25704	ENU09499	ANI61C9658: 761..28			GTBX	Y13138				1.0e-14			
25705	ENU09500	ANI61C9664: 2241..4059			GTBX	"AFUc10881, Y13139"				"1.0e-83, 4.3e-149"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25706	ENU09501	ANI61C9669: 3783..5102			GTBX	"AFUc10037, AFUc12096"				"1.4e-95, 5.2e-40"			
25707	ENU09502	ANI61C8941: 564..836			GTBX	AFUc07937				1.5E-56			
25708	ENU09503	ANI61C9675: 2597..749			GTBX	"AFUc10109, AFUc17198, AFUc17198, FGRC15837, FGRC26158"				"3.0e-78, 4.0e-21, 5.3e-23, 1.5e-21, 3.5e-13"			
25709	ENU09504	ANI61C9677: 2010..1543			GTBX	AFUc12413				1.7E-102			
25710	ENU09505	ANI61C8954: 683..447			GTBX	AFUc08873				6.9E-34			
25711	ENU09506	ANI61C9687: 829..2			GTBX	"FGRC12006, Y13136"				"1.2e-51, 5.3e-40"			
25712	ENU09507	ANI61C9691: 2115..1211			GTBX	AFUc05215				5.3E-41			
25713	ENU09508	ANI61C9692: 1160..606			GTBX	AFUc16896				2.9E-28			
25714	ENU09509	ANI61C9694: 4490..3594			GTBX	"AFUc20993, U00092"				"2.6e-46, 3.6e-07"			
25715	ENU09510	ANI61C8966: 5753..6363			GTBX	"AFUc06989, Z71256"				"4.3e-36, 4.6e-11"			
25716	ENU09511	ANI61C9695: 923..72			GTBX	"AFUc14005, AFUc20315"				"7.8e-29, 3.3e-73"			
25717	ENU09512	ANI61C8967: 2826..2269			GTBX	AFUc03802				4.7E-40			
25718	ENU09513	ANI61C8971: 1468..733			GTBX	"CALc05073, FGRC02949"				"1.2e-22, 7.5e-24"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25719	ENU09514	ANI61C8973: 574..1417			GTBX	AFUc21866				1.9E-30			
25720	ENU09515	ANI61C8979: 129..506			GTBX	AFUc00391				5.9E-29			
25721	ENU09516	ANI61C8979: 3411..3851			GTBX	AFUc05896				9.6E-24			
25722	ENU09517	ANI61C6002: 1830..1440			GTBX	AFUc13365				4.5E-61			
25723	ENU09518	ANI61C6003: 1016..1437			GTBX	AFUc14299				3.9E-71			
25724	ENU09519	ANI61C8982: 756..2038			GTBX	"AFUc09202, Y13139"				"6.1e-92, 1.1e-28"			
25725	ENU09520	ANI61C8987: 5718..5065			GTBX	FGRc14942				2.8E-33			
25726	ENU09521	ANI61C8988: 29..1003			GTBX	"AFUc09518, FGRc00963"				"4.6e-37, 8.8e-14"			
25727	ENU09522	ANI61C6010: 705..413			GTBX	AFUc11775				3.6E-69			
25728	ENU09523	ANI61C8992: 1060..1268			GTBX	AFUc15788				6.5E-46			
25729	ENU09524	ANI61C6023: 22..959			GTBX	AFUc08361				2.1E-105			
25730	ENU09525	ANI61C6028: 698..112			GTBX	AFUc15445				2.8E-45			
25731	ENU09526	ANI61C5302: 804..1978			GTBX	"AFUc03529, FGRc15568, FGRc23030"				"3.9e-75, 1.9e-31, 6.8e-27"			
25732	ENU09527	ANI61C6032: 121..656			GTBX	FGRc24538				5.3E-24			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25733	ENU09528	ANI61C5304: 20..1813			GTBX	"CALc04320, CALc06192"				"4.1e-46, 1.3e-114"			
25734	ENU09529	ANI61C5307: 1011..634			GTBX	AFUc13255				1.7E-36			
25735	ENU09530	ANI61C6040: 498..238			GTBX	AFUc14608				1.3E-22			
25736	ENU09531	ANI61C5312: 17..463			GTBX	AFUc08453				1.5E-54			
25737	ENU09532	ANI61C6044: 827..423			GTBX	"AFUc20402, CALc05987, FGRc05827"				"1.4e-19, 7.9e-53, 3.2e-52"			
25738	ENU09533	ANI61C5317: 3..599			GTBX	"AFUc20512, CALc05290"				"3.1e-46, 1.8e-07"			
25739	ENU09534	ANI61C5320: 383..24			GTBX	CALc05007				6.7E-28			
25740	ENU09535	ANI61C5322: 2464..874			GTBX	"AFUc11807, FGRc09518"				"4.3e-88, 4.4e-20"			
25741	ENU09536	ANI61C5323: 557..1220			GTBX	AFUc08478				9.2E-73			
25742	ENU09537	ANI61C6052: 840..342			GTBX	AFUc01410				9.1E-40			
25743	ENU09538	ANI61C5324: 1547..58			GTBX	"AFUc06920, AFUc07230, AFUc14567, Y13135"				"5.1e-54, 1.9e-34, 7.7e-11, 5.1e-13"			
25744	ENU09539	ANI61C6062: 377..39			GTBX	AFUc13039				3.2E-30			
25745	ENU09540	ANI61C4610: 78..674			GTBX	AFUc07396				4.1E-82			
25746	ENU09541	ANI61C5341: 1441..35			GTBX	"AFUc21842, CALc05774"				"8.4e-62, 1.9e-72"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25747	ENU09542	ANI61C6074: 1430..126			GTBX	Y13137				7.4e-89			
25748	ENU09543	ANI61C5348: 2041..49			GTBX	"AFUc04409, AFUc14023"				"2.3e-18, 2.3e-22"			
25749	ENU09544	ANI61C5351: 3706..2627			GTBX	FGRc11453				1.5E-44			
25750	ENU09545	ANI61C5355: 400..77			GTBX	AFUc22404				5.3E-47			
25751	ENU09546	ANI61C5363: 1986..2330			GTBX	AFUc02673				1.1E-35			
25752	ENU09547	ANI61S3748: 25..508			GTBX	AFUc19745				4.5E-46			
25753	ENU09548	ANI61C3914: 1..336			GTBX	AFUc12813				2E-30			
25754	ENU09549	ANI61C5372: 2782..3320			GTBX	AFUc10825				3E-56			
25755	ENU09550	ANI61C4644: 385..122			GTBX	"AFUc14213, CALc06077"				"1.0e-23, 6.0e-13"			
25756	ENU09551	ANI61C3915: 1063..782			GTBX	AFUc00550				1.3E-42			
25757	ENU09552	ANI61C5373: 6..1136			GTBX	AFUc08943				2.9E-89			
25758	ENU09553	ANI61C5376: 55..480			GTBX	AFUc05917				7.3E-30			
25759	ENU09554	ANI61C3920: 2247..56			GTBX	"AFUc17196, AFUc18488, AFUc18488, FGRc00704, Y13134"				"1.3e-71, 3.5e-44, 3.5e-75, 2.7e-29, 1.3e-68"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25760	ENU09555	ANI61C4650: 1372..2			GTBX	"AFUc14849, FGRc00854"				"3.1e-10, 6.0e-32"			
25761	ENU09556	ANI61C4651: 870..50			GTBX	"AFUc22660, FGRc07303"				"6.5e-29, 3.2e-52"			
25762	ENU09557	ANI61C4652: 752..2207			GTBX	AFUc14076				8.4E-46			
25763	ENU09558	ANI61C5381: 1004..492			GTBX	AFUc03475				4.2E-51			
25764	ENU09559	ANI61C3925: 218..802			GTBX	AFUc15140				9.4E-57			
25765	ENU09560	ANI61C5385: 1551..1769			GTBX	AFUc07950				2.4E-42			
25766	ENU09561	ANI61C4657: 4223..6270			GTBX	"AFUc11820, AFUc12573, AFUc14610, Y13135"				"5.1e-145, 4.5e-84, 1.4e-15, 2.0e-98"			
25767	ENU09562	ANI61C3929: 514..28			GTBX	AFUc01963				1.3E-45			
25768	ENU09563	ANI61C5387: 1209..723			GTBX	FGRc03431				5.6E-46			
25769	ENU09564	ANI61C4659: 1012..1228			GTBX	AFUc14550				3.7E-25			
25770	ENU09565	ANI61C5388: 2432..2081			GTBX	"AFUc11974, AFUc14576"				"3.6e-40, 2.4e-67"			
25771	ENU09566	ANI61C5389: 97..686			GTBX	AFUc10526				1.7E-51			
25772	ENU09567	ANI61C4663: 149..637			GTBX	AFUc14674				1.6E-25			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25773	ENU09568	ANI61C5396: 1207..3398			GTBX	"AFUc05105, AFUc11030, FGRc07318"				"1.0e-81, 2.1e-79, 3.6e-124"			
25774	ENU09569	ANI61C4667: 422..34			GTBX	FGRc10474				2.6E-26			
25775	ENU09570	ANI61C4669: 6..968			GTBX	"AFUc09487, FGRc08263"				"2.3e-103, 3.5e-33"			
25776	ENU09571	ANI61C5399: 1944..519			GTBX	AFUc15972				5.6E-33			
25777	ENU09572	ANI61C4672: 742..473			GTBX	AFUc13983				3.2E-32			
25778	ENU09573	ANI61C3953: 2205..895			GTBX	"AFUc00630, AFUc16315"				"2.5e-36, 8.9e-30"			
25779	ENU09574	ANI61C4683: 435..36			GTBX	AFUc11129				3.4E-35			
25780	ENU09575	ANI61C3956: 1317..362			GTBX	"AFUc15086, Y13138"				"6.9e-43, 3.0e-21"			
25781	ENU09576	ANI61C3965: 2616..2940			GTBX	AFUc14919				3.5E-65			
25782	ENU09577	ANI61C3966: 924..1			GTBX	"AFUc19250, Y13138"				"1.7e-18, 1.8e-36"			
25783	ENU09578	ANI61C4698: 651..1923			GTBX	"AFUc13453, FGRc11821"				"2.6e-83, 2.5e-47"			
25784	ENU09579	ANI61C3971: 1048..34			GTBX	"AFUc00727, AFUc21727"				"1.9e-90, 5.3e-42"			
25785	ENU09580	ANI61C3972: 3639..2620			GTBX	"AFUc02588, AFUc02588"				"8.1e-28, 9.6e-37"			
25786	ENU09581	ANI61C3973: 2117..461			GTBX	"AFUc19352, CALc06116"				"6.3e-14, 7.6e-171"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25787	ENU09582	ANI61C3977: 1953..643			GTBX	AFUc15344				2.9E-166			
25788	ENU09583	ANI61C3978: 843..82			GTBX	FGRc04709				6.4E-34			
25789	ENU09584	ANI61C1002: 2611..2219			GTBX	AFUc08610				1.1E-28			
25790	ENU09585	ANI61C1003: 2507..993			GTBX	"AFUc01633, AFUc19340, FGRc18569"				"1.9e-51, 1.4e-46, 1.6e-11"			
25791	ENU09586	ANI61C1014: 740..199			GTBX	AFUc02769				2E-26			
25792	ENU09587	ANI61C3992: 282..521			GTBX	AFUc20274				1.7E-29			
25793	ENU09588	ANI61C3995: 44..766			GTBX	"AFUc05280, AFUc21291"				"2.0e-14, 1.2e-43"			
25794	ENU09589	ANI61C1022: 766..454			GTBX	AFUc14424				2.6E-31			
25795	ENU09590	ANI61C1025: 556..32			GTBX	AFUc14916				7.3E-108			
25796	ENU09591	ANI61C1030: 3757..3323			GTBX	AFUc10051				9.9E-36			
25797	ENU09592	ANI61C1038: 712..1006			GTBX	"AFUc14099, FGRc00303"				"5.0e-52, 1.3e-12"			
25798	ENU09593	ANI61C1044: 1903..35			GTBX	AFUc08909				5.9E-121			
25799	ENU09594	ANI61C1052: 1095..102			GTBX	"AFUc03916, AFUc06334"				"2.8e-32, 5.4e-26"			
25800	ENU09595	ANI61C1053: 618..115			GTBX	AFUc12163				8.2E-69			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25801	ENU09596	ANI61C1056: 1..606			GTBX	"AFUc17783, CALc05720"				"7.4e-44, 8.3e-23"			
25802	ENU09597	ANI61C1058: 2606..2340			GTBX	AFUc12718				4.7E-23			
25803	ENU09598	ANI61C1069: 4950..5330			GTBX	AFUc15622				1.1E-58			
25804	ENU09599	ANI61C9702: 2851..385			GTBX	"AFUc18380, CALc02515, U00092"				"8.9e-49, 7.3e-93, 1.5e-284"			
25805	ENU09600	ANI61C9702: 4461..4919			GTBX	AFUc10199				1.4E-80			
25806	ENU09601	ANI61C9706: 4861..6696			GTBX	"CALc05544, Y13137"				"3.8e-234, 3.7e-307"			
25807	ENU09602	ANI61C9717: 419..1280			GTBX	"AFUc05673, AFUc07215"				"1.5e-31, 4.4e-123"			
25808	ENU09603	ANI61C9718: 618..277			GTBX	AFUc18240				3E-31			
25809	ENU09604	ANI61C1084: 317..835			GTBX	AFUc14920				1.2E-23			
25810	ENU09605	ANI61C9720: 356..1467			GTBX	"AFUc12550, CALc05628"				"3.7e-168, 1.6e-21"			
25811	ENU09606	ANI61C1095: 4166..4419			GTBX	"AFUc03966, FGRc09117"				"2.2e-32, 1.5e-10"			
25812	ENU09607	ANI61C9733: 2309..2918			GTBX	AFUc14559				2.3E-43			
25813	ENU09608	ANI61C9738: 3327..3604			GTBX	AFUc06208				4.3E-24			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
25814	ENU09609	ANI61C9739: 7440..7764			GTBX	AFUc20780				3E-49			
25815	ENU09610	ANI61C9743: 1418..873			GTBX	"CALc05775, FGRc05013"				"2.8e-60, 1.9e-26"			
25816	ENU09611	ANI61C9752: 1283..51			GTBX	"AFUc14599, CALc02009"				"8.4e-132, 1.9e-07"			
25817	ENU09612	ANI61C9760: 3667..4155			GTBX	AFUc07682				1.8E-31			
25818	ENU09613	ANI61C9760: 5872..4366			GTBX	"AFUc07479, Y13134"				"2.6e-66, 1.2e-55"			
25819	ENU09614	ANI61C9769: 120..994			GTBX	AFUc07018				5.2E-44			
25820	ENU09615	ANI61C9773: 1037..200			GTBX	"AFUc08480, FGRc23544"				"3.2e-16, 1.7e-34"			
25821	ENU09616	ANI61C9775: 1364..2760			GTBX	"AFUc06544, AFUc15485"				"3.2e-35, 6.5e-73"			
25822	ENU09617	ANI61C9790: 415..3897			GTBX	"AFUc02169, AFUc12397, CALc01597, CALc04669"				"2.0e-70, 2.3e-252, 5.0e-19, 9.6e-114"			
25823	ENU09618	ANI61C9792: 540..156			GTBX	AFUc09788				5.2E-45			
25824	ENU09619	ANI61C9794: 3349..2897			GTBX	AFUc09569				1.8E-27			
25825	ENU09620	ANI61C6100: 325..100			GTBX	AFUc06484				2.5E-26			

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25826	ENU09621	ANI61C6108: 208..1945			GTBX	"AFUc10825, AFUc14691, AFUc15224, FGRc16414"				"1.7e-54, 3.0e-53, 8.0e-14, 1.4e-14"			
25827	ENU09622	ANI61C6109: 214..997			GTBX	AFUc09931				2.5E-48			
25828	ENU09623	ANI61C6112: 975..84			GTBX	FGRc04110				5.3E-71			
25829	ENU09624	ANI61C6113: 8..928			GTBX	CALc05352				1.3E-80			
25830	ENU09625	ANI61C6129: 423..1525			GTBX	AFUc07714				4.2E-24			
25831	ENU09626	ANI61S4500: 363..67			GTBX	FGRc05103				5.8E-49			
25832	ENU09627	ANI61C6132: 403..107			GTBX	AFUc01942				1.4E-51			
25833	ENU09628	ANI61S4517: 45..440			GTBX	Y13135				1.5e-38			
25834	ENU09629	ANI61C6140: 51..1322			GTBX	"AFUc00820, Z71256"				"9.1e-23, 8.7e-11"			
25835	ENU09630	ANI61C6142: 1192..107			GTBX	"AFUc05916, CALc05479"				"2.5e-37, 3.4e-110"			
25836	ENU09631	ANI61C6146: 1590..2326			GTBX	"AFUc04896, AFUc05822, FGRc10423"				"1.9e-28, 1.8e-07, 2.7e-13"			
25837	ENU09632	ANI61C5425: 702..94			GTBX	AFUc07579				3.8E-31			
25838	ENU09633	ANI61C6154: 702..1596			GTBX	"AFUc01051, FGRc10010"				"1.2e-18, 1.3e-21"			
25839	ENU09634	ANI61C5426: 761..12			GTBX	"AFUc04407, FGRc10921"				"9.8e-61, 2.0e-47"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25840	ENU09635	ANI61C6157: 2088..1205			GTBX	AFUc14533				6.7E-30			
25841	ENU09636	ANI61C4701: 814..374			GTBX	"AFUc05559, FGRc08592"				"3.7e-89, 2.2e-25"			
25842	ENU09637	ANI61C5430: 1315..803			GTBX	AFUc10737				1.5E-23			
25843	ENU09638	ANI61C4705: 15..1511			GTBX	AFUc13476				2.4E-72			
25844	ENU09639	ANI61C5435: 95..861			GTBX	AFUc14400				1.5E-50			
25845	ENU09640	ANI61C5440: 1234..15			GTBX	U00093				1.4e-111			
25846	ENU09641	ANI61C4712: 606..1352			GTBX	AFUc01145				6.8E-39			
25847	ENU09642	ANI61C6171: 1210..226			GTBX	AFUc15787				5.9E-33			
25848	ENU09643	ANI61C5442: 1738..1020			GTBX	AFUc02895				1.5E-36			
25849	ENU09644	ANI61C5444: 320..668			GTBX	AFUc15322				1E-37			
25850	ENU09645	ANI61C4716: 3235..3650			GTBX	AFUc13372				5.7E-52			
25851	ENU09646	ANI61C5449: 3..537			GTBX	AFUc15317				1.1E-27			
25852	ENU09647	ANI61S3822: 109..415			GTBX	AFUc05500				4.6E-31			
25853	ENU09648	ANI61C4720: 32..475			GTBX	AFUc04498				5E-36			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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25855	ENU09650	ANI61C5451: 502..849			GTBX	AFUc21338				2.5E-22			
25856	ENU09651	ANI61C6182: 644..27			GTBX	FGRc06110				2.7E-37			
25857	ENU09652	ANI61C5454: 2..340			GTBX	AFUc06221				5.1E-45			
25858	ENU09653	ANI61C4727: 336..664			GTBX	AFUc12008				4.4E-39			
25859	ENU09654	ANI61C5456: 1126..55			GTBX	"AFUc16901, FGRc10006"				"4.9e-21, 4.5e-14"			
25860	ENU09655	ANI61C6187: 1320..540			GTBX	"AFUc09040, AFUc14490"				"2.5e-144, 3.4e-13"			
25861	ENU09656	ANI61C5458: 571..1412			GTBX	"AFUc07396, AFUc11792, AFUc14619"				"1.9e-11, 1.6e-55, 1.6e-48"			
25862	ENU09657	ANI61C4730: 1349..868			GTBX	"AFUc14839, CALc04948"				"1.1e-22, 1.2e-46"			
25863	ENU09658	ANI61C6190: 1..462			GTBX	AFUc13184				4.5E-69			
25864	ENU09659	ANI61C5464: 911..132			GTBX	"AFUc06054, AFUc20036"				"3.2e-21, 5.2e-22"			
25865	ENU09660	ANI61C4738: 666..33			GTBX	AFUc14106				2.7E-62			
25866	ENU09661	ANI61C4739: 859..2			GTBX	AFUc11624				5.2E-105			
25867	ENU09662	ANI61C6199: 909..1228			GTBX	AFUc13777				4.2E-61			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
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25869	ENU09664	ANI61C4742: 738..94			GTBX	AFUc10405				1.3E-96			
25870	ENU09665	ANI61C5472: 1135..1935			GTBX	AFUc05296				9E-52			
25871	ENU09666	ANI61C5475: 13..408			GTBX	"AFUc01962, AFUc11850"				"1.8e-20, 2.2e-21"			
25872	ENU09667	ANI61C5475: 1314..662			GTBX	AFUc01962				2.5E-26			
25873	ENU09668	ANI61C4748: 1215..2511			GTBX	AFUc14868				1.2E-119			
25874	ENU09669	ANI61C5479: 620..144			GTBX	AFUc11381				8.9E-37			
25875	ENU09670	ANI61C5479: 1189..2303			GTBX	"AFUc08610, AFUc16734"				"1.5e-107, 1.5e-17"			
25876	ENU09671	ANI61C4756: 407..33			GTBX	AFUc02287				2.2E-21			
25877	ENU09672	ANI61S3867: 266..498			GTBX	AFUc14997				1.3E-26			
25878	ENU09673	ANI61C4761: 56..845			GTBX	AFUc02466				1.2E-26			
25879	ENU09674	ANI61S3872: 446..65			GTBX	AFUc02766				3.3E-42			
25880	ENU09675	ANI61C4771: 1109..62			GTBX	AFUc11383				2.2E-125			
25881	ENU09676	ANI61C4786: 876..135			GTBX	"AFUc15660, FGRc09694"				"4.3e-41, 5.1e-29"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	Description
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25883	ENU09678	ANI61C4789: 1071..690			GTBX	AFUc13817				1.1E-44			
25884	ENU09679	ANI61C4797: 319..2529			GTBX	"AFUc09124, AFUc09640, AFUc18058"				"2.2e-78, 8.8e-38, 8.5e-29"			
25885	ENU09680	ANI61C1103: 26..999			GTBX	FGRc09135				2.7E-37			
25886	ENU09681	ANI61C1105: 13..573			GTBX	"AFUc15843, U00094"				"6.4e-87, 2.8e-40"			
25887	ENU09682	ANI61C1111: 5900..6720			GTBX	"AFUc00779, FGRc22503"				"3.0e-09, 4.3e-35"			
25888	ENU09683	ANI61C1120: 10231..12501			GTBX	"AFUc03712, AFUc18769, CALc03518, FGRc12834, FGRc20309"				"1.2e-22, 8.1e-09, 2.3e-56, 3.5e-13, 6.6e-17"			
25889	ENU09684	ANI61C1121: 4847..3694			GTBX	Y13134				1.3e-41			
25890	ENU09685	ANI61C1123: 2959..23			GTBX	"AFUc00718, AFUc10854, AFUc11508, Z71256"				"2.0e-58, 5.5e-76, 2.5e-19, 1.8e-109"			
25891	ENU09686	ANI61C1126: 2054..1083			GTBX	"AFUc10316, AFUc22327"				"9.7e-40, 5.8e-17"			
25892	ENU09687	ANI61C1132: 3362..6968			GTBX	"AFUc08048, AFUc09981, FGRc03735, Y13136"				"2.3e-128, 4.6e-111, 5.8e-73, 4.3e-166"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25893	ENU09688	ANI61C1132: 7960..8202			GTBX	AFUc12080				3.2E-39			
25894	ENU09689	ANI61C1133: 3701..5484			GTBX	"AFUc16469, Y13137"				"9.6e-37, 1.2e-44"			
25895	ENU09690	ANI61C1133: 6897..5740			GTBX	FGRc03896				5.8E-55			
25896	ENU09691	ANI61C1138: 12140..10469			GTBX	"AFUc13136, CALc04542"				"8.4e-121, 3.5e-38"			
25897	ENU09692	ANI61C1141: 1383..1990			GTBX	"AFUc22467, FGRc06420"				"1.9e-71, 5.1e-08"			
25898	ENU09693	ANI61C1142: 1359..266			GTBX	AFUc15387				2.7E-96			
25899	ENU09694	ANI61C1145: 338..979			GTBX	"AFUc21496, Y131340"				"2.0e-58, 1.8e-12"			
25900	ENU09695	ANI61C1147: 3448..4162			GTBX	"AFUc06122, CALc05976, FGRc03662"				"1.7e-27, 4.0e-52, 7.5e-53"			
25901	ENU09696	ANI61C1156: 7493..7059			GTBX	AFUc13989				5.7E-25			
25902	ENU09697	ANI61C1161: 553..281			GTBX	FGRc16793				1.1E-44			
25903	ENU09698	ANI61C9802: 3878..2312			GTBX	"FGRc12359, FGRc26682, Y13140"				"5.3e-08, 5.2e-13, 4.4e-67"			
25904	ENU09699	ANI61C9804: 1241..151			GTBX	AFUc03380				2E-46			
25905	ENU09700	ANI61C1178: 878..53			GTBX	AFUc03777				3.4E-26			
25906	ENU09701	ANI61C9810: 1756..1256			GTBX	FGRc23086				1.1E-24			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25907	ENU09702	ANI61C1180: 1196..2056			GTBX	FGRc06851				1.5E-60			
25908	ENU09703	ANI61C1183: 2237..21			GTBX	"AFUc10035, FGRc20878, Y13136"				"2.1e-170, 2.6e-21, 1.1e-68"			
25909	ENU09704	ANI61C1186: 5213..806			GTBX	"AFUc15897, CALc05493"				"0.0, 2.6e-30"			
25910	ENU09705	ANI61C1187: 4140..5351			GTBX	AFUc08928				8.4E-43			
25911	ENU09706	ANI61C1189: 7785..6298			GTBX	"AFUc04073, AFUc20231, AFUc21886"				"1.2e-45, 5.9e-08, 2.4e-27"			
25912	ENU09707	ANI61C9824: 5113..4670			GTBX	AFUc13521				8.2E-33			
25913	ENU09708	ANI61C9826: 1..1518			GTBX	AFUc15367				1.7E-184			
25914	ENU09709	ANI61C9830: 1703..409			GTBX	CALc05806				2.4E-131			
25915	ENU09710	ANI61C9830: 5218..4379			GTBX	AFUc09714				8.1E-24			
25916	ENU09711	ANI61C9834: 6571..7561			GTBX	"AFUc11109, AFUc17602, FGRc08107"				"3.5e-28, 2.1e-19, 6.1e-18"			
25917	ENU09712	ANI61C9836: 947..226			GTBX	"AFUc14827, CALc04616"				"2.2e-16, 3.8e-23"			
25918	ENU09713	ANI61C9839: 611..879			GTBX	AFUc08740				8.4E-22			
25919	ENU09714	ANI61C9847: 1986..2857			GTBX	"AFUc11344, AFUc11344"				"2.9e-45, 4.7e-53"			
25920	ENU09715	ANI61C9847: 4264..3095			GTBX	"AFUc12331, AFUc21805"				"4.6e-31, 6.7e-19"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
25921	ENU09716	ANI61C9847: 9285..10497			GTBX	FGRc11572				9.4E-41			
25922	ENU09717	ANI61C9854: 365..63			GTBX	AFUc20068				2.7E-30			
25923	ENU09718	ANI61C9864: 1801..2743			GTBX	AFUc15416				9.7E-198			
25924	ENU09719	ANI61C9871: 463..701			GTBX	AFUc15546				1.5E-69			
25925	ENU09720	ANI61C9873: 496..2			GTBX	AFUc14820				2.7E-81			
25926	ENU09721	ANI61C9876: 2029..906			GTBX	AFUc13760				2.8E-81			
25927	ENU09722	ANI61C9880: 3365..1981			GTBX	"AFUc06015, FGRc12116"				"6.3e-24, 8.9e-29"			
25928	ENU09723	ANI61C9892: 1057..687			GTBX	"AFUc11408, FGRc01592"				"1.4e-98, 8.4e-10"			
25929	ENU09724	ANI61C6203: 10275..11138			GTBX	AFUc13995				4.9E-165			
25930	ENU09725	ANI61C6205: 2078..1213			GTBX	"AFUc15242, D50617"				"6.6e-108, 1.2e-84"			
25931	ENU09726	ANI61C6213: 2259..580			GTBX	"AFUc02451, AFUc09901, CALc05142, Y13135"				"1.5e-95, 2.4e-19, 6.3e-09, 1.5e-07"			
25932	ENU09727	ANI61C6227: 4483..3758			GTBX	"AFUc03527, AFUc20765"				"2.4e-18, 3.1e-27"			
25933	ENU09728	ANI61C5506: 2022..3044			GTBX	AFUc15489				3.2E-126			
25934	ENU09729	ANI61C5507: 3470..3854			GTBX	AFUc11680				1.2E-40			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25935	ENU09730	ANI61C6240: 4.483			GTBX	AFUc01334				5.8E-38			
25936	ENU09731	ANI61C6242: 666..250			GTBX	AFUc06832				1.6E-47			
25937	ENU09732	ANI61S4625: 238..496			GTBX	AFUc15836				9.8E-28			
25938	ENU09733	ANI61C6254: 2036..2560			GTBX	"AFUc10347, AFUc15031"				"1.5e-22, 8.3e-54"			
25939	ENU09734	ANI61C5528: 608..123			GTBX	AFUc13043				7.6E-58			
25940	ENU09735	ANI61C4801: 1188..1772			GTBX	"AFUc01206, AFUc07147, FGRc12821"				"5.6e-24, 2.1e-35, 2.8e-09"			
25941	ENU09736	ANI61C5537: 605..147			GTBX	AFUc15430				3.2E-31			
25942	ENU09737	ANI61C5537: 2786..2061			GTBX	AFUc15185				2.5E-68			
25943	ENU09738	ANI61C5542: 168..530			GTBX	AFUc06476				1.8E-33			
25944	ENU09739	ANI61C4816: 33..461			GTBX	AFUc05360				3.4E-35			
25945	ENU09740	ANI61C5549: 615..1013			GTBX	AFUc05565				7.1E-81			
25946	ENU09741	ANI61C5552: 851..93			GTBX	AFUc14753				2.7E-74			
25947	ENU09742	ANI61C6284: 673..325			GTBX	AFUc09678				2.5E-26			
25948	ENU09743	ANI61S3933: 9..233			GTBX	AFUc11585				7.4E-25			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25949	ENU09744	ANI61C4831: 45..475			GTBX	AFUc13810				3.2E-49			
25950	ENU09745	ANI61C4836: 1112..15			GTBX	AFUc03302				8.9E-93			
25951	ENU09746	ANI61C4837: 4..586			GTBX	AFUc08292				1.2E-92			
25952	ENU09747	ANI61C6297: 2743..3635			GTBX	"AFUc06848, Y13139"				"1.9e-76, 1.2e-25"			
25953	ENU09748	ANI61C6299: 1417..1637			GTBX	AFUc13847				2.2E-59			
25954	ENU09749	ANI61C4840: 108..974			GTBX	AFUc13509				1.9E-118			
25955	ENU09750	ANI61C4849: 942..589			GTBX	FGRc13511				4.8E-29			
25956	ENU09751	ANI61C5582: 44..732			GTBX	CALc06150				6.4E-21			
25957	ENU09752	ANI61C5583: 569..3			GTBX	AFUc20430				1.7E-25			
25958	ENU09753	ANI61C5586: 1296..2030			GTBX	"AFUc06713, FGRc18425"				"4.0e-57, 1.3e-09"			
25959	ENU09754	ANI61C4862: 2887..2038			GTBX	AFUc07470				1.2E-33			
25960	ENU09755	ANI61C4866: 1044..484			GTBX	"AFUc08653, AFUc18008"				"7.0e-62, 1.6e-41"			
25961	ENU09756	ANI61C5596: 623..42			GTBX	AFUc15561				6.3E-42			
25962	ENU09757	ANI61C5598: 478..113			GTBX	Y13137				1.3e-25			

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25963	ENU09758	ANI61C4874:1487..111			GTBX	AFUc15142				1.4E-124			
25964	ENU09759	ANI61C4879:1881..1163			GTBX	AFUc08813				1.9E-66			
25965	ENU09760	ANI61C4881:1028..1734			GTBX	FGRc13484				4E-30			
25966	ENU09761	ANI61C4882:214..776			GTBX	AFUc06352				2.3E-48			
25967	ENU09762	ANI61C4884:511..101			GTBX	FGRc04402				1.5E-33			
25968	ENU09763	ANI61C4887:1783..1230			GTBX	AFUc15282				6.9E-57			
25969	ENU09764	ANI61C4897:374..1395			GTBX	"AFUc07714, AFUc07747, AFUc11389"				"2.0e-10, 2.8e-32, 5.6e-36"			
25970	ENU09765	ANI61C4899:258..1409			GTBX	"AFUc12154, FGRc02884"				"3.8e-21, 3.2e-11"			
25971	ENU09766	ANI61S1039:442..14			GTBX	Y13140				3.5e-39			
25972	ENU09767	ANI61C1205:437..87			GTBX	AFUc15751				1.5E-53			
25973	ENU09768	ANI61C1208:6391..8168			GTBX	"AFUc08640, AFUc14702"				"2.8e-95, 4.5e-16"			
25974	ENU09769	ANI61C1208:8761..10056			GTBX	"AFUc13639, CALc06164"				"5.6e-119, 2.5e-26"			
25975	ENU09770	ANI61C1000:6:478..14			GTBX	AFUc08460				9.9E-21			
25976	ENU09771	ANI61C1000:7:188..676			GTBX	AFUc00879				2.6E-34			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25977	ENU09772	ANI61C1217: 5382..4258			GTBX	AFUc09190				1.7E-68			
25978	ENU09773	ANI61C1001 1:255..7			GTBX	AFUc14823				7.3E-47			
25979	ENU09774	ANI61C1001 5:731..2197			GTBX	AFUc09627				4.7E-29			
25980	ENU09775	ANI61C1223: 2975..2406			GTBX	AFUc10564				1.9E-37			
25981	ENU09776	ANI61C1226: 511..4			GTBX	AFUc15919				1.7E-35			
25982	ENU09777	ANI61C1227: 1799..965			GTBX	"AFUc15619, FGRc18463"				"3.6e-52, 2.4e-39"			
25983	ENU09778	ANI61C1229: 12629..13750			GTBX	"AFUc08495, AFUc15892"				"1.5e-57, 1.2e-44"			
25984	ENU09779	ANI61C1002 0:14..511			GTBX	"AFUc18869, CALc02488"				"1.1e-74, 5.1e-52"			
25985	ENU09780	ANI61C1002 5:1419..2136			GTBX	"AFUc11304, AFUc11498, AFUc15909"				"7.6e-27, 3.8e-36, 2.4e-40"			
25986	ENU09781	ANI61C1002 6:2060..4211			GTBX	"AFUc09022, AFUc11200, FGRc09828"				"1.1e-155, 3.6e-09, 7.7e-30"			
25987	ENU09782	ANI61C1002 8:8..556			GTBX	FGRc10845				7.3E-23			
25988	ENU09783	ANI61C1234: 698..264			GTBX	FGRc03585				2.7E-22			
25989	ENU09784	ANI61C1236: 3294..247			GTBX	"CALc05504, CALc05504, FGRc10685"				"1.1e-166, 4.4e-172, 1.0e-24"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
25990	ENU09785	ANI61C1003 9:78..593			GTBX	AFUc04205				2.2E-29			
25991	ENU09786	ANI61C1243: 76..647			GTBX	AFUc14226				2.2E-47			
25992	ENU09787	ANI61C1244: 639..205			GTBX	AFUc10187				4.6E-49			
25993	ENU09788	ANI61C1004 3:638..1321			GTBX	AFUc11890				3.5E-128			
25994	ENU09789	ANI61C1004 3:4533..1878			GTBX	"AFUc18915, AFUc22245, CALc06125"				"2.9e-37, 5.4e-55, 6.3e-86"			
25995	ENU09790	ANI61S1082: 533..81			GTBX	"AFUc14265, AFUc15053, CALc06148"				"3.6e-09, 1.1e-45, 1.8e-46"			
25996	ENU09791	ANI61C1004 8:1235..1896			GTBX	"AFUc17530, AFUc21626"				"9.1e-23, 4.6e-18"			
25997	ENU09792	ANI61S1086: 306..22			GTBX	AFUc10933				2.8E-39			
25998	ENU09793	ANI61C1250: 965..442			GTBX	AFUc02186				2.9E-64			
25999	ENU09794	ANI61C1251: 435..235			GTBX	AFUc05890				1.8E-31			
26000	ENU09795	ANI61C1460: 658..362			TBX	AFUc04191				1.4E-57			
26001	ENU09796	ANI61C1026 8:2016..2441			TBX	AFUc05348				1.5E-36			
26002	ENU09797	ANI61C1472: 2305..2820			TBX	AFUc15503				3.8E-62			
26003	ENU09798	ANI61C1473: 744..469			TBX	AFUc05026				1.1E-51			

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26005	ENU09800	ANI61C1027 6:1572..2084			TBX	AFUc13815				6.7E-37			
26006	ENU09801	ANI61C1484:2614..3107			TBX	AFUc22069				3.7E-37			
26007	ENU09802	ANI61C1028 2:741..950			TBX	AFUc14473				1.3E-129			
26008	ENU09803	ANI61C1028 3:939..666			TBX	AFUc10944				7.2E-84			
26009	ENU09804	ANI61C1028 9:873..166			TBX	AFUc14293				3.4E-59			
26010	ENU09805	ANI61C322:2 318..2686			TBX	Y13138				1.7e-18			
26011	ENU09806	ANI61C349:9 981..9772			TBX	AFUc08818				8.1E-69			
26012	ENU09807	ANI61C352:5 292..5651			TBX	AFUc05906				1.5E-41			
26013	ENU09808	ANI61C363:3 04..2			TBX	CALc02816				1.9E-35			
26014	ENU09809	ANI61C7202:134..361			TBX	AFUc14285				1E-31			
26015	ENU09810	ANI61C7216:1390..1924			TBX	"AFUc11696, AFUc11696"				"1.7e-61, 4.9e-33"			
26016	ENU09811	ANI61C7219:2645..2310			TBX	AFUc09975				1.4E-59			
26017	ENU09812	ANI61C385:4 260..4942			TBX	AFUc12528				2.5E-53			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26018	ENU09813	ANI61C388:4 66..64			TBX	AFUc20119				1.2E-55			
26019	ENU09814	ANI61C7223: 2972..2172			TBX	AFUc06424				1.1E-58			
26020	ENU09815	ANI61C7224: 4437..4850			TBX	AFUc12875				3.1E-88			
26021	ENU09816	ANI61C7236: 1466..1086			TBX	AFUc18591				3.4E-42			
26022	ENU09817	ANI61C7238: 680..344			TBX	AFUc09528				2.5E-45			
26023	ENU09818	ANI61C7238: 1092..832			TBX	AFUc09528				2.5E-45			
26024	ENU09819	ANI61C7271: 1132..605			TBX	AFUc06636				2.4E-38			
26025	ENU09820	ANI61C7272: 1371..1610			TBX	AFUc07449				1.1E-44			
26026	ENU09821	ANI61C5818: 881..339			TBX	AFUc08233				7.7E-38			
26027	ENU09822	ANI61S204:4 81..27			TBX	FGRc12216				3.7E-40			
26028	ENU09823	ANI61C7285: 8248..8667			TBX	AFUc15172				4.4E-69			
26029	ENU09824	ANI61C5830: 16..802			TBX	AFUc08094				2.6E-48			
26030	ENU09825	ANI61C6560: 32..1156			TBX	AFUc13931				1.4E-79			
26031	ENU09826	ANI61C5832: 1096..497			TBX	AFUc08734				4.3E-50			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26046	ENU09841	ANI61C2243: 321..63			TBX	AFUc04253				4.2E-93			
26047	ENU09842	ANI61C1031 8:6871..7170			TBX	AFUc08903				3E-41			
26048	ENU09843	ANI61C2250: 27..410			TBX	AFUc14478				8.6E-55			
26049	ENU09844	ANI61C1032 1:4802..5332			TBX	AFUc13535				1.4E-70			
26050	ENU09845	ANI61C1105 1:1650..1889			TBX	AFUc15849				3.5E-49			
26051	ENU09846	ANI61C1105 6:1..393			TBX	AFUc10621				4E-68			
26052	ENU09847	ANI61S1369: 2..411			TBX	AFUc15183				1.2E-41			
26053	ENU09848	ANI61C1033 0:13..225			TBX	FGRc08647				3.6E-42			
26054	ENU09849	ANI61C1033 5:2001..2270			TBX	AFUc11528				6E-153			
26055	ENU09850	ANI61C1106 5:1976..3091			TBX	AFUc12698				1.3E-138			
26056	ENU09851	ANI61C1033 8:652..1062			TBX	AFUc15802				5.7E-81			
26057	ENU09852	ANI61C1034 3:382..104			TBX	AFUc15194				1.2E-194			
26058	ENU09853	ANI61C1555: 1459..1665			TBX	AFUc09094				2.2E-48			
26059	ENU09854	ANI61S1393: 3..350			TBX	AFUc11981				8.7E-34			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26060	ENU09855	ANI61C1035 7:2937..1118			TBX	"AFUc10516, AFUc13253"				"1.4e-96, 1.1e-16"			
26061	ENU09856	ANI61C1035 8:2452..2676			TBX	AFUc21007				4.8E-39			
26062	ENU09857	ANI61S1397: 31..342			TBX	AFUc15972				6.6E-38			
26063	ENU09858	ANI61C1564: 1067..1316			TBX	AFUc03100				1.6E-71			
26064	ENU09859	ANI61C1036 0:1291..1680			TBX	AFUc05803				7.4E-36			
26065	ENU09860	ANI61C1036 0:3349..3570			TBX	AFUc13299				2.7E-142			
26066	ENU09861	ANI61C1036 0:385..1			TBX	AFUc15643				5.5E-39			
26067	ENU09862	ANI61C1036 0:3316..3017			TBX	AFUc13299				1.5E-150			
26068	ENU09863	ANI61C1109 9:1051..1761			TBX	AFUc13178				1.2E-56			
26069	ENU09864	ANI61C1109 9:10567..1015 4			TBX	"AFUc04105, FGRc12288"				"3.7e-16, 1.1e-57"			
26070	ENU09865	ANI61C403:1 218..1006			TBX	AFUc02462				1.9E-60			
26071	ENU09866	ANI61C1037 0:104..925			TBX	AFUc11594				1.7E-49			
26072	ENU09867	ANI61C1585: 92..490			TBX	AFUc15700				3.3E-38			
26073	ENU09868	ANI61C410:7 738..8487			TBX	"AFUc04942, AFUc11941, CALc04450"				"1.1e-67, 1.3e-34, 3.5e-29"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26074	ENU09869	ANI61C412:1 440..1774			TBX	AFUc05418				3.7E-70			
26075	ENU09870	ANI61C412:6 523..6927			TBX	AFUc11022				4.3E-57			
26076	ENU09871	ANI61C412:7 008..7352			TBX	AFUc11022				4.3E-57			
26077	ENU09872	ANI61C1038 6:1631..1945			TBX	AFUc10295				1E-42			
26078	ENU09873	ANI61C1038 6:1945..2298			TBX	AFUc10295				1E-42			
26079	ENU09874	ANI61C1038 7:55..495			TBX	AFUc15010				5.6E-58			
26080	ENU09875	ANI61C1593: 241..771			TBX	AFUc02879				6.4E-48			
26081	ENU09876	ANI61C425:5 20..95			TBX	AFUc15422				1.5E-38			
26082	ENU09877	ANI61C431:3 2..613			TBX	AFUc03600				1.3E-33			
26083	ENU09878	ANI61C433:3 511..3186			TBX	CALc05879				9E-80			
26084	ENU09879	ANI61C8004: 2247..1915			TBX	AFUc12803				1.8E-113			
26085	ENU09880	ANI61C445:2 3..278			TBX	Y13139				5.9e-57			
26086	ENU09881	ANI61C8028: 409..2			TBX	Y13137				5.9e-75			
26087	ENU09882	ANI61C8033: 60..272			TBX	Z71256				2.7e-59			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26088	ENU09883	ANI61C7309:548..3			TBX	AFUc12240				2.7E-59			
26089	ENU09884	ANI61C7317:2202..1795			TBX	FGRc01319				1.5E-44			
26090	ENU09885	ANI61C7317:2579..2337			TBX	AFUc11246				7E-49			
26091	ENU09886	ANI61C7318:1943..1584			TBX	AFUc11373				1.3E-32			
26092	ENU09887	ANI61C481:80..589			TBX	AFUc14011				5.6E-45			
26093	ENU09888	ANI61C8051:469..212			TBX	CALc04459				3E-62			
26094	ENU09889	ANI61C8051:6074..5853			TBX	Z71256				1.2e-82			
26095	ENU09890	ANI61C8053:2264..2734			TBX	AFUc14405				2E-57			
26096	ENU09891	ANI61C499:722..455			TBX	AFUc09357				1.1E-68			
26097	ENU09892	ANI61C7331:4599..4327			TBX	AFUc15784				3E-39			
26098	ENU09893	ANI61C6614:1629..1394			TBX	AFUc15221				1.2E-142			
26099	ENU09894	ANI61C6621:1600..1818			TBX	CALc06130				4.9E-55			
26100	ENU09895	ANI61C8084:3162..3470			TBX	AFUc15749				8.8E-31			
26101	ENU09896	ANI61C8085:96..612			TBX	AFUc17865				1.2E-53			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
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26103	ENU09898	ANI61C8087: 771..1			TBX	AFUc12758				4.4E-32			
26104	ENU09899	ANI61C6632: 431..192			TBX	AFUc06255				5.4E-64			
26105	ENU09900	ANI61C7365: 8009..7809			TBX	AFUc05380				1.5E-42			
26106	ENU09901	ANI61C5911: 1563..1063			TBX	AFUc14011				1.3E-36			
26107	ENU09902	ANI61C6644: 572..294			TBX	AFUc15344				4.4E-98			
26108	ENU09903	ANI61C7394: 1580..1083			TBX	AFUc10645				2.5E-63			
26109	ENU09904	ANI61C7396: 6555..7882			TBX	"AFUc08731, FGRc07479"				"3.5e-64, 1.9e-59"			
26110	ENU09905	ANI61C6667: 233..10			TBX	AFUc08889				4.1E-44			
26111	ENU09906	ANI61C5941: 871..323			TBX	AFUc05668				8.3E-43			
26112	ENU09907	ANI61C6677: 395..21			TBX	AFUc12033				2.1E-47			
26113	ENU09908	ANI61C5957: 429..757			TBX	AFUc00567				2.7E-65			
26114	ENU09909	ANI61C5967: 9075..9284			TBX	FGRc11859				1.8E-32			
26115	ENU09910	ANI61S2104: 550..7			TBX	"AFUc04034, FGRc16556"				"2.6e-39, 1.1e-16"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26116	ENU09911	ANI61C5978: 275..3			TBX	AFUc03602				1.2E-61			
26117	ENU09912	ANI61C3001: 411..2			TBX	AFUc15002				2.1E-49			
26118	ENU09913	ANI61C5997: 990..478			TBX	AFUc10036				1.3E-33			
26119	ENU09914	ANI61C3026: 568..11			TBX	"AFUc15479, AFUc21770"				"7.6e-22, 1.9e-35"			
26120	ENU09915	ANI61C2305: 1105..612			TBX	AFUc11158				3.1E-32			
26121	ENU09916	ANI61C1110 7:652..155			TBX	AFUc22275				1E-32			
26122	ENU09917	ANI61C1110 7:8686..8456			TBX	AFUc14504				2.9E-41			
26123	ENU09918	ANI61C3046: 869..252			TBX	AFUc09171				7.2E-40			
26124	ENU09919	ANI61C2324: 416..628			TBX	AFUc11776				3.4E-81			
26125	ENU09920	ANI61C3056: 3382..2980			TBX	"AFUc10340, CALc05472"				"1.3e-14, 4.3e-61"			
26126	ENU09921	ANI61C3062: 983..432			TBX	AFUc07103				2.5E-94			
26127	ENU09922	ANI61C2334: 764..1012			TBX	AFUc02776				5.2E-57			
26128	ENU09923	ANI61C1113 3:4764..4195			TBX	AFUc21395				4E-40			
26129	ENU09924	ANI61C1040 5:4666..4179			TBX	AFUc15972				3.2E-48			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26130	ENU09925	ANI61C1040 6:2096..1620			TBX	AFUc12015				1.4E-44			
26131	ENU09926	ANI61C2345: 431..1051			TBX	FGRc12154				3.1E-38			
26132	ENU09927	ANI61C1041 0:2812..2332			TBX	AFUc15133				1.2E-64			
26133	ENU09928	ANI61C1041 2:1541..1239			TBX	AFUc15311				2.9E-43			
26134	ENU09929	ANI61C1114 2:1..292			TBX	CALc06013				1.6E-79			
26135	ENU09930	ANI61C1114 8:2..325			TBX	AFUc15058				5E-42			
26136	ENU09931	ANI61C1115 7:1333..1037			TBX	AFUc05490				4.6E-53			
26137	ENU09932	ANI61C2363: 4..390			TBX	AFUc14337				2.7E-90			
26138	ENU09933	ANI61C2367: 2683..2409			TBX	AFUc02537				7.4E-47			
26139	ENU09934	ANI61C3097: 5..238			TBX	AFUc15533				2E-70			
26140	ENU09935	ANI61C1116 4:3922..4133			TBX	AFUc15879				5.1E-41			
26141	ENU09936	ANI61C1044 6:9480..9848			TBX	AFUc01816				5.7E-38			
26142	ENU09937	ANI61C2382: 18..689			TBX	AFUc04434				4.3E-45			
26143	ENU09938	ANI61C2384: 372..10			TBX	AFUc05787				7E-32			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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26145	ENU09940	ANI61C1045 5:1831..2178			TBX	AFUc13075				5.4E-56			
26146	ENU09941	ANI61C1118 5:3141..2914			TBX	AFUc13895				3.2E-107			
26147	ENU09942	ANI61C1118 6:2201..1884			TBX	AFUc13910				2.3E-33			
26148	ENU09943	ANI61C1118 9:880..1347			TBX	AFUc05827				2.1E-56			
26149	ENU09944	ANI61C1668: 961..1218			TBX	AFUc03564				5.9E-31			
26150	ENU09945	ANI61C1668: 1423..2232			TBX	"AFUc03564, AFUc19776"				"5.9e-31, 2.6e-46"			
26151	ENU09946	ANI61C1119 3:724..206			TBX	AFUc03276				6.8E-64			
26152	ENU09947	ANI61C1046 4:16..517			TBX	AFUc14564				1.5E-68			
26153	ENU09948	ANI61C508:2 833..2485			TBX	AFUc12712				2.7E-34			
26154	ENU09949	ANI61C1047 7:7766..8083			TBX	AFUc15740				3.3E-55			
26155	ENU09950	ANI61C1047 7:10845..1121 4			TBX	"AFUc13557, X59720"				"3.1e-53, 8.7e-50"			
26156	ENU09951	ANI61C1048 3:1906..2700			TBX	AFUc15804				7.7E-153			
26157	ENU09952	ANI61C1048 3:3278..3486			TBX	"AFUc15804, AFUc15804"				"4.0e- 150, 7.7e- 153"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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26159	ENU09954	ANI61C1048 7:6932..8598			TBX	"AFUc14083, AFUc15928"				"1.3e-25, 9.8e-121"			
26160	ENU09955	ANI61C1696: 1625..2005			TBX	AFUc06052				3.6E-38			
26161	ENU09956	ANI61C1699: 4320..3898			TBX	AFUc08707				3.5E-63			
26162	ENU09957	ANI61C524:3 96..830			TBX	AFUc15671				8.4E-83			
26163	ENU09958	ANI61C1049 7:6312..7257			TBX	"AFUc06170, AFUc14026"				"5.4e-36, 1.8e-70"			
26164	ENU09959	ANI61C530:6 259..5831			TBX	Z47047				4.6e-17			
26165	ENU09960	ANI61C534:7 958..7584			TBX	AFUc19364				3.5E-33			
26166	ENU09961	ANI61C539:7 80..97			TBX	AFUc09491				1.9E-69			
26167	ENU09962	ANI61C8115: 1511..57			TBX	AFUc15481				4.6E-151			
26168	ENU09963	ANI61C8119: 1234..920			TBX	AFUc08845				1.7E-82			
26169	ENU09964	ANI61C556:5 647..5390			TBX	AFUc14924				1.1E-218			
26170	ENU09965	ANI61C558:4 320..4880			TBX	AFUc14136				3E-62			
26171	ENU09966	ANI61C562:3 131..2799			TBX	AFUc06316				5.9E-41			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26172	ENU09967	ANI61C8133: 3..473			TBX	AFUc11118				4.2E-59			
26173	ENU09968	ANI61C578:5 77..1029			TBX	AFUc01862				3.6E-64			
26174	ENU09969	ANI61C8140: 938..64			TBX	"AFUc00985, AFUc03101"				"1.7e-16, 6.6e-43"			
26175	ENU09970	ANI61C7419: 511..140			TBX	AFUc15103				2.7E-52			
26176	ENU09971	ANI61C7419: 1006..668			TBX	AFUc15103				2.7E-52			
26177	ENU09972	ANI61C8155: 2..232			TBX	AFUc15172				2.4E-43			
26178	ENU09973	ANI61C592:4 59..1			TBX	FGRc12433				5.6E-42			
26179	ENU09974	ANI61C7430: 1250..1047			TBX	AFUc05191				3.2E-97			
26180	ENU09975	ANI61C6703: 847..1110			TBX	AFUc14632				7.8E-86			
26181	ENU09976	ANI61C6703: 2316..1740			TBX	AFUc14632				3.3E-72			
26182	ENU09977	ANI61C6709: 4001..4468			TBX	AFUc03350				2.4E-52			
26183	ENU09978	ANI61C6711: 2059..1173			TBX	AFUc14433				2.9E-154			
26184	ENU09979	ANI61C6711: 2772..2153			TBX	AFUc14433				2.9E-154			
26185	ENU09980	ANI61C6714: 6174..6386			TBX	AFUc14412				4.5E-35			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26186	ENU09981	ANI61C6717: 1667..1895			TBX	Y13138				2.8e-34			
26187	ENU09982	ANI61C7455: 2801..2121			TBX	AFUc14993				5.7E-52			
26188	ENU09983	ANI61C6728: 254..499			TBX	AFUc04684				2E-44			
26189	ENU09984	ANI61C7465: 74..283			TBX	AFUc14734				2.8E-136			
26190	ENU09985	ANI61C7485: 3034..3324			TBX	AFUc13156				5.2E-35			
26191	ENU09986	ANI61C7492: 14..599			TBX	AFUc08563				1E-93			
26192	ENU09987	ANI61C6764: 431..997			TBX	AFUc02841				1.4E-59			
26193	ENU09988	ANI61C6772: 1885..1670			TBX	AFUc13631				5E-78			
26194	ENU09989	ANI61C6772: 3366..2850			TBX	AFUc11189				2.3E-31			
26195	ENU09990	ANI61C6777: 1739..2320			TBX	AFUc11182				9.5E-73			
26196	ENU09991	ANI61C6779: 885..415			TBX	AFUc01472				8.6E-45			
26197	ENU09992	ANI61C6785: 400..657			TBX	AFUc18290				1.8E-60			
26198	ENU09993	ANI61S2209: 584..63			TBX	AFUc12936				4.4E-55			
26199	ENU09994	ANI61C3104: 3733..3464			TBX	Y13134				1.1e-95			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26200	ENU09995	ANI61C3122: 355..765			TBX	AFUc15397				3.3E-72			
26201	ENU09996	ANI61C2410: 1111..1348			TBX	AFUc10475				9E-39			
26202	ENU09997	ANI61C2410: 1841..2470			TBX	"AFUc14120, AFUc14120"				"1.3e-116, 1.8e-98"			
26203	ENU09998	ANI61C1121 7:429..1			TBX	CALc01737				5.9E-34			
26204	ENU09999	ANI61C3151: 766..1116			TBX	AFUc12817				1.4E-34			
26205	ENU10000	ANI61C1122 5:2..694			TBX	AFUc11815				3.1E-62			
26206	ENU10001	ANI61C1122 5:879..1377			TBX	"AFUc11815, AFUc11815"				"2.4e-54, 3.1e-62"			
26207	ENU10002	ANI61C1122 9:3671..2959			TBX	AFUc15733				1.7E-120			
26208	ENU10003	ANI61C1700: 23..397			TBX	AFUc13133				3.5E-35			
26209	ENU10004	ANI61C1701: 2076..2837			TBX	AFUc15352				1.3E-62			
26210	ENU10005	ANI61C1705: 3399..3761			TBX	AFUc08134				1.8E-44			
26211	ENU10006	ANI61C2436: 957..1347			TBX	AFUc15614				2.4E-85			
26212	ENU10007	ANI61C1123 4:467..3			TBX	AFUc15455				2.2E-40			
26213	ENU10008	ANI61C1124 0:2..461			TBX	AFUc06703				9.7E-46			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26214	ENU10009	ANI61C3182: 2031..2377			TBX	AFUc04772				7E-47			
26215	ENU10010	ANI61C3185: 508..145			TBX	AFUc13049				1.7E-126			
26216	ENU10011	ANI61C3186: 3106..2741			TBX	AFUc13434				7.6E-45			
26217	ENU10012	ANI61C1730: 3..527			TBX	AFUc10266				6.5E-59			
26218	ENU10013	ANI61C3191: 278..3			TBX	AFUc15545				3.8E-87			
26219	ENU10014	ANI61C2464: 1668..1021			TBX	FGRe11747				1.2E-31			
26220	ENU10015	ANI61C3199: 1..611			TBX	AFUc15519				1.3E-45			
26221	ENU10016	ANI61C1741: 618..33			TBX	AFUc15826				8.6E-41			
26222	ENU10017	ANI61C2473: 1109..42			TBX	"AFUc09645, AFUc09645"				"3.3e-31, 7.9e-54"			
26223	ENU10018	ANI61C1054 1:2933..2106			TBX	"AFUc12046, Y13140"				"6.8e-95, 3.0e-130"			
26224	ENU10019	ANI61C1127 4:1813..796			TBX	"FGRe06649, FGRe11623"				"3.8e-34, 9.9e-11"			
26225	ENU10020	ANI61C1127 9:17..250			TBX	AFUc07741				8.7E-61			
26226	ENU10021	ANI61C2480: 240..440			TBX	AFUc08744				6.3E-48			
26227	ENU10022	ANI61C1759: 1431..460			TBX	"AFUc11420, AFUc18306"				"3.8e-51, 2.0e-21"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26228	ENU10023	ANI61C1055 3:21..320			TBX	CALc06110				8.7E-101			
26229	ENU10024	ANI61C1055 5:2699..1999			TBX	AFUc05645				8.4E-74			
26230	ENU10025	ANI61C1055 7:467..96			TBX	AFUc13557				6.9E-52			
26231	ENU10026	ANI61C2495: 521..3			TBX	AFUc14306				2.3E-76			
26232	ENU10027	ANI61C600:2 174..1764			TBX	CALc06158				1.5E-72			
26233	ENU10028	ANI61C602:9 74..355			TBX	AFUc13158				1.2E-65			
26234	ENU10029	ANI61C1057 2:57..1135			TBX	"AFUc00606, AFUc06517, FGRc10385"				"1.3e-12, 1.3e-51, 1.0e-33"			
26235	ENU10030	ANI61C1057 3:1024..1449			TBX	AFUc03864				2.5E-83			
26236	ENU10031	ANI61C613:3 ..584			TBX	AFUc14174				1.1E-67			
26237	ENU10032	ANI61C1058 2:545..72			TBX	AFUc14725				2.9E-38			
26238	ENU10033	ANI61C1058 9:7928..8383			TBX	AFUc13200				3.3E-98			
26239	ENU10034	ANI61C1059 2:2426..2656			TBX	AFUc07883				9.4E-32			
26240	ENU10035	ANI61C634:8 86..629			TBX	Y13136				1.0e-18			
26241	ENU10036	ANI61C656:3 4..618			TBX	AFUc07639				1.2E-64			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26242	ENU10037	ANI61C669:3 23..48			TBX	AFUc11626				1.7E-36			
26243	ENU10038	ANI61C8230: 165..455			TBX	FGRc11456				1.9E-37			
26244	ENU10039	ANI61C7508: 1555..372			TBX	AFUc09787				6.4E-78			
26245	ENU10040	ANI61C671:4 82..808			TBX	AFUc15558				4.8E-61			
26246	ENU10041	ANI61C686:4 695..5262			TBX	AFUc13870				7.5E-43			
26247	ENU10042	ANI61C7523: 1790..2362			TBX	AFUc06950				1.4E-52			
26248	ENU10043	ANI61C7528: 395..3			TBX	AFUc15740				1.2E-39			
26249	ENU10044	ANI61C699:3 53..2			TBX	AFUc09402				3.2E-44			
26250	ENU10045	ANI61C7530: 972..442			TBX	AFUc11771				2.1E-55			
26251	ENU10046	ANI61C7531: 2779..3147			TBX	CALc05550				1.4E-32			
26252	ENU10047	ANI61C7535: 548..1081			TBX	AFUc15071				2.3E-118			
26253	ENU10048	ANI61C7535: 380..3			TBX	AFUc13442				4.5E-43			
26254	ENU10049	ANI61C6808: 2162..2704			TBX	AFUc13976				5.2E-32			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26255	ENU10050	ANI61C6814: 3423..1721			TBX	"AFUc06527, AFUc17241, FGRc09905, FGRc15187"				"1.8e-113, 5.7e-40, 2.6e-74, 3.5e-13"			
26256	ENU10051	ANI61C8273: 1404..1688			TBX	FGRc12425				1.8E-170			
26257	ENU10052	ANI61C8273: 3873..3640			TBX	AFUc11234				7.4E-91			
26258	ENU10053	ANI61C8273: 4919..4605			TBX	AFUc04450				5.2E-32			
26259	ENU10054	ANI61C7546: 569..9			TBX	Y13140				1.5e-69			
26260	ENU10055	ANI61C6819: 360..61			TBX	AFUc14565				1.9E-86			
26261	ENU10056	ANI61C6819: 1172..511			TBX	"AFUc14565, AFUc14565"				"1.9e-86, 5.6e-26"			
26262	ENU10057	ANI61C6823: 475..86			TBX	AFUc08494				3.4E-57			
26263	ENU10058	ANI61C6827: 1241..709			TBX	AFUc15969				9.6E-34			
26264	ENU10059	ANI61C7560: 710..153			TBX	AFUc14056				3.6E-33			
26265	ENU10060	ANI61C8293: 1736..1422			TBX	AFUc11416				4.3E-66			
26266	ENU10061	ANI61C6867: 4199..4710			TBX	AFUc13638				2.6E-33			
26267	ENU10062	ANI61C6875: 487..239			TBX	AFUc15186				2.1E-45			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
26268	ENU10063	ANI61C6880: 422..6			TBX	AFUc09175				3.8E-41			
26269	ENU10064	ANI61C6892: 286..771			TBX	AFUc01364				1.2E-43			
26270	ENU10065	ANI61C6895: 48..635			TBX	AFUc20237				3.8E-48			
26271	ENU10066	ANI61C3208: 2018..2563			TBX	AFUc10936				5.8E-66			
26272	ENU10067	ANI61S3046: 93..596			TBX	AFUc15363				4.9E-51			
26273	ENU10068	ANI61C3229: 2533..2303			TBX	AFUc08535				1.3E-33			
26274	ENU10069	ANI61C2509: 3278..2802			TBX	AFUc14181				8.3E-66			
26275	ENU10070	ANI61C3241: 1482..1832			TBX	AFUc11766				4.3E-36			
26276	ENU10071	ANI61C1131 1:1269..1808			TBX	AFUc07214				9.1E-36			
26277	ENU10072	ANI61C3253: 1238..2259			TBX	AFUc15072				7.1E-105			
26278	ENU10073	ANI61C1132 1:1517..2423			TBX	AFUc10674				3.3E-98			
26279	ENU10074	ANI61S1636: 335..3			TBX	AFUc02091				6.5E-41			
26280	ENU10075	ANI61C2549: 36..604			TBX	FGRc12323				5.1E-35			
26281	ENU10076	ANI61C1134 1:3722..3447			TBX	CALc05684				4.8E-52			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26282	ENU10077	ANI61S1654: 1..347			TBX	AFUc10087				5.9E-35			
26283	ENU10078	ANI61C2553: 14..374			TBX	AFUc05589				2.6E-44			
26284	ENU10079	ANI61C2553: 2527..3117			TBX	AFUc04288				5.7E-58			
26285	ENU10080	ANI61C1062 4:2670..2122			TBX	AFUc09584				5.6E-35			
26286	ENU10081	ANI61C1135 7:34..367			TBX	AFUc15619				3.2E-42			
26287	ENU10082	ANI61C1836: 516..7			TBX	Z71256				2.7e-20			
26288	ENU10083	ANI61C3299: 772..1486			TBX	AFUc15114				9.9E-61			
26289	ENU10084	ANI61C1063 4:3..416			TBX	FGRc10919				2.1E-33			
26290	ENU10085	ANI61C1136 3:2..495			TBX	AFUc13573				2.3E-64			
26291	ENU10086	ANI61S1673: 438..133			TBX	AFUc01485				2E-37			
26292	ENU10087	ANI61C1840: 506..42			TBX	AFUc09670				3.8E-37			
26293	ENU10088	ANI61C1064 6:757..247			TBX	AFUc10676				1.9E-70			
26294	ENU10089	ANI61C1064 6:1379..1034			TBX	AFUc10676				1.9E-70			
26295	ENU10090	ANI61C1850: 1015..1			TBX	AFUc15969				3.6E-101			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26296	ENU10091	ANI61C1065 4:5628..6366			TBX	"AFUc15290, FGRc03192"				"1.0e-153, 1.6e-66" 2.1E-47			
26297	ENU10092	ANI61C1138 4:961..456			TBX	AFUc04784							
26298	ENU10093	ANI61C1138 6:949..477			TBX	AFUc07894				1.8E-51			
26299	ENU10094	ANI61C2598: 1649..1030			TBX	AFUc14134				3.8E-61			
26300	ENU10095	ANI61C1139 3:1062..1801			TBX	"AFUc15965, AFUc15965"				"1.4e-160, 4.5e-167" 4.5E-167			
26301	ENU10096	ANI61C1139 3:2717..3327			TBX	AFUc15965							
26302	ENU10097	ANI61C1139 3:3454..4047			TBX	AFUc15965				4.5E-167			
26303	ENU10098	ANI61C1139 8:1407..1883			TBX	AFUc19996				5.4E-33			
26304	ENU10099	ANI61C1066 9:2650..2192			TBX	AFUc15856				2E-118			
26305	ENU10100	ANI61C1871: 642..304			TBX	AFUc01385				3.1E-34			
26306	ENU10101	ANI61C702:9 ..296			TBX	AFUc02664				2.3E-50			
26307	ENU10102	ANI61C1067 0:241..2			TBX	AFUc11950				5.1E-41			
26308	ENU10103	ANI61C9007: 3904..4113			TBX	AFUc13744				2.2E-85			
26309	ENU10104	ANI61C1886: 516..781			TBX	AFUc12305				9.9E-50			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
26310	ENU10105	ANI61C1068 6:674..357			TBX	AFUc16162				1.5E-45			
26311	ENU10106	ANI61C1899: 1..216			TBX	X59720				5.9e-45			
26312	ENU10107	ANI61C722:3 540..3286			TBX	Y13134				2.1e-120			
26313	ENU10108	ANI61C1069 1:232..450			TBX	AFUc01808				1.2E-43			
26314	ENU10109	ANI61C1069 2:1866..2621			TBX	AFUc15403				9.5E-47			
26315	ENU10110	ANI61C9024: 334..2			TBX	AFUc10157				2.4E-73			
26316	ENU10111	ANI61C736:4 ..557			TBX	FGRc08015				4.1E-34			
26317	ENU10112	ANI61C742:9 86..1309			TBX	AFUc04230				2.2E-42			
26318	ENU10113	ANI61C9041: 769..225			TBX	AFUc15972				4.3E-51			
26319	ENU10114	ANI61C8314: 847..1149			TBX	AFUc01794				9.8E-39			
26320	ENU10115	ANI61C754:1 694..2598			TBX	AFUc07695				6E-94			
26321	ENU10116	ANI61C759:9 74..1656			TBX	AFUc15782				1.3E-216			
26322	ENU10117	ANI61C760:8 24..1195			TBX	AFUc15173				7.7E-116			
26323	ENU10118	ANI61C9060: 489..1082			TBX	"AFUc09562, AFUc16430"				"5.1e-41, 1.7e-14"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26324	ENU10119	ANI61C7602: 2..661			TBX	AFUc08499				2E-43			
26325	ENU10120	ANI61C7611: 266..18			TBX	AFUc01029				1E-34			
26326	ENU10121	ANI61C9078: 1169..627			TBX	"CALc05486, Y13140"				"1.7e-172, 9.9e-187"			
26327	ENU10122	ANI61C9081: 2..544			TBX	AFUc09562				3.3E-71			
26328	ENU10123	ANI61C796:2 000..1580			TBX	Z71256				1.1e-94			
26329	ENU10124	ANI61C797:3 073..3285			TBX	AFUc14002				2E-68			
26330	ENU10125	ANI61C6901: 369..1157			TBX	AFUc11697				1.6E-66			
26331	ENU10126	ANI61C6908: 238..2			TBX	AFUc11236				2E-80			
26332	ENU10127	ANI61C8372: 68..310			TBX	FGRc10332				2.9E-38			
26333	ENU10128	ANI61C6936: 1145..1738			TBX	AFUc00849				5.3E-50			
26334	ENU10129	ANI61C6941: 1300..322			TBX	AFUc13344				4.8E-76			
26335	ENU10130	ANI61C7675: 1507..1737			TBX	AFUc15563				2.7E-84			
26336	ENU10131	ANI61S617:5 00..105			TBX	AFUc05623				7E-47			
26337	ENU10132	ANI61C24:48 2..219			TBX	AFUc10888				2.2E-38			

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26338	ENU10133	ANI61C24:39 12..3514			TBX	AFUc03140				3E-62			
26339	ENU10134	ANI61C4002: 2009..1581			TBX	AFUc10817				4.7E-59			
26340	ENU10135	ANI61C6983: 961..1700			TBX	AFUc14695				1E-47			
26341	ENU10136	ANI61C4013: 122..460			TBX	AFUc11715				4.5E-34			
26342	ENU10137	ANI61C6992: 2612..3298			TBX	AFUc10584				8.8E-42			
26343	ENU10138	ANI61C4029: 80..709			TBX	AFUc13720				5.9E-36			
26344	ENU10139	ANI61C4034: 851..537			TBX	FGRc12892				3.8E-40			
26345	ENU10140	ANI61C74:24 01..1973			TBX	FGRc10359				2E-50			
26346	ENU10141	ANI61C80:31 13..3924			TBX	AFUc11668				1.9E-71			
26347	ENU10142	ANI61C82:17 26..1385			TBX	AFUc06769				3.8E-51			
26348	ENU10143	ANI61C4062: 745..1218			TBX	AFUc07689				5.4E-37			
26349	ENU10144	ANI61C95:21 13..1149			TBX	FGRc02814				5.6E-52			
26350	ENU10145	ANI61C96:15 17..1230			TBX	FGRc10078				1.4E-40			
26351	ENU10146	ANI61C1140 1:3..434			TBX	AFUc13163				2.4E-38			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26352	ENU10147	ANI61S698:345..23			TBX	AFUc09912				5.7E-34			
26353	ENU10148	ANI61C11419:2373..1843			TBX	AFUc15881				1.6E-67			
26354	ENU10149	ANI61S2455:392..2			TBX	AFUc11066				1.1E-31			
26355	ENU10150	ANI61C3355:2104..2365			TBX	AFUc09161				2.7E-80			
26356	ENU10151	ANI61C3356:297..28			TBX	AFUc12958				1.1E-81			
26357	ENU10152	ANI61C4085:638..48			TBX	AFUc11270				1.1E-65			
26358	ENU10153	ANI61S2462:5..440			TBX	AFUc21510				3.8E-62			
26359	ENU10154	ANI61C3362:4..264			TBX	FGRc11478				4.6E-34			
26360	ENU10155	ANI61C3362:436..786			TBX	FGRc11478				4.6E-34			
26361	ENU10156	ANI61C11436:4996..4331			TBX	"AFUc04052, FGRc01908"				"7.1e-13, 4.3e-46"			
26362	ENU10157	ANI61C2646:3168..3605			TBX	AFUc14961				2.5E-47			
26363	ENU10158	ANI61C3377:959..459			TBX	AFUc22233				6.1E-41			
26364	ENU10159	ANI61C10717:4585..3701			TBX	AFUc11632				3.9E-65			
26365	ENU10160	ANI61C1929:584..5			TBX	AFUc13153				5.6E-52			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26366	ENU10161	ANI61C1072 5:528..16			TBX	AFUc12822				2.6E-35			
26367	ENU10162	ANI61C2662: 2551..2306			TBX	AFUc13641				5.8E-31			
26368	ENU10163	ANI61C3398: 387..870			TBX	AFUc18684				2E-44			
26369	ENU10164	ANI61C1146 2:3829..4053			TBX	AFUc13016				5.5E-42			
26370	ENU10165	ANI61C2676: 330..5			TBX	AFUc13919				6.5E-148			
26371	ENU10166	ANI61C2679: 1222..893			TBX	AFUc09698				2.1E-47			
26372	ENU10167	ANI61C1954: 679..9			TBX	"FGRc04985, Y13140"				"1.4e-62, 1.4e-35"			
26373	ENU10168	ANI61C2684: 71..694			TBX	AFUc06488				2.4E-82			
26374	ENU10169	ANI61C1075 3:1340..981			TBX	AFUc19770				9.7E-36			
26375	ENU10170	ANI61C1075 3:1723..1472			TBX	"AFUc17439, AFUc17439"				"2.2e-40, 6.0e-31"			
26376	ENU10171	ANI61C1076 2:980..528			TBX	AFUc10345				3.4E-32			
26377	ENU10172	ANI61C805:2 233..2634			TBX	AFUc15684				6.5E-95			
26378	ENU10173	ANI61C1077 1:216..4			TBX	AFUc14697				1.4E-103			
26379	ENU10174	ANI61C1077 6:3838..4329			TBX	AFUc21889				1.2E-40			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26380	ENU10175	ANI61C9104:528..4			TBX	AFUc01187				7.3E-40			
26381	ENU10176	ANI61C810:205..2			TBX	CALc05989				8.6E-33			
26382	ENU10177	ANI61C10784:3472..3786			TBX	AFUc14184				3.6E-62			
26383	ENU10178	ANI61C9110:222..683			TBX	AFUc08719				2E-48			
26384	ENU10179	ANI61C9112:7119..6715			TBX	AFUc12106				4.2E-73			
26385	ENU10180	ANI61C1990:33..308			TBX	AFUc15553				7.5E-55			
26386	ENU10181	ANI61C8403:475..2			TBX	AFUc13583				1.4E-64			
26387	ENU10182	ANI61C9135:1669..1460			TBX	CALc05289				7.1E-84			
26388	ENU10183	ANI61C843:2539..2069			TBX	AFUc10565				1.5E-63			
26389	ENU10184	ANI61C847:482..111			TBX	AFUc00801				3.7E-51			
26390	ENU10185	ANI61C9142:131..346			TBX	AFUc01270				3.1E-55			
26391	ENU10186	ANI61C854:619..1			TBX	AFUc15449				1.5E-50			
26392	ENU10187	ANI61C8426:389..1			TBX	AFUc13368				1.2E-34			
26393	ENU10188	ANI61C861:3..675			TBX	"AFUc16323, Y13140"				"1.4e-27, 2.5e-41"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26394	ENU10189	ANI61C9162:1393..776			TBX	AFUc14973				4.9E-32			
26395	ENU10190	ANI61C7710:775..35			TBX	AFUc12089				2.3E-64			
26396	ENU10191	ANI61C7715:3917..4234			TBX	FGRc09602				3.3E-33			
26397	ENU10192	ANI61C7717:6428..6108			TBX	FGRc18440				7.3E-33			
26398	ENU10193	ANI61C880:1600..692			TBX	AFUc05401				7E-61			
26399	ENU10194	ANI61C8450:2030..1656			TBX	AFUc14668				1.6E-40			
26400	ENU10195	ANI61C9184:31..390			TBX	AFUc08030				4.1E-49			
26401	ENU10196	ANI61C7728:1528..953			TBX	AFUc14112				1.2E-37			
26402	ENU10197	ANI61C8457:6314..5572			TBX	"AFUc09443, AFUc09443, FGRc19689, U00093"				"2.2e-54, 7.4e-41, 2.3e-26, 1.7e-34"			
26403	ENU10198	ANI61C8459:2032..1801			TBX	AFUc15223				2.5E-129			
26404	ENU10199	ANI61C8459:9064..8759			TBX	AFUc10030				3E-104			
26405	ENU10200	ANI61C893:2401..2670			TBX	AFUc14162				1.1E-84			
26406	ENU10201	ANI61C7735:754..1065			TBX	AFUc12028				5.3E-40			
26407	ENU10202	ANI61C8480:888..511			TBX	AFUc15553				3.6E-35			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26408	ENU10203	ANI61C8486:3..308			TBX	CALc04830				5.4E-77			
26409	ENU10204	ANI61C8494:3477..2449			TBX	AFUc14523				5E-90			
26410	ENU10205	ANI61C7767:1652..2095			TBX	AFUc05805				6.9E-138			
26411	ENU10206	ANI61C7776:1643..1987			TBX	AFUc10213				1.6E-33			
26412	ENU10207	ANI61S710:8..441			TBX	AFUc01898				7.8E-46			
26413	ENU10208	ANI61S34:6..293			TBX	AFUc09951				4.4E-40			
26414	ENU10209	ANI61S42:40..9..23			TBX	FGRc11175				1.1E-40			
26415	ENU10210	ANI61C4105:15..279			TBX	AFUc15131				2.2E-72			
26416	ENU10211	ANI61C4108:432..3			TBX	AFUc15554				3E-38			
26417	ENU10212	ANI61C3402:1678..1353			TBX	AFUc08075				2.3E-66			
26418	ENU10213	ANI61C4132:581..807			TBX	U00094				"9,4e-22"			
26419	ENU10214	ANI61C4132:1138..1458			TBX	AFUc01742				1.1E-35			
26420	ENU10215	ANI61C4132:3240..3479			TBX	FGRc07284				1.6E-95			
26421	ENU10216	ANI61C3412:711..1163			TBX	AFUc12614				9.6E-40			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26422	ENU10217	ANI61C4144:154..513			TBX	AFUc18185				3E-49			
26423	ENU10218	ANI61C4146:206..6			TBX	AFUc11980				2.7E-48			
26424	ENU10219	ANI61C3427:2300..2070			TBX	AFUc11170				1.1E-32			
26425	ENU10220	ANI61C4157:3987..3415			TBX	"AFUc22639, Y13135"				"1.5e-13, 3.2e-25"			
26426	ENU10221	ANI61C4160:27..296			TBX	AFUc20192				5.3E-35			
26427	ENU10222	ANI61C3443:512..24			TBX	AFUc17062				4.4E-47			
26428	ENU10223	ANI61C4182:2842..3151			TBX	Y13136				2.5e-18			
26429	ENU10224	ANI61C4192:4052..3765			TBX	AFUc14724				3.7E-90			
26430	ENU10225	ANI61C4194:2150..2505			TBX	AFUc11112				1E-37			
26431	ENU10226	ANI61C4195:809..1015			TBX	AFUc11252				5.6E-91			
26432	ENU10227	ANI61C4199:794..1340			TBX	"AFUc01489, AFUc19265"				"9.5e-48, 7.7e-08"			
26433	ENU10228	ANI61C3474:853..3			TBX	AFUc06878				3.1E-82			
26434	ENU10229	ANI61S2581:2..439			TBX	"AFUc18278, CALc04638"				"1.3e-25, 1.3e-31"			
26435	ENU10230	ANI61C3481:424..5			TBX	AFUc10462				1.5E-38			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26436	ENU10231	ANI61S1867:101..544			TBX	AFUc14374				1.7E-68			
26437	ENU10232	ANI61C2763:8..802			TBX	AFUc13692				5.8E-77			
26438	ENU10233	ANI61C2774:525..4			TBX	AFUc14947				1.7E-54			
26439	ENU10234	ANI61C10849:3248..3499			TBX	AFUc10042				4.5E-54			
26440	ENU10235	ANI61C10855:2191..2922			TBX	"AFUc08795, AFUc08853"				"6.4e-78, 1.6e-38"			
26441	ENU10236	ANI61C2798:939..448			TBX	AFUc04411				7.2E-31			
26442	ENU10237	ANI61C900:494..760			TBX	Z71256				9.0e-47			
26443	ENU10238	ANI61C904:1533..1126			TBX	CALc05922				2.2E-46			
26444	ENU10239	ANI61C9202:2010..1717			TBX	FGRc11250				2.3E-79			
26445	ENU10240	ANI61C10888:1767..1118			TBX	AFUc15937				5.5E-34			
26446	ENU10241	ANI61C9214:363..4			TBX	AFUc14249				2.9E-66			
26447	ENU10242	ANI61C9214:2824..2441			TBX	AFUc05949				1.8E-56			
26448	ENU10243	ANI61C10890:82..1020			TBX	"AFUc15972, AFUc15972"				"3.1e-67, 9.1e-74"			
26449	ENU10244	ANI61C10894:3385..2755			TBX	FGRc10423				9.6E-38			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26450	ENU10245	ANI61C9221:1982..2254			TBX	AFUc14012				2.7E-72			
26451	ENU10246	ANI61C936:1465..1980			TBX	AFUc15330				2.4E-132			
26452	ENU10247	ANI61C8502:769..171			TBX	"AFUc03429, AFUc18078"				"2.2e-09, 9.7e-43"			
26453	ENU10248	ANI61C945:2606..1959			TBX	AFUc13932				8.5E-51			
26454	ENU10249	ANI61C945:2854..2606			TBX	AFUc13932				8.5E-51			
26455	ENU10250	ANI61C8510:2200..1793			TBX	AFUc14805				2.3E-52			
26456	ENU10251	ANI61C8529:1547..2065			TBX	FGRc02575				1.3E-33			
26457	ENU10252	ANI61C8537:1088..33			TBX	FGRc10154				5.6E-44			
26458	ENU10253	ANI61C9268:4569..4189			TBX	AFUc20576				3.3E-49			
26459	ENU10254	ANI61C9269:1741..2743			TBX	"AFUc14083, AFUc15534"				"1.9e-19, 5.3e-32"			
26460	ENU10255	ANI61C7811:352..8			TBX	AFUc13321				1.9E-33			
26461	ENU10256	ANI61C9273:2..301			TBX	AFUc05348				2.6E-34			
26462	ENU10257	ANI61C9274:1360..1106			TBX	AFUc10007				9.1E-49			
26463	ENU10258	ANI61C989:1027..1779			TBX	AFUc15375				1.7E-71			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg %	Description
26464	ENU10259	ANI61C7821:1841..2815			TBX	AFUc13640				3.7E-56			
26465	ENU10260	ANI61C8551:1249..2174			TBX	AFUc12117				3E-62			
26466	ENU10261	ANI61C7825:2387..1959			TBX	AFUc07632				2.4E-80			
26467	ENU10262	ANI61C7829:128..622			TBX	AFUc00937				2E-53			
26468	ENU10263	ANI61C9289:219..1253			TBX	AFUc10073				1.4E-40			
26469	ENU10264	ANI61C991:17..562			TBX	AFUc14674				1.4E-69			
26470	ENU10265	ANI61C9294:468..671			TBX	AFUc10456				6E-31			
26471	ENU10266	ANI61C8565:1..585			TBX	AFUc03126				1.9E-62			
26472	ENU10267	ANI61C9295:440..63			TBX	AFUc08217				1.7E-83			
26473	ENU10268	ANI61C8570:8427..8742			TBX	"FGRc03639, U00094"				"6.3e-39, 3.4e-49"			
26474	ENU10269	ANI61C8573:5526..4607			TBX	"FGRc22681, FGRc23949"				"3.2e-16, 5.3e-58"			
26475	ENU10270	ANI61C8575:1282..2046			TBX	AFUc00968				1.5E-62			
26476	ENU10271	ANI61C8580:188..637			TBX	AFUc07749				1.5E-57			
26477	ENU10272	ANI61C7851:2521..2318			TBX	AFUc15780				1.2E-49			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26478	ENU10273	ANI61C7865:1351..1782			TBX	AFUc06805				9E-55			
26479	ENU10274	ANI61C7870:2395..2601			TBX	AFUc12018				1.4E-76			
26480	ENU10275	ANI61C7885:1235..826			TBX	"AFUc00688, AFUc00688"				"2.4e-51, 9.0e-51"			
26481	ENU10276	ANI61C7896:72..566			TBX	AFUc18887				6.5E-44			
26482	ENU10277	ANI61S822:621..386			TBX	"AFUc14236, AFUc14236"				"1.2e-34, 5.1e-39"			
26483	ENU10278	ANI61S3327:45..308			TBX	AFUc15972				2.1E-42			
26484	ENU10279	ANI61C4225:2091..1639			TBX	AFUc15269				7.6E-52			
26485	ENU10280	ANI61C4226:375..13			TBX	Y13137				8.5e-18			
26486	ENU10281	ANI61S853:424..20			TBX	AFUc13855				5.5E-40			
26487	ENU10282	ANI61C4239:596..2			TBX	FGRc11037				4.9E-32			
26488	ENU10283	ANI61C4242:3202..3477			TBX	AFUc14037				5.5E-67			
26489	ENU10284	ANI61C4262:113..679			TBX	AFUc08092				1.8E-56			
26490	ENU10285	ANI61C4263:377..6			TBX	AFUc01021				2E-52			
26491	ENU10286	ANI61C2812:3..762			TBX	"AFUc01646, AFUc11287"				"2.1e-33, 3.4e-46"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	Description
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26493	ENU10288	ANI61C3544: 3554..3094			TBX	AFUc12369				1.4E-40			
26494	ENU10289	ANI61C2817: 373..15			TBX	AFUc15017				1.3E-45			
26495	ENU10290	ANI61C3548: 1461..1129			TBX	FGRc26479				2.3E-41			
26496	ENU10291	ANI61S1939: 606..169			TBX	AFUc13323				3.7E-38			
26497	ENU10292	ANI61C3566: 4239..4448			TBX	Y13136				1.4e-52			
26498	ENU10293	ANI61C1090 0:536..907			TBX	FGRc11747				9.5E-32			
26499	ENU10294	ANI61C3588: 2278..2856			TBX	AFUc13885				2.5E-56			
26500	ENU10295	ANI61C3592: 358..8			TBX	AFUc09097				5.2E-32			
26501	ENU10296	ANI61C1093 2:1213..582			TBX	AFUc15923				1.3E-49			
26502	ENU10297	ANI61C1093 6:2207..1787			TBX	AFUc05492				5.8E-53			
26503	ENU10298	ANI61C1093 7:782..1237			TBX	AFUc14290				2.1E-41			
26504	ENU10299	ANI61C1094 3:423..671			TBX	AFUc17390				6.5E-42			
26505	ENU10300	ANI61C2880: 800..504			TBX	AFUc16447				1.2E-32			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26506	ENU10301	ANI61C2882: 808..1305			TBX	AFUc13856				2.1E-47			
26507	ENU10302	ANI61C2885: 481..783			TBX	AFUc14906				7.3E-35			
26508	ENU10303	ANI61C1096 3:4720..4947			TBX	AFUc01385				2.5E-37			
26509	ENU10304	ANI61C1097 4:6..680			TBX	AFUc09332				2E-40			
26510	ENU10305	ANI61C1097 8:377..102			TBX	AFUc10468				8E-37			
26511	ENU10306	ANI61C9300: 2401..1704			TBX	"AFUc05781, AFUc12769"				"2.7e-47, 2.6e-47"			
26512	ENU10307	ANI61C1098 7:2320..2655			TBX	AFUc21995				2.4E-46			
26513	ENU10308	ANI61C1098 9:469..18			TBX	AFUc12150				4.4E-39			
26514	ENU10309	ANI61C9310: 741..25			TBX	AFUc15016				4E-81			
26515	ENU10310	ANI61C9318: 4838..4473			TBX	AFUc07003				7.7E-89			
26516	ENU10311	ANI61C9326: 1564..1956			TBX	AFUc15104				4.7E-65			
26517	ENU10312	ANI61C8605: 1497..625			TBX	AFUc06416				5.3E-44			
26518	ENU10313	ANI61C8608: 3240..2755			TBX	AFUc04235				4.7E-50			
26519	ENU10314	ANI61C8608: 4091..3681			TBX	AFUc01064				3.8E-53			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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26521	ENU10316	ANI61C9345: 302..3			TBX	AFUc15332				3E-33			
26522	ENU10317	ANI61C8618: 2899..2618			TBX	AFUc15281				1.8E-47			
26523	ENU10318	ANI61C8618: 3589..3119			TBX	AFUc03740				8.5E-36			
26524	ENU10319	ANI61C9355: 543..7			TBX	AFUc15687				9.2E-108			
26525	ENU10320	ANI61C9362: 1959..1529			TBX	AFUc21030				1.2E-35			
26526	ENU10321	ANI61C9363: 1339..866			TBX	AFUc20167				2.7E-42			
26527	ENU10322	ANI61C8635: 1402..1717			TBX	AFUc15942				3.1E-34			
26528	ENU10323	ANI61C9369: 2437..1592			TBX	"AFUc01185, FGRc20865"				"6.1e-20, 2.0e-37"			
26529	ENU10324	ANI61C9377: 955..1296			TBX	AFUc08600				4.6E-38			
26530	ENU10325	ANI61C8649: 3568..3825			TBX	"AFUc09782, FGRc24890"				"2.0e-21, 1.9e-43"			
26531	ENU10326	ANI61C8653: 2070..2574			TBX	AFUc04641				8.6E-43			
26532	ENU10327	ANI61C8656: 2089..2426			TBX	T18724				1.7e-22			
26533	ENU10328	ANI61C9386: 650..2094			TBX	AFUc13410				8.1E-94			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26534	ENU10329	ANI61C8659; 566..294			TBX	AFUc10787				2.7E-74			
26535	ENU10330	ANI61C7939; 1440..1162			TBX	AFUc11560				5.5E-57			
26536	ENU10331	ANI61C8669; 4081..4653			TBX	AFUc05795				9E-47			
26537	ENU10332	ANI61C8672; 12..1160			TBX	AFUc13321				2.5E-89			
26538	ENU10333	ANI61C8685; 144..353			TBX	AFUc13122				2.1E-67			
26539	ENU10334	ANI61C7963; 2540..3006			TBX	AFUc09860				1.6E-37			
26540	ENU10335	ANI61C7988; 556..248			TBX	AFUc03753				7.1E-40			
26541	ENU10336	ANI61C7994; 2406..3131			TBX	AFUc02330				3.1E-48			
26542	ENU10337	ANI61C5025; 1520..773			TBX	AFUc08324				5.2E-49			
26543	ENU10338	ANI61C4311; 338..670			TBX	AFUc03634				4.4E-34			
26544	ENU10339	ANI61C5041; 132..716			TBX	AFUc05209				5.7E-57			
26545	ENU10340	ANI61C4315; 2667..2467			TBX	AFUc14948				4.4E-68			
26546	ENU10341	ANI61C5049; 1100..303			TBX	AFUc02784				4.9E-52			
26547	ENU10342	ANI61C5053; 7..360			TBX	AFUc12855				1.4E-81			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26548	ENU10343	ANI61C3616: 1021..686			TBX	AFUc11581				2E-31			
26549	ENU10344	ANI61C5075: 958..1185			TBX	AFUc14875				2.5E-141			
26550	ENU10345	ANI61C4346: 343..761			TBX	AFUc04097				3.4E-34			
26551	ENU10346	ANI61C3623: 1889..2795			TBX	"AFUc11914, FGRc09621"				"1.9e-72, 9.4e-31"			
26552	ENU10347	ANI61C3623: 400..8			TBX	AFUc15572				3.6E-44			
26553	ENU10348	ANI61C4360: 1029..1415			TBX	AFUc15474				1.7E-128			
26554	ENU10349	ANI61C3634: 888..1166			TBX	AFUc14338				1.6E-116			
26555	ENU10350	ANI61C5094: 8..361			TBX	AFUc08772				6.5E-38			
26556	ENU10351	ANI61C3637: 2145..1699			TBX	AFUc09606				5E-40			
26557	ENU10352	ANI61C2915: 2915..2528			TBX	AFUc11110				5.6E-35			
26558	ENU10353	ANI61C4374: 2149..2712			TBX	Z71256				1.4e-56			
26559	ENU10354	ANI61C3652: 2..604			TBX	AFUc00801				3.7E-35			
26560	ENU10355	ANI61C2931: 8..617			TBX	AFUc08105				1.6E-51			
26561	ENU10356	ANI61C3670: 923..1135			TBX	AFUc11895				3.5E-39			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
26562	ENU10357	ANI61C3672: 455..679			TBX	AFUc15435				6.4E-78			
26563	ENU10358	ANI61C2949: 167..850			TBX	AFUc07056				1.8E-49			
26564	ENU10359	ANI61S2794: 559..104			TBX	AFUc10264				8.5E-70			
26565	ENU10360	ANI61C2968: 1521..2163			TBX	AFUc05625				1E-67			
26566	ENU10361	ANI61C2976: 1861..2472			TBX	AFUc13072				1.6E-80			
26567	ENU10362	ANI61C2982: 515..10			TBX	AFUc08724				5.7E-34			
26568	ENU10363	ANI61C9433: 998..517			TBX	AFUc03107				2.7E-42			
26569	ENU10364	ANI61C9435: 444..31			TBX	AFUc08363				3.8E-34			
26570	ENU10365	ANI61C9442: 3306..2878			TBX	AFUc14805				2E-54			
26571	ENU10366	ANI61C8715: 442..867			TBX	AFUc05950				5.3E-55			
26572	ENU10367	ANI61C8716: 1384..1013			TBX	AFUc14901				3.1E-33			
26573	ENU10368	ANI61C9454: 2260..1922			TBX	AFUc15792				5.4E-55			
26574	ENU10369	ANI61C8731: 1663..2388			TBX	AFUc06663				3.6E-38			
26575	ENU10370	ANI61C8733: 1307..567			TBX	AFUc14363				2E-135			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
26576	ENU10371	ANI61C8739: 765..463			TBX	AFUc10121				4.2E-50			
26577	ENU10372	ANI61C8739: 1268..1017			TBX	AFUc10121				4.2E-50			
26578	ENU10373	ANI61C8740: 6361..5553			TBX	AFUc14582				2.4E-87			
26579	ENU10374	ANI61C9478: 1447..1242			TBX	FGRc11372				6.1E-49			
26580	ENU10375	ANI61C8751: 2625..2849			TBX	AFUc08745				3.6E-45			
26581	ENU10376	ANI61C9484: 671..1048			TBX	AFUc11750				2.5E-71			
26582	ENU10377	ANI61C9484: 1048..1296			TBX	AFUc11750				2.5E-71			
26583	ENU10378	ANI61C8768: 1..699			TBX	AFUc06951				6.8E-57			
26584	ENU10379	ANI61C8774: 1683..1354			TBX	AFUc22116				1.4E-40			
26585	ENU10380	ANI61C8775: 1169..1564			TBX	FGRc11711				1.1E-39			
26586	ENU10381	ANI61C5103: 771..452			TBX	AFUc14207				9.4E-86			
26587	ENU10382	ANI61C4415: 2958..3168			TBX	AFUc14631				5.7E-117			
26588	ENU10383	ANI61C4415: 290..27			TBX	AFUc08588				8.1E-50			
26589	ENU10384	ANI61C4421: 582..1			TBX	AFUc13569				8E-83			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26590	ENU10385	ANI61C5150: 717..1240			TBX	"AFUc01789, AFUc17092"				"5.8e-31, 7.6e-11"			
26591	ENU10386	ANI61C4423: 1282..1818			TBX	AFUc14561				7.7E-32			
26592	ENU10387	ANI61C5159: 698..164			TBX	AFUc08493				9.8E-49			
26593	ENU10388	ANI61C3704: 361..854			TBX	AFUc07782				5.3E-83			
26594	ENU10389	ANI61C4437: 1727..2095			TBX	AFUc10065				7.2E-31			
26595	ENU10390	ANI61C5173: 1175..777			TBX	AFUc15520				3E-125			
26596	ENU10391	ANI61C3725: 729..1112			TBX	AFUc01619				1.6E-47			
26597	ENU10392	ANI61C3734: 34..558			TBX	AFUc16279				7.1E-47			
26598	ENU10393	ANI61C3735: 2099..3050			TBX	AFUc12357				7.2E-77			
26599	ENU10394	ANI61C4464: 433..2			TBX	AFUc07536				1.6E-37			
26600	ENU10395	ANI61C3736: 3424..3224			TBX	AFUc06687				8.9E-35			
26601	ENU10396	ANI61C3737: 281..3			TBX	AFUc09976				1.8E-68			
26602	ENU10397	ANI61C3743: 627..92			TBX	AFUc16169				3.2E-41			
26603	ENU10398	ANI61C3747: 860..1082			TBX	AFUc14515				1.4E-45			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26604	ENU10399	ANI61C3754: 4931..5320			TBX	CALc04204				5.7E-83			
26605	ENU10400	ANI61C4494: 1056..1402			TBX	AFUc03670				2.3E-40			
26606	ENU10401	ANI61C3796: 2333..2704			TBX	AFUc14450				4.8E-34			
26607	ENU10402	ANI61C9500: 803..6			TBX	AFUc15381				1.1E-73			
26608	ENU10403	ANI61C9533: 2882..2592			TBX	FGRc08616				6E-83			
26609	ENU10404	ANI61C8814: 6199..6564			TBX	AFUc16594				4E-32			
26610	ENU10405	ANI61C8818: 3144..3440			TBX	Y13135				2.9e-22			
26611	ENU10406	ANI61C8818: 2206..1928			TBX	AFUc13384				9.4E-45			
26612	ENU10407	ANI61C9551: 2318..2079			TBX	AFUc11576				3E-58			
26613	ENU10408	ANI61C9551: 3060..2512			TBX	AFUc11576				3E-58			
26614	ENU10409	ANI61C9554: 4585..4318			TBX	D50617				1.8e-18			
26615	ENU10410	ANI61C9556: 4609..4214			TBX	AFUc12874				2.1E-53			
26616	ENU10411	ANI61C9556: 5248..4933			TBX	AFUc12874				2.1E-53			
26617	ENU10412	ANI61C8837: 3432..2767			TBX	"AFUc00743, AFUc09194"				"1.8e-11, 9.3e-42"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	Description
26618	ENU10413	ANI61C9577: 5153..5725			TBX	AFUc20879				2.9E-58			
26619	ENU10414	ANI61C9579: 2165..1657			TBX	"AFUc13295, FGRc06579"				"5.7e-31, 1.5e-12"			
26620	ENU10415	ANI61C9585: 845..213			TBX	AFUc11738				6.2E-96			
26621	ENU10416	ANI61C8873: 1147..668			TBX	AFUc04140				1.4E-46			
26622	ENU10417	ANI61C8876: 126..374			TBX	Y13135				1.9e-146			
26623	ENU10418	ANI61C8878: 4257..3709			TBX	AFUc15197				1.1E-100			
26624	ENU10419	ANI61C5200: 1392..2379			TBX	"CALc06185, CALc06185"				"4.1e-37, 5.6e-13"			
26625	ENU10420	ANI61C5207: 48..260			TBX	AFUc15608				1.5E-46			
26626	ENU10421	ANI61C5211: 2..232			TBX	AFUc09688				2.8E-32			
26627	ENU10422	ANI61C5228: 44..370			TBX	AFUc14750				1.2E-90			
26628	ENU10423	ANI61C5238: 983..675			TBX	AFUc13449				1.1E-42			
26629	ENU10424	ANI61C5238: 1776..1549			TBX	AFUc13449				1.1E-42			
26630	ENU10425	ANI61C5240: 938..63			TBX	AFUc14032				1E-65			
26631	ENU10426	ANI61C4514: 588..343			TBX	AFUc08117				2.6E-31			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cavg	% Description
26632	ENU10427	ANI61C5247: 4969..5199			TBX	AFUc13730				1E-97			
26633	ENU10428	ANI61C5248: 347..78			TBX	AFUc14275				2.2E-43			
26634	ENU10429	ANI61C5250: 1..324			TBX	AFUc07874				7.2E-35			
26635	ENU10430	ANI61C4526: 813..1025			TBX	AFUc15744				6.4E-115			
26636	ENU10431	ANI61C4534: 428..664			TBX	AFUc02260				2E-47			
26637	ENU10432	ANI61C4534: 935..1201			TBX	AFUc02260				2E-47			
26638	ENU10433	ANI61C3809: 6632..7087			TBX	AFUc16219				2.6E-60			
26639	ENU10434	ANI61C3822: 2..610			TBX	AFUc11403				4.2E-59			
26640	ENU10435	ANI61C4556: 2..343			TBX	AFUc08005				7.6E-41			
26641	ENU10436	ANI61C3830: 3..292			TBX	FGRc22883				8.1E-33			
26642	ENU10437	ANI61C5291: 887..1411			TBX	AFUc02421				6.6E-51			
26643	ENU10438	ANI61C4576: 332..673			TBX	AFUc14692				3.7E-38			
26644	ENU10439	ANI61C4579: 776..66			TBX	AFUc08897				3.3E-63			
26645	ENU10440	ANI61C4581: 167..460			TBX	AFUc10845				8.7E-34			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
26646	ENU10441	ANI61C4587: 401..2			TBX	FGRc06237				2.7E-37			
26647	ENU10442	ANI61C3885: 720..1126			TBX	"AFUc05920, AFUc05920"				"1.6e-31, 7.0e-60"			
26648	ENU10443	ANI61C3890: 1104..649			TBX	AFUc09816				4.1E-48			
26649	ENU10444	ANI61C9618: 2..465			TBX	AFUc03874				7.4E-63			
26650	ENU10445	ANI61C9634: 5066..4527			TBX	AFUc02404				4.9E-39			
26651	ENU10446	ANI61C9636: 4726..4224			TBX	"FGRc17533, Y13140"				"4.0e-28, 2.3e-26"			
26652	ENU10447	ANI61C9637: 1073..178			TBX	FGRc10589				4.6E-75			
26653	ENU10448	ANI61C8908: 2362..2835			TBX	AFUc15919				3E-49			
26654	ENU10449	ANI61C8910: 391..2			TBX	AFUc04556				3.7E-43			
26655	ENU10450	ANI61C8913: 3476..3057			TBX	AFUc03973				1.5E-35			
26656	ENU10451	ANI61C9642: 1286..852			TBX	FGRc10508				2.7E-48			
26657	ENU10452	ANI61C8921: 2219..2962			TBX	AFUc13687				2.4E-34			
26658	ENU10453	ANI61C8921: 5235..4886			TBX	AFUc08999				3.6E-32			
26659	ENU10454	ANI61C9656: 2345..2824			TBX	AFUc12498				6.1E-46			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26660	ENU10455	ANI61C8932: 646..5			TBX	FGRc06110				9.2E-38			
26661	ENU10456	ANI61C9663: 4438..3729			TBX	AFUc11984				1.2E-63			
26662	ENU10457	ANI61C8941: 837..1202			TBX	AFUc07937				1.5E-56			
26663	ENU10458	ANI61C9673: 3351..2389			TBX	"FGRc06761, FGRc13645"				"4.5e-12, 1.3e-33"			
26664	ENU10459	ANI61C9683: 1130..903			TBX	AFUc14283				1.4E-60			
26665	ENU10460	ANI61C8956: 3704..3153			TBX	AFUc04448				6.7E-60			
26666	ENU10461	ANI61C8958: 282..31			TBX	AFUc03959				2.9E-47			
26667	ENU10462	ANI61C8958: 512..282			TBX	AFUc03959				2.9E-47			
26668	ENU10463	ANI61C8962: 3300..3755			TBX	FGRc11722				2.7E-50			
26669	ENU10464	ANI61C8966: 3485..4861			TBX	AFUc12092				1.2E-83			
26670	ENU10465	ANI61C9697: 3970..3734			TBX	FGRc02733				1.1E-33			
26671	ENU10466	ANI61C9698: 1565..1311			TBX	AFUc09469				6.9E-86			
26672	ENU10467	ANI61C8971: 25..270			TBX	AFUc19130				1.8E-35			
26673	ENU10468	ANI61C8975: 606..31			TBX	AFUc10229				5.8E-58			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26674	ENU10469	ANI61C8980: 13..456			TBX	AFUc15109				1.6E-114			
26675	ENU10470	ANI61C8981: 6167..6614			TBX	AFUc15468				5.5E-156			
26676	ENU10471	ANI61C8986: 5448..5828			TBX	AFUc17681				1.5E-36			
26677	ENU10472	ANI61C8992: 43..387			TBX	AFUc15788				6.5E-46			
26678	ENU10473	ANI61C6020: 1131..769			TBX	AFUc11116				1.4E-44			
26679	ENU10474	ANI61C6020: 1804..1235			TBX	"AFUc11116, AFUc12982"				"1.4e-44, 5.6e-31"			
26680	ENU10475	ANI61C6029: 470..844			TBX	AFUc02496				7.2E-59			
26681	ENU10476	ANI61S4401: 4..495			TBX	Y13139				1.4e-16			
26682	ENU10477	ANI61C5311: 3509..3204			TBX	AFUc15777				7.9E-197			
26683	ENU10478	ANI61C5312: 736..1092			TBX	FGRc00937				2E-39			
26684	ENU10479	ANI61C5313: 2184..3161			TBX	"AFUc08581, FGRc10546"				"1.3e-89, 1.9e-13"			
26685	ENU10480	ANI61C5314: 882..1340			TBX	AFUc14733				9.7E-42			
26686	ENU10481	ANI61S4434: 5..580			TBX	AFUc13932				4.8E-43			
26687	ENU10482	ANI61C6060: 852..4			TBX	AFUc15741				9.1E-144			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26688	ENU10483	ANI61C5339:1771..1418			TBX	AFUc18220				1.3E-41			
26689	ENU10484	ANI61C5346:1293..1616			TBX	AFUc11752				5.5E-32			
26690	ENU10485	ANI61C3905:1127..333			TBX	AFUc02952				2.5E-70			
26691	ENU10486	ANI61C3905:1507..1292			TBX	AFUc13396				3.6E-53			
26692	ENU10487	ANI61C6092:510..307			TBX	AFUc15283				8.6E-35			
26693	ENU10488	ANI61C3908:1013..1393			TBX	AFUc09536				6.1E-57			
26694	ENU10489	ANI61C3916:1331..1672			TBX	AFUc14010				1.5E-102			
26695	ENU10490	ANI61C3922:3..212			TBX	AFUc15201				3.9E-38			
26696	ENU10491	ANI61S3768:482..240			TBX	AFUc08524				9.3E-35			
26697	ENU10492	ANI61C4662:613..335			TBX	AFUc13777				2.1E-40			
26698	ENU10493	ANI61C4670:745..53			TBX	AFUc12006				1.8E-56			
26699	ENU10494	ANI61C3958:1367..1068			TBX	U00093				4.9e-16			
26700	ENU10495	ANI61C3964:5879..6301			TBX	AFUc17957				8.5E-32			
26701	ENU10496	ANI61C3979:1132..3123			TBX	AFUc15917				3.1E-152			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26702	ENU10497	ANI61C1002: 2691..3661			TBX	AFUc11715				9E-91			
26703	ENU10498	ANI61C1002: 2096..1689			TBX	AFUc03394				3.1E-34			
26704	ENU10499	ANI61C3982: 934..1254			TBX	AFUc15781				9.6E-174			
26705	ENU10500	ANI61C1030: 2411..3198			TBX	AFUc10447				2.7E-51			
26706	ENU10501	ANI61C9702: 4068..4367			TBX	"AFUc10199, AFUc10199"				"1.4e-80, 6.8e-74"			
26707	ENU10502	ANI61C1072: 754..13			TBX	AFUc15759				4.6E-43			
26708	ENU10503	ANI61C9726: 653..1			TBX	CALc05491				6.1E-33			
26709	ENU10504	ANI61C9729: 2216..1656			TBX	AFUc14102				5.2E-39			
26710	ENU10505	ANI61C9737: 343..26			TBX	AFUc14470				6.8E-75			
26711	ENU10506	ANI61C9737: 1274..918			TBX	AFUc14470				6.8E-75			
26712	ENU10507	ANI61C9768: 1271..2131			TBX	U00094				3.0e-246			
26713	ENU10508	ANI61C9771: 4119..4642			TBX	AFUc07319				3.7E-53			
26714	ENU10509	ANI61C9776: 5848..5597			TBX	AFUc10732				1.6E-49			
26715	ENU10510	ANI61C9779: 777..364			TBX	Y13137				5.8e-80			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
26716	ENU10511	ANI61C9783: 253..3			TBX	AFUc13340				1.2E-31			
26717	ENU10512	ANI61C9791: 7939..7275			TBX	AFUc11371				4.4E-76			
26718	ENU10513	ANI61C9793: 14..865			TBX	AFUc07854				1.4E-78			
26719	ENU10514	ANI61C6117: 1129..1617			TBX	AFUc09532				2.1E-48			
26720	ENU10515	ANI61S4503: 575..17			TBX	AFUc08015				3.8E-77			
26721	ENU10516	ANI61C5405: 352..44			TBX	AFUc04307				6.2E-38			
26722	ENU10517	ANI61C6134: 666..878			TBX	AFUc12780				4.1E-49			
26723	ENU10518	ANI61C6136: 2170..2385			TBX	AFUc12645				8.3E-105			
26724	ENU10519	ANI61C6143: 352..5			TBX	FGRc15010				5.3E-33			
26725	ENU10520	ANI61C5422: 209..562			TBX	FGRc06384				1.1E-40			
26726	ENU10521	ANI61C4701: 321..94			TBX	AFUc05559				3.7E-89			
26727	ENU10522	ANI61C6167: 85..837			TBX	AFUc14614				1.4E-83			
26728	ENU10523	ANI61C6169: 533..844			TBX	AFUc15069				1.2E-59			
26729	ENU10524	ANI61C4711: 804..5			TBX	AFUc12529				1.2E-107			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26730	ENU10525	ANI61C4714; 1635..1198			TBX	AFUc11891				3.4E-32			
26731	ENU10526	ANI61C4721; 76..363			TBX	AFUc07768				1.4E-58			
26732	ENU10527	ANI61C6180; 963..1289			TBX	AFUc18477				7.1E-38			
26733	ENU10528	ANI61C4733; 77..687			TBX	AFUc13638				1E-38			
26734	ENU10529	ANI61C5462; 921..253			TBX	AFUc14210				6.7E-68			
26735	ENU10530	ANI61C5471; 621..1014			TBX	AFUc14562				3.3E-44			
26736	ENU10531	ANI61C4749; 1693..11490			TBX	AFUc15821				1.7E-128			
26737	ENU10532	ANI61S4583; 51..377			TBX	AFUc15972				1.6E-33			
26738	ENU10533	ANI61C4764; 494..195			TBX	AFUc11693				1.4E-103			
26739	ENU10534	ANI61C4784; 1322..855			TBX	AFUc00822				1.2E-52			
26740	ENU10535	ANI61C4790; 720..457			TBX	AFUc00901				5.3E-36			
26741	ENU10536	ANI61C4796; 1558..2298			TBX	AFUc15050				3E-86			
26742	ENU10537	ANI61C1104; 1273..611			TBX	CALc06186				8E-40			
26743	ENU10538	ANI61C1112; 2794..1976			TBX	AFUc11351				5.1E-46			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26744	ENU10539	ANI61C1120:12513..12740			TBX	CALc03518				2.3E-56			
26745	ENU10540	ANI61C1120:1790..1437			TBX	AFUc15689				1.1E-41			
26746	ENU10541	ANI61C1127:2014..1043			TBX	AFUc11947				1E-105			
26747	ENU10542	ANI61C1135:1766..2113			TBX	AFUc15916				3.1E-98			
26748	ENU10543	ANI61C1137:10..315			TBX	AFUc15972				1.2E-120			
26749	ENU10544	ANI61C1137:430..1264			TBX	AFUc15972				1.2E-120			
26750	ENU10545	ANI61C1138:193..701			TBX	AFUc15803				6.3E-91			
26751	ENU10546	ANI61C1138:1603..1989			TBX	AFUc15803				6.3E-91			
26752	ENU10547	ANI61C1139:5367..5110			TBX	CALc06190				8.4E-44			
26753	ENU10548	ANI61C1141:2040..2351			TBX	AFUc22467				1.9E-71			
26754	ENU10549	ANI61C9807:2386..2132			TBX	AFUc13156				3.2E-40			
26755	ENU10550	ANI61C1183:3285..3707			TBX	AFUc16697				9.8E-57			
26756	ENU10551	ANI61C1188:2..371			TBX	AFUc15915				8.4E-80			
26757	ENU10552	ANI61C1188:4690..4926			TBX	AFUc15848				2.9E-120			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	Description
26758	ENU10553	ANI61C1188: 7009..7704			TBX	AFUc13465				2.6E-50			
26759	ENU10554	ANI61C9827: 4904..4662			TBX	AFUc01941				4.4E-33			
26760	ENU10555	ANI61C1190: 1669..1460			TBX	AFUc19119				3.3E-46			
26761	ENU10556	ANI61C9876: 4899..5639			TBX	AFUc01111				4.6E-51			
26762	ENU10557	ANI61C9878: 1670..1978			TBX	FGRe13922				3.2E-51			
26763	ENU10558	ANI61C9880: 4442..4932			TBX	AFUc19094				8.2E-36			
26764	ENU10559	ANI61C9880: 5038..5410			TBX	AFUc10800				2.7E-74			
26765	ENU10560	ANI61C9880: 1147..719			TBX	AFUc20412				4.8E-39			
26766	ENU10561	ANI61C9882: 5925..6479			TBX	AFUc10536				1.3E-48			
26767	ENU10562	ANI61C9883: 1765..2013			TBX	AFUc03896				9.4E-34			
26768	ENU10563	ANI61C6208: 4005..4583			TBX	AFUc02427				6.4E-42			
26769	ENU10564	ANI61C6220: 228..691			TBX	AFUc13617				7.9E-152			
26770	ENU10565	ANI61S4601: 369..16			TBX	AFUc17622				9.7E-46			
26771	ENU10566	ANI61C5501: 1905..2144			TBX	CALc02466				3.2E-69			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26772	ENU10567	ANI61C5504: 719..1018			TBX	AFUc13011				2.1E-57			
26773	ENU10568	ANI61C5512: 1004..735			TBX	AFUc15725				3.5E-35			
26774	ENU10569	ANI61C5520: 795..3			TBX	AFUc14374				2.6E-96			
26775	ENU10570	ANI61C5524: 479..9			TBX	AFUc05656				7.3E-37			
26776	ENU10571	ANI61C6258: 2595..1909			TBX	AFUc12895				9.4E-66			
26777	ENU10572	ANI61C6260: 36..472			TBX	AFUc12576				4.9E-31			
26778	ENU10573	ANI61C5533: 2815..3542			TBX	Y13134				1.1e-52			
26779	ENU10574	ANI61C4808: 1828..2380			TBX	"AFUc14618, FGRC25347"				"5.2e-76, 1.6e-18"			
26780	ENU10575	ANI61C5543: 286..621			TBX	AFUc17116				3.3E-51			
26781	ENU10576	ANI61C6279: 992..1635			TBX	AFUc10520				3.2E-62			
26782	ENU10577	ANI61C4820: 1166..402			TBX	AFUc12278				1.3E-52			
26783	ENU10578	ANI61C4825: 3..263			TBX	AFUc09182				2.7E-118			
26784	ENU10579	ANI61C4829: 541..759			TBX	AFUc02495				3.4E-45			
26785	ENU10580	ANI61C6294: 245..3			TBX	AFUc05031				1.9E-36			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
26786	ENU10581	ANI61C6299: 603..1086			TBX	AFUc13847				2.2E-59			
26787	ENU10582	ANI61S3944: 5..361			TBX	AFUc14576				2.3E-41			
26788	ENU10583	ANI61C4841: 161..523			TBX	AFUc11703				7.1E-59			
26789	ENU10584	ANI61C4844: 1224..514			TBX	AFUc14922				1.1E-58			
26790	ENU10585	ANI61C5574: 4287..4858			TBX	AFUc12427				3.3E-48			
26791	ENU10586	ANI61C4851: 1359..1936			TBX	AFUc15187				6.8E-127			
26792	ENU10587	ANI61C4852: 465..217			TBX	AFUc11440				2.2E-64			
26793	ENU10588	ANI61C4858: 4225..3968			TBX	AFUc18745				6.1E-58			
26794	ENU10589	ANI61C1213: 666..2015			TBX	"AFUc00755, AFUc11547, AFUc21642"				"7.2e-48, 3.7e-60, 5.5e-50"			
26795	ENU10590	ANI61C1002 1:2042..2257			TBX	Y13137				1.7e-114			
26796	ENU10591	ANI61C1002 1:2807..3483			TBX	Y13137				1.7e-114			
26797	ENU10592	ANI61C1002 1:5043..5705			TBX	Y13137				1.7e-114			
26798	ENU10593	ANI61C1233: 104..469			TBX	AFUc15972				3E-223			
26799	ENU10594	ANI61C1233: 593..2227			TBX	"AFUc15972, AFUc15972"				"2.5e- 220, 3.0e- 223"			

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26800	ENU10595	ANI61C1233: 2461..2855			TBX	AFUc15972				3E-223			
26801	ENU10596	ANI61C1004 5:1756..2355			TBX	U00093				6.3e-36			
26802	ENU10597	ANI61C1004 8:4266..3979			TBX	AFUc15560				2.1E-113			
26803	ENU10598	ANI61C1252: 1331..926			TBX	T18651				3.1e-27			
26804	ENU10599	ANI61C1252: 4561..3724			TBX	"AFUc02348, AFUc12920, AFUc15910"				"2.2e-36, 9.1e-44, 4.0e-38"			
26805	ENU10600	ANI50C1_16 80:2447..609			GSP								
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			5	6									
			-	8									
			4	7									
			6	-									
				1									
				7									
				0									
				4									
26806	ENU10601	ANI61C9631: 1107..3725			GSP								
			2	1									
			5	6									
			-	0									
			4	0									
			3	-									
				1									
				6									
				2									
				0									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nebi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26807	ENU10602	ANI61C7134: 1740..2790	2 5 - 4 7	1 0 2 7 -	GSP								
26808	ENU10603	ANI61C6293: 240..2557	2 5 - 5 1	2 2 7 3 -	GSP								
26809	ENU10604	ANI61C6879: 478..1118	2 5 - 5 0	5 9 7 - 6	GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26810	ENU10605	ANI61C7328: 5293..6820	2	1	GSP								
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			-	2									
			5	9									
			0	-									
				1									
26811	ENU10606	ANI61C1031 8:4988..5776		4	GSP								
				5									
				5									
				7									
			2	7									
			-	2									
26812	ENU10607	ANI61C6288: 9175..4851	5	-	GSP								
			0	7									
				7									
				9									
			2	2									
			5	2									
			-	7									
			5	8									
			0	-									
				2									
				3									
				0									
				7									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26813	ENU10608	ANI61C1025; 943..2449	2	1	GSP								
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			-	1									
			4	5									
			4	-									
				1									
				4									
				3									
				4									
26814	ENU10609	ANI50C8686 _1:101..1327	2	1	GSP								
			5	1									
			-	9									
			4	1									
			6	-									
				1									
				2									
				0									
				9									
26815	ENU10610	ANI61C8855: 1121..3430	2	1	GSP								
			5	9									
			-	6									
			4	8									
			7	-									
				1									
				9									
				9									
				5									

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26816	ENU10611	ANI61C4238:1653..2569			GSP								
26817	ENU10612	ANI61C9758:5232..2829			GSP								
26818	ENU10613	ANI61C9777:4913..3682			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26819	ENU10614	ANI61C9272:2805..4329			GSP								
26820	ENU10615	ANI61C11205:3505..5508			GSP								
26821	ENU10616	ANI61C11368:3956..3354			GSP								
26822	ENU10617	ANI61C3922:221..1201			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26823	ENU10618	ANI61C4244:1752..25			GSP								

26824	ENU10619	ANI61C9662:1762..3272			GSP								
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26825	ENU10620	ANI61C1189:733..2186			GSP								
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Seq num	Seq id	Config source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26826	ENU10621	ANI61C852:1055..1534			GSP								
26827	ENU10622	ANI61C10188:2524..1832			GSP								
26828	ENU10623	ANI61C11064:4467..5468			GSP								
26829	ENU10624	ANI61C10379:2558..3166			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26830	ENU10625	ANI61C8159: 1418..708											
26831	ENU10626	ANI61C4204: 4458..1758											
26832	ENU10627	ANI61C9269: 447..1520											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26833	ENU10628	ANI61C1174: 4..927											
26834	ENU10629	ANI61C1099 8:6512..4967											
26835	ENU10630	ANI61C3343: 3012..1656											

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26836	ENU10631	ANI61C1023 6:138..1026			GSP								
26837	ENU10632	ANI61C9178: 4154..3195			GSP								
26838	ENU10633	ANI61C8787: 2798..117			GSP								
26839	ENU10634	ANI61C1052 2:9..1581			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26840	ENU10635	ANI61C391:1 157..2307			GSP								

26841	ENU10636	ANI61C8594: 354..1610			GSP								
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26842	ENU10637	ANI61C5881: 796..2073			GSP								
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Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26843	ENU10638	ANI61C1067 6:1673..506			GSP								
26844	ENU10639	ANI61C1026 6:639..1493			GSP								
26845	ENU10640	ANI61C9273: 2356..3502			GSP								
26846	ENU10641	ANI61C9135: 1310..282			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26847	ENU10642	ANI61C4057: 12..1370			GSP								
26848	ENU10643	ANI61C5181: 205..730			GSP								
26849	ENU10644	ANI61C5163: 1648..925			GSP								
26850	ENU10645	ANI61C9611: 1060..208			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26851	ENU10646	ANI61C6211: 5848..3572											
26852	ENU10647	ANI61C3390: 1827..500			GSP								
26853	ENU10648	ANI61C405:2 513..1849			GSP								
26854	ENU10649	ANI61C8967: 1333..2100			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26855	ENU10650	ANI61C6915: 231..1067			GSP								
26856	ENU10651	ANI61C9116: 4511..5203			GSP								
26857	ENU10652	ANI61C2197: 153..952			GSP								
26858	ENU10653	ANI61C1026 9:343..52			GSP								
26859	ENU10654	ANI61C309:1 624..2155			GSP								
26860	ENU10655	ANI61C1027 9:3325..3609			GSP								
26861	ENU10656	ANI61C1480: 944..27			GSP								
26862	ENU10657	ANI61C1029 5:2764..2435			GSP								
26863	ENU10658	ANI61C7211: 1755..1192			GSP								
26864	ENU10659	ANI61C7220: 1287..1690			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26865	ENU10660	ANI61C7233:157..435			GSP								
26866	ENU10661	ANI61C6507:412..1250			GSP								
26867	ENU10662	ANI61C7239:1987..1316			GSP								
26868	ENU10663	ANI61C7239:3400..4598			GSP								
26869	ENU10664	ANI61C9301:875..1414			GSP								
26870	ENU10665	ANI61C7262:357..19			GSP								
26871	ENU10666	ANI61C6551:55..1973			GSP								
26872	ENU10667	ANI61C5824:144..1000			GSP								
26873	ENU10668	ANI61C5838:1710..790			GSP								
26874	ENU10669	ANI61S229:21..272			GSP								
26875	ENU10670	ANI61C6580:954..1271			GSP								
26876	ENU10671	ANI61S247:418..18			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26877	ENU10672	ANI61C6599:2219..1887			GSP								
26878	ENU10673	ANI61S277:141..353			GSP								
26879	ENU10674	ANI61C11067:3583..3283	2	3	GSP								
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			-	4									
			4	-									
			6	4									
				1									
				7									
26880	ENU10675	ANI61C2213:588..10			GSP								
26881	ENU10676	ANI61C2215:7849..7241			GSP								
26882	ENU10677	ANI61C2223:191..631			GSP								
26883	ENU10678	ANI61C2224:498..845			GSP								
26884	ENU10679	ANI61C2229:298..57			GSP								
26885	ENU10680	ANI61C11020:275..40			GSP								
26886	ENU10681	ANI61C1505:482..971			GSP								
26887	ENU10682	ANI61C10300:973..1299			GSP								
26888	ENU10683	ANI61C11036:2132..1698			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
26889	ENU10684	ANI61C1030 9:539..240			GSP								
26890	ENU10685	ANI61C1103 8:8033..7008			GSP								
26891	ENU10686	ANI61C1031 6:427..146			GSP								
26892	ENU10687	ANI61C2268: 676..22			GSP								
26893	ENU10688	ANI61C1033 2:196..702			GSP								
26894	ENU10689	ANI61C1033 2:1857..2930			GSP								
26895	ENU10690	ANI61C1106 7:692..997			GSP								
26896	ENU10691	ANI61C1106 9:1488..1817			GSP								
26897	ENU10692	ANI61C1106 9:4255..4617			GSP								
26898	ENU10693	ANI61S1377: 444..11			GSP								
26899	ENU10694	ANI61C1553: 1103..1303			GSP								
26900	ENU10695	ANI61C1108 3:728..460			GSP								
26901	ENU10696	ANI61C2291: 173..520			GSP								
26902	ENU10697	ANI61C2297: 622..891			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26903	ENU10698	ANI61C1036 1:6952..7162			GSP								
26904	ENU10699	ANI61C1036 3:3081..2758			GSP								
26905	ENU10700	ANI61C1109 8:804..166			GSP								
26906	ENU10701	ANI61C425:6 27..833			GSP								
26907	ENU10702	ANI61C8007: 408..139			GSP								
26908	ENU10703	ANI61C7305: 1365..2019			GSP								
26909	ENU10704	ANI61C7309: 528..756			GSP								
26910	ENU10705	ANI61C474:3 7..324			GSP								
26911	ENU10706	ANI61C7312: 392..165			GSP								
26912	ENU10707	ANI61C485:5 84..121			GSP								
26913	ENU10708	ANI61C6606: 379..762			GSP								
26914	ENU10709	ANI61C8075: 1744..2038			GSP								
26915	ENU10710	ANI61C8086: 1038..1379			GSP								
26916	ENU10711	ANI61C7373: 531..97			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26917	ENU10712	ANI61C5924: 515..29			GSP								
26918	ENU10713	ANI61C5924: 1395..1042			GSP								
26919	ENU10714	ANI61C6655: 1840..616			GSP								
26920	ENU10715	ANI61C5930: 14203..14442			GSP								
26921	ENU10716	ANI61C3681: 5295..4159	2	1	GSP								
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			-	9									
			4	3									
			7	-									
				1									
				1									
				1									
				9									
26922	ENU10717	ANI61S2109: 460..123			GSP								
26923	ENU10718	ANI61C5980: 1430..1658			GSP								
26924	ENU10719	ANI61S2115: 504..19			GSP								
26925	ENU10720	ANI61C3012: 2747..2469			GSP								
26926	ENU10721	ANI61C3022: 1523..1266			GSP								
26927	ENU10722	ANI61C2314: 124..425			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26928	ENU10723	ANI61C2339: 4593..5853			GSP								
26929	ENU10724	ANI61S1445: 217..447			GSP								
26930	ENU10725	ANI61C7400: 2503..1237			GSP								
26931	ENU10726	ANI61C3077: 672..14			GSP								
26932	ENU10727	ANI61C1041 1:563..261			GSP								
26933	ENU10728	ANI61S1452: 359..18			GSP								
26934	ENU10729	ANI61C2352: 176..792			GSP								
26935	ENU10730	ANI61S1463: 286..74			GSP								
26936	ENU10731	ANI61C2361: 934..60			GSP								
26937	ENU10732	ANI61C2361: 3052..3372			GSP								
26938	ENU10733	ANI61C1116 5:1645..2411			GSP								

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26939	ENU10734	ANI61C2372: 855..1133			GSP								
26940	ENU10735	ANI61C2372: 1652..2011			GSP								
26941	ENU10736	ANI61C1045 4:4570..4971			GSP								
26942	ENU10737	ANI61C1661: 882..424			GSP								
26943	ENU10738	ANI61C1047 4:160..561			GSP								
26944	ENU10739	ANI61C1047 5:353..12			GSP								
26945	ENU10740	ANI61C1686: 634..265			GSP								
26946	ENU10741	ANI61C511:3 2..511			GSP								
26947	ENU10742	ANI61C511:9 55..2004			GSP								
26948	ENU10743	ANI61C515:5 07..1530			GSP								
26949	ENU10744	ANI61C517:6 36..10			GSP								
26950	ENU10745	ANI61C1697: 907..698			GSP								
26951	ENU10746	ANI61C531:3 13..1072			GSP								
26952	ENU10747	ANI61C534:3 22..579			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	Description
26953	ENU10748	ANI61C8105:335..615			GSP								
26954	ENU10749	ANI61C8112:1340..2031			GSP								
26955	ENU10750	ANI61C567:7098..6774			GSP								
26956	ENU10751	ANI61C8137:682..158			GSP								
26957	ENU10752	ANI61C582:456..62			GSP								
26958	ENU10753	ANI61C8155:4157..3861			GSP								
26959	ENU10754	ANI61C7434:1177..1404			GSP								
26960	ENU10755	ANI61C1400:822..2177			GSP								
26961	ENU10756	ANI61C7438:641..1129			GSP								
26962	ENU10757	ANI61C7441:861..505			GSP								
26963	ENU10758	ANI61C6717:3333..2875			GSP								
26964	ENU10759	ANI61C6721:881..525			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26965	ENU10760	ANI61C6736: 2119..302			GSP								
26966	ENU10761	ANI61C8198: 666..154			GSP								
26967	ENU10762	ANI61C6749: 318..664			GSP								
26968	ENU10763	ANI61C7495: 1744..2273			GSP								
26969	ENU10764	ANI61C6784: 866..1216			GSP								
26970	ENU10765	ANI61C6791: 598..892			GSP								
26971	ENU10766	ANI61S465:1 99..480			GSP								
26972	ENU10767	ANI61C3116: 2211..1954			GSP								
26973	ENU10768	ANI61S2221: 292..5			GSP								
26974	ENU10769	ANI61C4578: 2006..79			GSP								
26975	ENU10770	ANI61C2435: 4559..4236			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
26976	ENU10771	ANI61C2438:2880..3290			GSP								
26977	ENU10772	ANI61C1716:392..141			GSP								
26978	ENU10773	ANI61C10518:691..29			GSP								
26979	ENU10774	ANI61C2452:1114..866			GSP								
26980	ENU10775	ANI61C10529:71..500			GSP								
26981	ENU10776	ANI61C2462:2938..2609			GSP								
26982	ENU10777	ANI61C10532:32..247			GSP								
26983	ENU10778	ANI61C1740:1748..1434			GSP								
26984	ENU10779	ANI61C2478:93..382			GSP								
26985	ENU10780	ANI61C2488:122..484			GSP								
26986	ENU10781	ANI61C11281:107..430			GSP								
26987	ENU10782	ANI61S1594:215..3			GSP								
26988	ENU10783	ANI61C10562:358..78			GSP								
26989	ENU10784	ANI61C10575:448..687			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
26990	ENU10785	ANI61C1057 5:1238..939			GSP								
26991	ENU10786	ANI61C1057 6:1519..1313			GSP								
26992	ENU10787	ANI61C1780: 503..74			GSP								
26993	ENU10788	ANI61C1780: 2749..3104			GSP								
26994	ENU10789	ANI61C1790: 326..98			GSP								
26995	ENU10790	ANI61C1795: 651..301			GSP								
26996	ENU10791	ANI61C1059 9:1166..697			GSP								
26997	ENU10792	ANI61C1005: 159..644			GSP								
26998	ENU10793	ANI61C8215: 808..223			GSP								
26999	ENU10794	ANI61C8218: 800..126			GSP								
27000	ENU10795	ANI61C655:6 67..230			GSP								
27001	ENU10796	ANI61C7509: 665..59			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27002	ENU10797	ANI61C677:1 292..546			GSP								
27003	ENU10798	ANI61C8240: 268..633			GSP								
27004	ENU10799	ANI61C684:1 701..86			GSP								
27005	ENU10800	ANI61C684:2 632..3148			GSP								
27006	ENU10801	ANI61C8250: 1493..2275			GSP								
27007	ENU10802	ANI61C8253: 771..224			GSP								
27008	ENU10803	ANI61C694:3 6..966			GSP								
27009	ENU10804	ANI61C695:5 18..132			GSP								
27010	ENU10805	ANI61C8260: 2107..2690			GSP								
27011	ENU10806	ANI61C8262: 1584..640			GSP								
27012	ENU10807	ANI61C7534: 74..592			GSP								
27013	ENU10808	ANI61C7539: 125..505			GSP								
27014	ENU10809	ANI61C7551: 383..763			GSP								
27015	ENU10810	ANI61C7552: 17..358			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27016	ENU10811	ANI61C6825:1110..1553			GSP								
27017	ENU10812	ANI61C6826:892..1134			GSP								
27018	ENU10813	ANI61C8285:680..1088			GSP								
27019	ENU10814	ANI61C1118:8:1202..234			GSP								
27020	ENU10815	ANI61C6833:47..594			GSP								
27021	ENU10816	ANI61C6845:1225..1545			GSP								
27022	ENU10817	ANI61C6869:444..49			GSP								
27023	ENU10818	ANI61C6876:1362..467			GSP								
27024	ENU10819	ANI61S544:296..29			GSP								
27025	ENU10820	ANI61C3201:1463..2118			GSP								
27026	ENU10821	ANI61C3206:906..20			GSP								
27027	ENU10822	ANI61C3220:676..904			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27028	ENU10823	ANI61C3223:111..491			GSP								
27029	ENU10824	ANI61S582:342..4			GSP								
27030	ENU10825	ANI61S1603:33..296			GSP								
27031	ENU10826	ANI61C2502:1047..297			GSP								
27032	ENU10827	ANI61S3077:561..69			GSP								
27033	ENU10828	ANI61C11316:726..373			GSP								
27034	ENU10829	ANI61S2355:2..446			GSP								
27035	ENU10830	ANI61C11323:1295..421			GSP								
27036	ENU10831	ANI61C11334:127..375			GSP								
27037	ENU10832	ANI61S2374:80..323			GSP								
27038	ENU10833	ANI61C2548:2501..2814			GSP								
27039	ENU10834	ANI61C10612:640..35			GSP								
27040	ENU10835	ANI61S2386:120..347			GSP								
27041	ENU10836	ANI61C1820:1305..1067			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27042	ENU10837	ANI61C2551:593..144			GSP								
27043	ENU10838	ANI61C1825:96..480			GSP								
27044	ENU10839	ANI61C1827:63..511			GSP								
27045	ENU10840	ANI61C2557:358..11			GSP								
27046	ENU10841	ANI61S1665:225..14			GSP								
27047	ENU10842	ANI61C2564:1021..556			GSP								
27048	ENU10843	ANI61C2564:3000..3693			GSP								
27049	ENU10844	ANI61C2565:1843..1553			GSP								
27050	ENU10845	ANI61C1136 0:423..744			GSP								
27051	ENU10846	ANI61C1136 1:314..753			GSP								
27052	ENU10847	ANI61C1136 5:615..94			GSP								
27053	ENU10848	ANI61C1137 0:1053..437			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id cvrg	Description
27054	ENU10849	ANI61C9801:936..1955			GSP							
27055	ENU10850	ANI61C1851:237..13			GSP							
27056	ENU10851	ANI61C1859:689..332			GSP							
27057	ENU10852	ANI61C10650:256..8			GSP							
27058	ENU10853	ANI61C10666:40..318			GSP							
27059	ENU10854	ANI61C701:124..521			GSP							
27060	ENU10855	ANI61C705:573..153			GSP							
27061	ENU10856	ANI61C9000:2961..3380			GSP							
27062	ENU10857	ANI61C1887:209..448			GSP							
27063	ENU10858	ANI61C9010:1196..1606			GSP							
27064	ENU10859	ANI61C1893:30..260			GSP							
27065	ENU10860	ANI61C738:725..203			GSP							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27066	ENU10861	ANI61C749:5 6..721			GSP								
27067	ENU10862	ANI61C8311: 1091..738			GSP								
27068	ENU10863	ANI61C757:1 84..432			GSP								
27069	ENU10864	ANI61C8057: 25-47 3974..1828		1810- 1833	GSP								
27070	ENU10865	ANI61C7601: 60..910			GSP								
27071	ENU10866	ANI61C7603: 2760..2347			GSP								
27072	ENU10867	ANI61C9066: 2978..2667			GSP								
27073	ENU10868	ANI61C9077: 4407..4640			GSP								
27074	ENU10869	ANI61C8352: 1633..964			GSP								
27075	ENU10870	ANI61C7626: 1366..2139			GSP								
27076	ENU10871	ANI61C7627: 1790..1413			GSP								
27077	ENU10872	ANI61C6902: 58..303			GSP								
27078	ENU10873	ANI61C6902: 849..1115			GSP								
27079	ENU10874	ANI61C7631: 30..399			GSP								
27080	ENU10875	ANI61C9094: 1157..593			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
27081	ENU10876	ANI61C6912: 1483..1817			GSP								
27082	ENU10877	ANI61C7644: 445..945			GSP								
27083	ENU10878	ANI61C8385: 774..119			GSP								
27084	ENU10879	ANI61C6940: 1685..2623			GSP								
27085	ENU10880	ANI61S606:3 3..278			GSP								
27086	ENU10881	ANI61C7683: 56..815			GSP								
27087	ENU10882	ANI61C7685: 651..899			GSP								
27088	ENU10883	ANI61C6973: 58..857			GSP								
27089	ENU10884	ANI61C4000: 2436..2718			GSP								
27090	ENU10885	ANI61C38:27 80..4266			GSP								
27091	ENU10886	ANI61C6988: 654..79			GSP								
27092	ENU10887	ANI61C4014: 1281..1520			GSP								
27093	ENU10888	ANI61C47:51 6..59			GSP								
27094	ENU10889	ANI61C4030: 795..365			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27095	ENU10890	ANI61C4033: 64..360			GSP								
27096	ENU10891	ANI61S3149: 137..451			GSP								
27097	ENU10892	ANI61C4041: 33..770			GSP								
27098	ENU10893	ANI61C3319: 449..210			GSP								
27099	ENU10894	ANI61C87:13 60..758			GSP								
27100	ENU10895	ANI61C90:28 ..383			GSP								
27101	ENU10896	ANI61C9734: 25-46 136..1020		755-777	GSP								
27102	ENU10897	ANI61C4069: 483..163			GSP								
27103	ENU10898	ANI61C1140 4:3057..1670			GSP								
27104	ENU10899	ANI61C1140 5:362..983			GSP								
27105	ENU10900	ANI61C1140 8:48..1109			GSP								
27106	ENU10901	ANI61C4075: 1168..899			GSP								
27107	ENU10902	ANI61S1726: 161..580			GSP								
27108	ENU10903	ANI61C2623: 769..1152			GSP								
27109	ENU10904	ANI61C3354: 1852..823			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27110	ENU10905	ANI61C4083:600..292			GSP								
27111	ENU10906	ANI61C2631:569..96			GSP								
27112	ENU10907	ANI61C2634:575..63			GSP								
27113	ENU10908	ANI61C4098:3119..2841			GSP								
27114	ENU10909	ANI61C11437:2736..3185			GSP								
27115	ENU10910	ANI61C1911:743..462			GSP								
27116	ENU10911	ANI61C1917:658..913			GSP								
27117	ENU10912	ANI61C3375:274..515			GSP								
27118	ENU10913	ANI61C726:125-43519..2739	25-43	1184-1203	GSP								
27119	ENU10914	ANI61C3384:522..319			GSP								
27120	ENU10915	ANI61C11453:1122..904			GSP								
27121	ENU10916	ANI61C10726:39..550			GSP								
27122	ENU10917	ANI61S1762:138..449			GSP								
27123	ENU10918	ANI61C10728:504..109			GSP								
27124	ENU10919	ANI61C11458:498..226			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27125	ENU10920	ANI61C1936:1249..1759			GSP								
27126	ENU10921	ANI61C3394:507..1723			GSP								
27127	ENU10922	ANI61C3396:134..527			GSP								
27128	ENU10923	ANI61C1939:555..292			GSP								
27129	ENU10924	ANI61C11463:2680..3042			GSP								
27130	ENU10925	ANI61S1771:153..362			GSP								
27131	ENU10926	ANI61C2671:319..23			GSP								
27132	ENU10927	ANI61C2672:34..605			GSP								
27133	ENU10928	ANI61C10746:1645..1439			GSP								
27134	ENU10929	ANI61C1950:26..509			GSP								
27135	ENU10930	ANI61C1955:841..1119			GSP								
27136	ENU10931	ANI61C10773:3044..2808			GSP								
27137	ENU10932	ANI61C1987:421..25			GSP								
27138	ENU10933	ANI61C9739:25-451081..2142		1020-1044	GSP								
27139	ENU10934	ANI61C815:505..807			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvr%	Description
27140	ENU10935	ANI61C9119:670..385			GSP								
27141	ENU10936	ANI61C1993:578..104			GSP								
27142	ENU10937	ANI61C1079:7:3932..3549			GSP								
27143	ENU10938	ANI61C9132:954..398			GSP								
27144	ENU10939	ANI61C840:4:9..456			GSP								
27145	ENU10940	ANI61C849:1:187..1681			GSP								
27146	ENU10941	ANI61C876:1:590..2086			GSP								
27147	ENU10942	ANI61C7712:42..2293			GSP								
27148	ENU10943	ANI61C9179:6801..6508			GSP								
27149	ENU10944	ANI61C881:8:19..1067			GSP								
27150	ENU10945	ANI61C7726:1811..2377			GSP								
27151	ENU10946	ANI61C9186:546..1025			GSP								
27152	ENU10947	ANI61C7728:17..352			GSP								
27153	ENU10948	ANI61C8461:1237..130			GSP								

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27154	ENU10949	ANI61C7733: 545..1042			GSP								
27155	ENU10950	ANI61C8464: 2369..2686			GSP								
27156	ENU10951	ANI61C9194: 509..45			GSP								
27157	ENU10952	ANI61C7738: 773..1078			GSP								
27158	ENU10953	ANI61C8477: 600..325			GSP								
27159	ENU10954	ANI61C7750: 935..549			GSP								
27160	ENU10955	ANI61C8483: 2739..1493			GSP								
27161	ENU10956	ANI61C7758: 582..1060			GSP								
27162	ENU10957	ANI61C8488: 2420..2040			GSP								
27163	ENU10958	ANI61S10:38 8..158			GSP								
27164	ENU10959	ANI61C7772: 1779..2054			GSP								
27165	ENU10960	ANI61S704:2 90..69			GSP								
27166	ENU10961	ANI61C7784: 33..440			GSP								
27167	ENU10962	ANI61S3210: 133..504			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27168	ENU10963	ANI61S54:41 6..84			GSP								
27169	ENU10964	ANI61S57:40 5..27			GSP								
27170	ENU10965	ANI61C4111: 381..989			GSP								
27171	ENU10966	ANI61C4118: 1219..627			GSP								
27172	ENU10967	ANI61S62:39 2..105			GSP								
27173	ENU10968	ANI61C4136: 1820..2838			GSP								
27174	ENU10969	ANI61S80:90. .302			GSP								
27175	ENU10970	ANI61C8145: 25-48 425..2575	1462- 1497		GSP								
27176	ENU10971	ANI61S786:8 57..26			GSP								
27177	ENU10972	ANI61C2704: 1830..1507			GSP								
27178	ENU10973	ANI61C4171: 1698..76			GSP								
27179	ENU10974	ANI61C3448: 29..325			GSP								
27180	ENU10975	ANI61C3467: 382..22			GSP								
27181	ENU10976	ANI61C3469: 29..429			GSP								
27182	ENU10977	ANI61C2740: 1333..855			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27183	ENU10978	ANI61C2762: 566..303			GSP								
27184	ENU10979	ANI61C6697: 25-46	428-456		GSP								
27185	ENU10980	ANI61S1889: 2040..2513			GSP								
27186	ENU10981	ANI61C1085 3:912..3556			GSP								
27187	ENU10982	ANI61C1085 7:388..684			GSP								
27188	ENU10983	ANI61C2796: 651..1025			GSP								
27189	ENU10984	ANI61C910:2 343..2119			GSP								
27190	ENU10985	ANI61C1088 3:1002..601			GSP								
27191	ENU10986	ANI61C9218: 232..642			GSP								
27192	ENU10987	ANI61C927:2 538..2790			GSP								
27193	ENU10988	ANI61C9232: 396..1202			GSP								
27194	ENU10989	ANI61C944:1 483..1128			GSP								
27195	ENU10990	ANI61C8518: 97..1204			GSP								
27196	ENU10991	ANI61C950:3 56..47			GSP								
27197	ENU10992	ANI61C8529: 4191..4479			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	Description
27198	ENU10993	ANI61C963:1 068..1394			GSP								
27199	ENU10994	ANI61C9261: 723..1335			GSP								
27200	ENU10995	ANI61C8533: 199..436			GSP								
27201	ENU10996	ANI61C8534: 3831..4522			GSP								
27202	ENU10997	ANI61C8539: 1603..2387			GSP								
27203	ENU10998	ANI61C8543: 3298..2891			GSP								
27204	ENU10999	ANI61C7818: 15..251			GSP								
27205	ENU11000	ANI61C9283: 759..70			GSP								
27206	ENU11001	ANI61C9284: 569..336			GSP								
27207	ENU11002	ANI61C9284: 2239..1572			GSP								
27208	ENU11003	ANI61C7852: 17..259			GSP								
27209	ENU11004	ANI61C7868: 1327..541			GSP								
27210	ENU11005	ANI61C7532: 25-48 5139..3735		1200- 1227	GSP								
27211	ENU11006	ANI61C7889: 134..827			GSP								
27212	ENU11007	ANI61C4201: 651..966			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrq	Description
27213	ENU11008	ANI61C4231:1045..2050			GSP								
27214	ENU11009	ANI61C4240:1802..1443			GSP								
27215	ENU11010	ANI61S870:75..413			GSP								
27216	ENU11011	ANI61S887:533..71			GSP								
27217	ENU11012	ANI61S1900:242..36			GSP								
27218	ENU11013	ANI61S3362:59..322			GSP								
27219	ENU11014	ANI61C4253:25-50390..2994	2512-2538		GSP								
27220	ENU11015	ANI61C2823:703..311			GSP								
27221	ENU11016	ANI61S1936:3..307			GSP								
27222	ENU11017	ANI61C3564:2741..2421			GSP								
27223	ENU11018	ANI61C4294:945..11			GSP								
27224	ENU11019	ANI61C10903:2408..2130			GSP								
27225	ENU11020	ANI61C10909:1207..1480			GSP								
27226	ENU11021	ANI61C3574:621..271			GSP								
27227	ENU11022	ANI61C2851:338..80			GSP								

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27228	ENU11023	ANI61S1970:107..523			GSP								
27229	ENU11024	ANI61S1976:453..38			GSP								
27230	ENU11025	ANI61C1094:6:2971..3210			GSP								
27231	ENU11026	ANI61C1095:9:692..1021			GSP								
27232	ENU11027	ANI61C1097:4:8651..8980			GSP								
27233	ENU11028	ANI61C9307:2060..1566			GSP								
27234	ENU11029	ANI61C9309:71..346			GSP								
27235	ENU11030	ANI61C1098:8:2218..2525			GSP								
27236	ENU11031	ANI61C9318:1056..1424			GSP								
27237	ENU11032	ANI61C9320:2160..1305			GSP								
27238	ENU11033	ANI61C8612:2892..3431			GSP								
27239	ENU11034	ANI61C9350:97..312			GSP								
27240	ENU11035	ANI61C8622:2619..3263			GSP								
27241	ENU11036	ANI61C7901:1559..1341			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27242	ENU11037	ANI61C9361:557..778			GSP								
27243	ENU11038	ANI61C7928:221..433			GSP								
27244	ENU11039	ANI61C8660:282..67			GSP								
27245	ENU11040	ANI61C8665:843..43			GSP								
27246	ENU11041	ANI61C436:1 008..310	25-56	654-681	GSP								
27247	ENU11042	ANI61S4105:384..647			GSP								
27248	ENU11043	ANI61C7982:418..837			GSP								
27249	ENU11044	ANI61S913:2 1..650			GSP								
27250	ENU11045	ANI61S914:2 87..17			GSP								
27251	ENU11046	ANI61C7994:2149..1727			GSP								
27252	ENU11047	ANI61C5022:120..566			GSP								
27253	ENU11048	ANI61C5038:51..367			GSP								
27254	ENU11049	ANI61C4328:1036..666			GSP								
27255	ENU11050	ANI61S3430:399..154			GSP								
27256	ENU11051	ANI61S3435:47..548			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27257	ENU11052	ANI61C3604:172..483			GSP								
27258	ENU11053	ANI61C5067:528..11			GSP								
27259	ENU11054	ANI61C4339:641..103			GSP								
27260	ENU11055	ANI61S3440:247..33			GSP								
27261	ENU11056	ANI61C4340:1106..646			GSP								
27262	ENU11057	ANI61C8097:25-52180..794		572-597	GSP								
27263	ENU11058	ANI61C3625:410..209			GSP								
27264	ENU11059	ANI61C4355:23..1006			GSP								
27265	ENU11060	ANI61S986:244..16			GSP								
27266	ENU11061	ANI61S987:230..502			GSP								
27267	ENU11062	ANI61C2904:49..527			GSP								
27268	ENU11063	ANI61C5091:394..26			GSP								
27269	ENU11064	ANI61C5092:565..249			GSP								
27270	ENU11065	ANI61C5099:1694..1380			GSP								
27271	ENU11066	ANI61S3475:342..2			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27272	ENU11067	ANI61C2911: 1220..756			GSP								
27273	ENU11068	ANI61C4375: 338..66			GSP								
27274	ENU11069	ANI61C2923: 988..683			GSP								
27275	ENU11070	ANI61C2924: 567..58			GSP								
27276	ENU11071	ANI61C4383: 1284..1505			GSP								
27277	ENU11072	ANI61C4385: 10..543			GSP								
27278	ENU11073	ANI61C4389: 577..53			GSP								
27279	ENU11074	ANI61C3666: 851..1157			GSP								
27280	ENU11075	ANI61C3670: 903..583			GSP								
27281	ENU11076	ANI61C2943: 480..108			GSP								
27282	ENU11077	ANI61C3673: 423..752			GSP								
27283	ENU11078	ANI61S2784: 42..286			GSP								
27284	ENU11079	ANI61S2792: 253..29			GSP								
27285	ENU11080	ANI61C1079 25-54 862-885 6:999..38			GSP								
27286	ENU11081	ANI61C2976: 3215..3739			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27287	ENU11082	ANI61C9474: 2006..1695			GSP								
27288	ENU11083	ANI61C9475: 1862..2135			GSP								
27289	ENU11084	ANI61C9481: 340..26			GSP								
27290	ENU11085	ANI61C9499: 889..464			GSP								
27291	ENU11086	ANI61C8783: 2134..2337			GSP								
27292	ENU11087	ANI61C8799: 28..1591			GSP								
27293	ENU11088	ANI61C5127: 68..277			GSP								
27294	ENU11089	ANI61S4237: 505..147			GSP								
27295	ENU11090	ANI61C4403: 855..487			GSP								
27296	ENU11091	ANI61S4245: 186..659			GSP								
27297	ENU11092	ANI61C5140: 608..366			GSP								
27298	ENU11093	ANI61C5144: 91..574			GSP								
27299	ENU11094	ANI61C4085: 25-47		936-966	GSP								
27300	ENU11095	ANI61C4425: 2781..1798			GSP								
27301	ENU11096	ANI61C5154: 126..658			GSP								

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27302	ENU11097	ANI61C4426:792..16			GSP								
27303	ENU11098	ANI61S2803:83..411			GSP								
27304	ENU11099	ANI61C4434:789..1070			GSP								
27305	ENU11100	ANI61C3707:581..356			GSP								
27306	ENU11101	ANI61C4437:1858..1610			GSP								
27307	ENU11102	ANI61S4274:82..586			GSP								
27308	ENU11103	ANI61C4445:611..33			GSP								
27309	ENU11104	ANI61C4451:567..883			GSP								
27310	ENU11105	ANI61C3725:1341..1595			GSP								
27311	ENU11106	ANI61S2831:248..25			GSP								
27312	ENU11107	ANI61S3566:727..473			GSP								
27313	ENU11108	ANI61S4296:106..351			GSP								
27314	ENU11109	ANI61C3734:851..1099			GSP								
27315	ENU11110	ANI61S2840:557..300			GSP								

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27316	ENU11111	ANI61C3754: 3331..3726			GSP								
27317	ENU11112	ANI61C3761: 33..389			GSP								
27318	ENU11113	ANI61C3784: 637..260			GSP								
27319	ENU11114	ANI61C3784: 972..1225			GSP								
27320	ENU11115	ANI61C3791: 28..648			GSP								
27321	ENU11116	ANI61C9503: 1086..832			GSP								
27322	ENU11117	ANI61C8804: 20..376			GSP								
27323	ENU11118	ANI61C9553: 5754..6136			GSP								
27324	ENU11119	ANI61C8826: 1028..2376			GSP								
27325	ENU11120	ANI61C9579: 588..247			GSP								
27326	ENU11121	ANI61C8850: 1149..554			GSP								
27327	ENU11122	ANI61C9580: 3119..2889			GSP								
27328	ENU11123	ANI61C8890: 3006..2620			GSP								
27329	ENU11124	ANI61C8891: 1547..1314			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27330	ENU11125	ANI61C5220: 1262..1491			GSP								
27331	ENU11126	ANI61C5238: 81..503			GSP								
27332	ENU11127	ANI61C5252: 605..1027			GSP								
27333	ENU11128	ANI61C4533: 1007..711			GSP								
27334	ENU11129	ANI61C4533: 2262..1912			GSP								
27335	ENU11130	ANI61C3806: 151..459			GSP								
27336	ENU11131	ANI61C3809: 6367..6092			GSP								
27337	ENU11132	ANI61C3812: 348..16			GSP								
27338	ENU11133	ANI61C3815: 562..307			GSP								
27339	ENU11134	ANI61C3815: 6632..6285			GSP								
27340	ENU11135	ANI61C5276: 503..1318			GSP								
27341	ENU11136	ANI61S4389: 224..466			GSP								
27342	ENU11137	ANI61C4583: 4..691			GSP								
27343	ENU11138	ANI61C4597: 362..54			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	nchi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27344	ENU11139	ANI61C4598: 261..16			GSP								
27345	ENU11140	ANI61C3886: 1166..825			GSP								
27346	ENU11141	ANI61C3899: 60..866			GSP								
27347	ENU11142	ANI61C9645: 5205..5854			GSP								
27348	ENU11143	ANI61C9648: 1307..840			GSP								
27349	ENU11144	ANI61C8929: 1859..827			GSP								
27350	ENU11145	ANI61C8933: 1160..88			GSP								
27351	ENU11146	ANI61C8942: 950..555			GSP								
27352	ENU11147	ANI61C8948: 816..145			GSP								
27353	ENU11148	ANI61C9689: 786..439			GSP								
27354	ENU11149	ANI61C9699: 2047..1317			GSP								
27355	ENU11150	ANI61C7193: 25-47 105..1342		1140- 1164	GSP								
27356	ENU11151	ANI61C6005: 960..1552			GSP								
27357	ENU11152	ANI61C6014: 452...31			GSP								
27358	ENU11153	ANI61C5308: 1104..1550			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27359	ENU11154	ANI61C6037: 45..452			GSP								
27360	ENU11155	ANI61C6049: 2643..2927			GSP								
27361	ENU11156	ANI61C6054: 617..180			GSP								
27362	ENU11157	ANI61C5326: 269..673			GSP								
27363	ENU11158	ANI61C6063: 548..247			GSP								
27364	ENU11159	ANI61C4630: 121..563			GSP								
27365	ENU11160	ANI61C5365: 985..1310			GSP								
27366	ENU11161	ANI61S4484: 249..611			GSP								
27367	ENU11162	ANI61C3921: 953..1335			GSP								
27368	ENU11163	ANI61C3921: 2779..2390			GSP								
27369	ENU11164	ANI61C4653: 2087..1719			GSP								
27370	ENU11165	ANI61C4654: 1614..1315			GSP								
27371	ENU11166	ANI61C4658: 914..174			GSP								
27372	ENU11167	ANI61S3763: 74..559			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27373	ENU11168	ANI61S4495: 234..452			GSP								
27374	ENU11169	ANI61C3933: 549..114			GSP								
27375	ENU11170	ANI61C3937: 797..354			GSP								
27376	ENU11171	ANI61C3940: 21..232			GSP								
27377	ENU11172	ANI61C3954: 1326..1063			GSP								
27378	ENU11173	ANI61C4685: 757..491			GSP								
27379	ENU11174	ANI61C3958: 501..89			GSP								
27380	ENU11175	ANI61C4696: 280..56			GSP								
27381	ENU11176	ANI61C1004: 2019..2340			GSP								
27382	ENU11177	ANI61C1014: 3306..3527			GSP								
27383	ENU11178	ANI61C3998: 32..373			GSP								
27384	ENU11179	ANI61C1032: 460..155			GSP								
27385	ENU11180	ANI61C1050: 1319..1113			GSP								
27386	ENU11181	ANI61C1081: 596..850			GSP								

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27387	ENU11182	ANI61C1081: 1717..1370			GSP								
27388	ENU11183	ANI61C1088: 486..65			GSP								
27389	ENU11184	ANI61C9367: 25-48 576..1483		810-840	GSP								
27390	ENU11185	ANI61C9731: 1230..467			GSP								
27391	ENU11186	ANI61C9798: 2618..2337			GSP								
27392	ENU11187	ANI61C6101: 8..893			GSP								
27393	ENU11188	ANI61C6110: 857..23			GSP								
27394	ENU11189	ANI61C6122: 1618..2008			GSP								
27395	ENU11190	ANI61C6131: 1130..355			GSP								
27396	ENU11191	ANI61C5407: 71..948			GSP								
27397	ENU11192	ANI61C5427: 773..264			GSP								
27398	ENU11193	ANI61C4706: 860..402			GSP								
27399	ENU11194	ANI61C4711: 1595..1891			GSP								
27400	ENU11195	ANI61C4715: 142..424			GSP								
27401	ENU11196	ANI61S3828: 200..523			GSP								

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27402	ENU11197	ANI61S3837: 675..343			GSP								
27403	ENU11198	ANI61C6195: 476..60			GSP								
27404	ENU11199	ANI61C4750: 755..522			GSP								
27405	ENU11200	ANI61C4753: 1269..856			GSP								
27406	ENU11201	ANI61C5487: 642..219			GSP								
27407	ENU11202	ANI61C4762: 97..372			GSP								
27408	ENU11203	ANI61C4787: 1230..1449			GSP								
27409	ENU11204	ANI61C1100: 115..802			GSP								
27410	ENU11205	ANI61C1111: 455..45			GSP								
27411	ENU11206	ANI61C1111: 3679..4110			GSP								
27412	ENU11207	ANI61C1120: 7823..8526			GSP								
27413	ENU11208	ANI61C1169: 843..553			GSP								
27414	ENU11209	ANI61C9822: 1217..123			GSP								
27415	ENU11210	ANI61C9829: 4024..3818			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	Description
27416	ENU11211	ANI61C1192: 974..1474			GSP								
27417	ENU11212	ANI61C9847: 6199..6726			GSP								
27418	ENU11213	ANI61C9867: 1066..34			GSP								
27419	ENU11214	ANI61C9891: 452..243			GSP								
27420	ENU11215	ANI61C9899: 47..334			GSP								
27421	ENU11216	ANI61C6223: 92..463			GSP								
27422	ENU11217	ANI61S4621: 277..516			GSP								
27423	ENU11218	ANI61C5522: 613..402			GSP								
27424	ENU11219	ANI61C6258: 4017..4280			GSP								
27425	ENU11220	ANI61C4802: 291..4			GSP								
27426	ENU11221	ANI61C5533: 1131..1565			GSP								
27427	ENU11222	ANI61C5535: 1669..2031			GSP								
27428	ENU11223	ANI61C6268: 1609..1048			GSP								
27429	ENU11224	ANI61C4818: 1055..79			GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
27430	ENU11225	ANI61C6280: 695..384			GSP								
27431	ENU11226	ANI61C1085 25-42	1030-		GSP								
		5:1314..247		1050									
27432	ENU11227	ANI61C6289: 635..118			GSP								
27433	ENU11228	ANI61C5562: 115..501			GSP								
27434	ENU11229	ANI61C4861: 232..549			GSP								
27435	ENU11230	ANI61C4883: 540..944			GSP								
27436	ENU11231	ANI61C4886: 692..387			GSP								
27437	ENU11232	ANI61C4888: 735..28			GSP								
27438	ENU11233	ANI61C1000 5:1..846			GSP								
27439	ENU11234	ANI61C1212: 2420..1437			GSP								
27440	ENU11235	ANI61C1212: 7293..7081			GSP								
27441	ENU11236	ANI61C1215: 1067..828			GSP								
27442	ENU11237	ANI61C1001 9:66..374			GSP								
27443	ENU11238	ANI61C1001 9:1431..1786			GSP								
27444	ENU11239	ANI61S1058: 463..56			GSP								

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27445	ENU11240	ANI61C1002 4:388..146			GSP								
27446	ENU11241	ANI61C1004 2:147..493			GSP								
27447	ENU11242	ANI61C3535: 25-47 237..1526	1027-	1050	GSP								
27448	ENU11243	ANI61C5361: 25-49 1482..2129	606-630		GSP								
27449	ENU11244	ANI61C1043 25-43 6:4516..4046	434-453		GSP								
27450	ENU11245	ANI61C8290: 25-50 534..196	296-321		GSP								
27451	ENU11246	ANI61C8406: 25-48 1268..512	723-747		GSP								
27452	ENU11247	ANI61C3560: 25-50 547..1	736-762		GSP								
27453	ENU11248	ANI61C9221: 25-48 3343..4865	1159-	1182	GSP								
27454	ENU11249	ANI61C9335: 25-53 79..726	605-630		GSP								
27455	ENU11250	ANI61C4319: 25-48 596..2490	1770-	1794	GSP								
27456	ENU11251	ANI61C1135 25-54 4:738..97	598-624		GSP								
27457	ENU11252	ANI61C9630: 25-54 6026..5230	693-723		GSP								
27458	ENU11253	ANI61C3:451 25-49 ..1	487-516		GSP								
27459	ENU11254	ANI61C3101: 25-56 38..1916	1124-	1152	GSP								
27460	ENU11255	ANI61C7406: 25-51 933..374	473-492		GSP								
27461	ENU11256	ANI61C2199: 25-42 808..1	822-843		GSP								
27462	ENU11257	ANI61C1140 25-44 4:2738..1670	829-855		GSP								

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27465	ENU11260	ANI61C8506: 25-53 1702..2790	25-53	1048-1071	GSP								
27466	ENU11261	ANI61C5:911 25-44 ..522	25-44	347-372	GSP								
27467	ENU11262	ANI61C2228: 25-47 1078..400	25-47	588-612	GSP								
27468	ENU11263	ANI61C1229: 25-52 10663..12053	25-52	1031-1053	GSP								
27469	ENU11264	ANI61C2474: 25-48 1094..1708	25-48	571-597	GSP								
27470	ENU11265	ANI61C3401: 25-44 3819..1936	25-44	1674-1692	GSP								
27471	ENU11266	ANI61C7804: 25-49 2471..609	25-49	1714-1740	GSP								
27472	ENU11267	ANI61C1413: 25-52 4385..3561	25-52	773-807	GSP								
27473	ENU11268	ANI61C1078 25-48 6:2202..968	25-48	957-984	GSP								
27474	ENU11269	ANI61C3185: 25-47 2066..1480	25-47	549-573	GSP								
27475	ENU11270	ANI61C9745: 25-50 501..1022	25-50	481-504	GSP								
27476	ENU11271	ANI61C1075 25-48 6:864..2078	25-48	1174-1197	GSP								
27477	ENU11272	ANI61C8415: 25-53 2475..2142	25-53	550-579	GSP								
27478	ENU11273	ANI61C147:1 25-59 080..515	25-59	506-534	GSP								
27479	ENU11274	ANI61C8168: 25-45 313..669	25-45	312-339	GSP								
27480	ENU11275	ANI61C297:5 25-47 607..4879	25-47	697-726	GSP								
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		713..2196		1269									
27485	ENU11280	ANI61C7096:	25-42	1035-	GSP								
		132..1272		1062									
27486	ENU11281	ANI61C1232:	25-45	1117-	GSP								
		2724..1345		1146									
27487	ENU11282	ANI61C1097	25-49	733-750	GSP								
		9:137..967											
27488	ENU11283	ANI61C5397:	25-43	1232-	GSP								
		1095..2412		1254									
27489	ENU11284	ANI61C3282:	25-48	979-1005	GSP								
		159..1181											
27490	ENU11285	ANI61C9348:	25-53	797-819	GSP								
		3299..2421											
27491	ENU11286	ANI61C4800:	25-43	1279-	GSP								
		1832..3077		1311									
27492	ENU11287	ANI61C4256:	25-51	493-516	GSP								
		566..33											
27493	ENU11288	ANI61C1134	25-50	810-834	GSP								
		6:1472..487											
27494	ENU11289	ANI61C4213:	25-47	758-780	GSP								
		1527..671											
27495	ENU11290	ANI61C479:3	25-49	395-423	GSP								
		3..473											
27496	ENU11291	ANI61C6489:	25-48	2459-	GSP								
		268..3596		2490									
27497	ENU11292	ANI61C2618:	25-51	836-858	GSP								
		90..965											
27498	ENU11293	ANI61C5742:	25-43	473-495	GSP								
		957..452											
27499	ENU11294	ANI61C1141	25-56	1066-	GSP								
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27503	ENU11298	ANI61C1072: 2588..3558	ANI61C1072: 25-51	862-891	GSP								
27504	ENU11299	ANI61C1075: 2..1.831	ANI61C1075: 25-53	1134-1167	GSP								
27505	ENU11300	ANI61C1651: 2327..2689	ANI61C1651: 25-51	324-345	GSP								
27506	ENU11301	ANI61C4544: 485..1764	ANI61C4544: 25-47	872-897	GSP								
27507	ENU11302	ANI61C9753: 495..1130	ANI61C9753: 25-55	589-618	GSP								
27508	ENU11303	ANI61C1040: 4..3494..3038	ANI61C1040: 25-48	438-459	GSP								
27509	ENU11304	ANI61C3663: 53..781	ANI61C3663: 25-50	685-711	GSP								
27510	ENU11305	ANI61C8074: 1760..2561	ANI61C8074: 25-52	625-654	GSP								
27511	ENU11306	ANI61C8623: 4801..5229	ANI61C8623: 25-48	405-435	GSP								
27512	ENU11307	ANI61C9552: 2908..1237	ANI61C9552: 25-46	1428-1458	GSP								
27513	ENU11308	ANI61C6472: 135..851	ANI61C6472: 25-48	674-699	GSP								
27514	ENU11309	ANI61C1041: 7..735..1262	ANI61C1041: 25-45	487-510	GSP								
27515	ENU11310	ANI61C1006: 2144..2787	ANI61C1006: 25-45	609-630	GSP								
27516	ENU11311	ANI61C8909: 2220..2828	ANI61C8909: 25-54	571-594	GSP								
27517	ENU11312	ANI61C895:3 078..1361	ANI61C895:3 25-50	1010-1035	GSP								
27518	ENU11313	ANI61C7397: 7..963	ANI61C7397: 25-48	906-939	GSP								
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27522	ENU11317	ANI61C7548: 25-48 252..899	597-630	25-48	GSP								
27523	ENU11318	ANI61C9033: 25-52 2175..2843	1093-1116	25-52	GSP								
27524	ENU11319	ANI61C5893: 25-54 133..714	543-567	25-54	GSP								
27525	ENU11320	ANI61C2666: 25-46 4964..4109	755-780	25-46	GSP								
27526	ENU11321	ANI61C9776: 25-50 4636..2066	2275-2298	25-50	GSP								
27527	ENU11322	ANI61C9714: 25-48 1172..687	445-468	25-48	GSP								
27528	ENU11323	ANI61C1103 25-46 8:1841..956	808-828	25-46	GSP								
27529	ENU11324	ANI61C9251: 25-51 4545..3844	660-684	25-51	GSP								
27530	ENU11325	ANI61C6165: 25-42 297..605	267-291	25-42	GSP								
27531	ENU11326	ANI61C1252: 25-48 2607..4768	1486-1509	25-48	GSP								
27532	ENU11327	ANI61C7675: 25-48 2330..4510	1935-1959	25-48	GSP								
27533	ENU11328	ANI61C1022 25-44 7:997..1659	627-645	25-44	GSP								
27534	ENU11329	ANI61C1026 25-55 0:857..2059	906-930	25-55	GSP								
27535	ENU11330	ANI61C1019 25-46 8:23..1003	858-885	25-46	GSP								
27536	ENU11331	ANI61C7931: 25-48 674..357	276-300	25-48	GSP								
27537	ENU11332	ANI61C7943: 25-45 3406..2876	488-513	25-45	GSP								
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27541	ENU11336	ANI61C7650: 1237..711	25-53	585-615	GSP								
27542	ENU11337	ANI61C5313: 1474..102	25-57	941-969	GSP								
27543	ENU11338	ANI61C3043: 526..89	25-46	398-420	GSP								
27544	ENU11339	ANI61C1139: 383..1322	25-47	732-759	GSP								
27545	ENU11340	ANI61C598:2 020..685	25-43	1250-1269	GSP								
27546	ENU11341	ANI61C3699: 3386..3921	25-46	773-795	GSP								
27547	ENU11342	ANI61C9796: 2338..905	25-48	1264-1290	GSP								
27548	ENU11343	ANI61C1118 2:4620..4006	25-45	565-597	GSP								
27549	ENU11344	ANI61C8725: 211..1294	25-43	951-975	GSP								
27550	ENU11345	ANI61C9321: 11..1124	25-43	1005-1023	GSP								
27551	ENU11346	ANI61C58:13 11..730	25-48	540-564	GSP								
27552	ENU11347	ANI61C5896: 1167..1736	25-43	520-552	GSP								
27553	ENU11348	ANI61C1880: 75..1179	25-47	1009-1032	GSP								
27554	ENU11349	ANI61C768:4 9..747	25-44	664-681	GSP								
27555	ENU11350	ANI61C4397: 3721..4874	25-44	967-999	GSP								
27556	ENU11351	ANI61C893:3 49..780	25-45	391-414	GSP								
27557	ENU11352	ANI61C9103: 2711..1350	25-58	1288-1314	GSP								

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27560	ENU11355	ANI61C7392: 25-48	25-48	655-678	GSP								
27561	ENU11356	ANI61C7053: 25-60	25-60	541-573	GSP								
27562	ENU11357	ANI61C1804: 25-47	25-47	755-774	GSP								
27563	ENU11358	ANI61C1355: 25-52	25-52	584-609	GSP								
27564	ENU11359	ANI61C2838: 25-45	25-45	295-321	GSP								
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27567	ENU11362	ANI61C4813: 25-45	25-45	531-555	GSP								
27568	ENU11363	ANI61C1814: 25-52	25-52	911-939	GSP								
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27571	ENU11366	ANI61C4359: 25-49	25-49	1760-1791	GSP								
27572	ENU11367	ANI61C260:7 25-46	25-46	381-405	GSP								
27573	ENU11368	ANI61C136:2 25-47	25-47	542-567	GSP								
27574	ENU11369	ANI61C5892: 25-49	25-49	511-537	GSP								
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27579	ENU11374	ANI61C6754: 2578..2977	25-47	354-387	GSP								
27580	ENU11375	ANI61C1695: 2048..1590	25-53	412-441	GSP								
27581	ENU11376	ANI61C9665: 1466..933	25-44	499-516	GSP								
27582	ENU11377	ANI61C5460: 418..86	25-53	289-315	GSP								
27583	ENU11378	ANI61C8016: 4563..5658	25-47	1001-1026	GSP								
27584	ENU11379	ANI61C1032: 6:526..126	25-52	368-390	GSP								
27585	ENU11380	ANI50C1_16: 62:883..2658	25-51	2072-2097	GSP								
27586	ENU11381	ANI61C1043: 3:6045..5383	25-46	636-657	GSP								
27587	ENU11382	ANI61C1800: 2853..4234	25-44	1264-1281	GSP								
27588	ENU11383	ANI61C1118: 5:6336..4674	25-48	1323-1350	GSP								
27589	ENU11384	ANI61C7218: 2298..1016	25-46	1191-1212	GSP								
27590	ENU11385	ANI61C1135: 0:1359..814	25-45	502-528	GSP								
27591	ENU11386	ANI61C7821: 120..1235	25-43	1004-1029	GSP								
27592	ENU11387	ANI61C1030: 0:6596..8562	25-47	1600-1626	GSP								
27593	ENU11388	ANI61C7114: 919..1173	25-48	210-240	GSP								
27594	ENU11389	ANI61C8869: 652..1	25-54	1118-1143	GSP								
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27598	ENU11393	ANI61C5231: 1674..696	25-44	894-918	GSP								
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27600	ENU11395	ANI61C9195: 1475..1239	25-47	194-219	GSP								
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27603	ENU11398	ANI61C9071: 1813..3126	25-46	1206-1230	GSP								
27604	ENU11399	ANI61C1739: 1900..2871	25-42	850-873	GSP								
27605	ENU11400	ANI50S1653: 430..35	25-49	349-378	GSP								
27606	ENU11401	ANI61C3457: 487..1486	25-50	962-987	GSP								
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27610	ENU11405	ANI61C5924: 5506..6654	25-45	1108-1131	GSP								
27611	ENU11406	ANI61C5371: 689..107	25-43	329-348	GSP								
27612	ENU11407	ANI61C2188: 18..500	25-44	443-465	GSP								
27613	ENU11408	ANI61C5986: 769..1257	25-46	448-471	GSP								
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27618	ENU11413	ANI61C2256: 25-47 1735..606	25-47	1025-1047	GSP								
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27621	ENU11416	ANI61C5574: 25-48 2590..856	25-48	1435-1467	GSP								
27622	ENU11417	ANI61C4363: 25-42 1260..137	25-42	1043-1062	GSP								
27623	ENU11418	ANI61C1099 25-49 7:2080..108	25-49	1061-1086	GSP								
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27632	ENU11427	ANI61C7519: 25-48 2104..4116	25-48	1284-1308	GSP								
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27636	ENU11431	ANI61C9760: 25-50 2594..369	25-50	1439-1461	GSP								
27637	ENU11432	ANI61C5994: 25-48 3589..4155	25-48	520-549	GSP								
27638	ENU11433	ANI61C4612: 25-48 4670..4903	25-48	194-216	GSP								
27639	ENU11434	ANI61C685:2 25-50 982..777	25-50	1514-1545	GSP								
27640	ENU11435	ANI61C651:2 25-48 322..3137	25-48	628-660	GSP								
27641	ENU11436	ANI61C6088: 25-45 217..1433	25-45	986-1008	GSP								
27642	ENU11437	ANI61C1141 25-48 7:554..1688	25-48	1045-1068	GSP								
27643	ENU11438	ANI61C9830: 25-47 3483..3914	25-47	381-414	GSP								
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27646	ENU11441	ANI61C637:4 25-49 88..1102	25-49	574-597	GSP								
27647	ENU11442	ANI61C1148: 25-43 2120..742	25-43	1163-1182	GSP								
27648	ENU11443	ANI61C3716: 25-55 1618..917	25-55	655-684	GSP								
27649	ENU11444	ANI61C9449: 25-53 9108..9936	25-53	684-708	GSP								
27650	ENU11445	ANI61C5861: 25-46 1042..596	25-46	407-429	GSP								
27651	ENU11446	ANI61C3679: 25-44 1524..2664	25-44	1044-1068	GSP								
27652	ENU11447	ANI61C232:9 25-60 06..2267	25-60	1218-1248	GSP								

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27656	ENU11451	ANI61C1467: 2609..701	25-60	1564-1587	GSP								
27657	ENU11452	ANI61C9661: 943..2650	25-42	1463-1491	GSP								
27658	ENU11453	ANI61C1899: 279..1569	25-49	1051-1077	GSP								
27659	ENU11454	ANI61C314:3 569..3009	25-45	523-543	GSP								
27660	ENU11455	ANI61C4652: 4539..3879	25-45	623-642	GSP								
27661	ENU11456	ANI61C7344: 553..1427	25-46	717-744	GSP								
27662	ENU11457	ANI61C1102: 1007..399	25-49	533-552	GSP								
27663	ENU11458	ANI61C1103 0:990..2243	25-48	1184-1206	GSP								
27664	ENU11459	ANI61C5963: 1484..775	25-48	683-711	GSP								
27665	ENU11460	ANI61C2577: 1..920	25-45	853-876	GSP								
27666	ENU11461	ANI61C7847: 934..2031	25-55	943-966	GSP								
27667	ENU11462	ANI61C1359: 1154..759	25-47	355-378	GSP								
27668	ENU11463	ANI61C4272: 1785..2238	25-52	406-435	GSP								
27669	ENU11464	ANI61C3320: 3935..2344	25-49	1488-1518	GSP								
27670	ENU11465	ANI61C3350: 544..3	25-46	508-528	GSP								
27671	ENU11466	ANI61C9980: 1297..2692	25-48	1290-1317	GSP								

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27674	ENU11469	ANI61C1124 25-58 9:1741..316	25-58	1238-1266	GSP								
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27676	ENU11471	ANI61C8854: 25-48 2501..3411	25-48	854-879	GSP								
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27678	ENU11473	ANI61C7173: 25-50 5929..5225	25-50	533-564	GSP								
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27683	ENU11478	ANI61C9211: 25-43 841..463	25-43	342-363	GSP								
27684	ENU11479	ANI61C6804: 25-47 8679..9269	25-47	550-573	GSP								
27685	ENU11480	ANI61C2881: 25-48 505..23	25-48	432-465	GSP								
27686	ENU11481	ANI61C8985: 25-42 1757..702	25-42	854-882	GSP								
27687	ENU11482	ANI61C5083: 25-47 691..329	25-47	327-345	GSP								
27688	ENU11483	ANI61C1139 25-48 7:3768..2577	25-48	1118-1143	GSP								
27689	ENU11484	ANI61C6772: 25-51 2789..4449	25-51	904-936	GSP								
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27694	ENU11489	AN161C1040 1:3381..2461	25-52	879-903	GSP								
27695	ENU11490	AN161C9107: 478..1571	25-53	748-774	GSP								
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27697	ENU11492	AN161C964:1 083..1	25-42	788-807	GSP								
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27703	ENU11498	AN161C4106: 533..1172	25-55	475-498	GSP								
27704	ENU11499	AN161C7970: 2763..3219	25-51	416-438	GSP								
27705	ENU11500	AN150S6383: 13..372	25-54	321-342	GSP								
27706	ENU11501	AN161C6472: 1637..1182	25-54	411-438	GSP								
27707	ENU11502	AN161C8244: 480..770	25-46	249-273	GSP								
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27712	ENU11507	ANI61C2688: 3750..5147	25-48	1090-1116	GSP								
27713	ENU11508	ANI61S105:2 47..513	25-45	227-249	GSP								
27714	ENU11509	ANI61C4242: 1336..1031	25-49	261-288	GSP								
27715	ENU11510	ANI61C6934: 803..97	25-60	2030-2055	GSP								
27716	ENU11511	ANI61S829:4 54..167	25-54	238-270	GSP								
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27718	ENU11513	ANI61C2577: 1478..1074	25-53	499-519	GSP								
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27720	ENU11515	ANI61C1100 0:3720..4763	25-48	778-807	GSP								
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27722	ENU11517	ANI61C8731: 4102..1416	25-43	1465-1494	GSP								
27723	ENU11518	ANI61C7573: 436..885	25-44	405-432	GSP								
27724	ENU11519	ANI61C9156: 597..73	25-43	485-507	GSP								
27725	ENU11520	ANI61C3399: 2610..1263	25-49	1236-1263	GSP								
27726	ENU11521	ANI61C7310: 4839..4856	25-53	1031-1056	GSP								
27727	ENU11522	ANI61C2940: 436..59	25-48	325-360	GSP								
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27731	ENU11526	ANI61C9171: 25-48 1959..597		1111- 1146	GSP								
27732	ENU11527	ANI61C59:18 25-43 74..3318		1276- 1296	GSP								
27733	ENU11528	ANI61C7697: 25-51 2063..382		1409- 1440	GSP								
27734	ENU11529	ANI61C3180: 25-48 248..1172		633-660	GSP								
27735	ENU11530	ANI61C1148 25-45 4:737..1733		821-846	GSP								
27736	ENU11531	ANI61C3701: 25-48 3089..3358		228-252	GSP								
27737	ENU11532	ANI61C1060 25-42 3:2742..1457		1103- 1128	GSP								
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27739	ENU11534	ANI61C2468: 25-45 2924..3410		492-522	GSP								
27740	ENU11535	ANI61C7430: 25-46 3283..2845		704-735	GSP								
27741	ENU11536	ANI61C634:3 25-49 6..485		406-432	GSP								
27742	ENU11537	ANI61C3266: 25-54 674..1356		579-603	GSP								
27743	ENU11538	ANI61C6843: 25-52 2045..170		1757- 1779	GSP								
27744	ENU11539	ANI61C3259: 25-49 62..382		280-303	GSP								
27745	ENU11540	ANI61C4194: 25-50 1485..760		583-606	GSP								
27746	ENU11541	ANI61C315:3 25-51 283..272		469-495	GSP								
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27751	ENU11546	ANI61C6630: 25-47 696..15	25-47	744-777	GSP								
27752	ENU11547	ANI61C820:3 25-49 69..3066	25-49	2398- 2427	GSP								
27753	ENU11548	ANI61C1141: 25-49 2:2065..47	25-49	1873- 1899	GSP								
27754	ENU11549	ANI61C7335: 25-48 1416..449	25-48	787-816	GSP								
27755	ENU11550	ANI61C9065: 25-48 1508..2387	25-48	771-789	GSP								
27756	ENU11551	ANI61C1097: 25-45 1:1328..959	25-45	339-369	GSP								
27757	ENU11552	ANI61C1019: 25-49 8:2425..1513	25-49	729-759	GSP								
27758	ENU11553	ANI61C1185: 25-47 6136..6688	25-47	508-528	GSP								
27759	ENU11554	ANI61C5675: 25-44 3999..3514	25-44	445-468	GSP								
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27765	ENU11560	ANI61C1066: 25-53 1:361..53	25-53	269-291	GSP								
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27770	ENU11565	ANI6IC6174: 25-55 219..701	25-55	439-465	GSP								
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27777	ENU11572	ANI6IC8881: 25-44 3578..2998	25-44	482-507	GSP								
27778	ENU11573	ANI6IC7430: 25-45 3283..2845	25-45	352-375	GSP								
27779	ENU11574	ANI6IS3448: 25-48 395..218	25-48	422-447	GSP								
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27782	ENU11577	ANI6IC8293: 25-42 1673..986	25-42	274-294	GSP								
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27784	ENU11579	ANI6IC7782: 25-48 8..383	25-48	360-381	GSP								
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27849	ENU11644	ANI61C2961: 25-47 959..1987	25-47	781-804	GSP								
27850	ENU11645	ANI61C22:16 25-48 50..714	25-48	776-801	GSP								
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27865	ENU11660	ANI61C2443: 1157..1	25-50	774-801	GSP								
27866	ENU11661	ANI61C6248: 10252..9321	25-45	843-864	GSP								
27867	ENU11662	ANI61C1005: 5:3484..1762	25-45	1427-1458	GSP								
27868	ENU11663	ANI61C1046: 1:4279..2095	25-52	756-786	GSP								
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27884	ENU11679	ANI61C4188: 1815..3383	25-48	1065-1089	GSP								
27885	ENU11680	ANI61C5311: 2759..1507	25-48	925-948	GSP								
27886	ENU11681	ANI61C2779: 2334..1374	25-48	775-795	GSP								
27887	ENU11682	ANI61C4134: 4953..3776	25-42	969-996	GSP								
27888	ENU11683	ANI61C5248: 1625..2642	25-42	1025-1047	GSP								
27889	ENU11684	ANI61C1087: 2908..1902	25-48	858-891	GSP								
27890	ENU11685	ANI61C9702: 2743..385	25-51	1257-1281	GSP								
27891	ENU11686	ANI61C9303: 3713..1422	25-52	1421-1446	GSP								
27892	ENU11687	ANI61C1430: 5584..6726	25-53	872-894	GSP								
27893	ENU11688	ANI61C1047 7:4876..3341	25-50	1328-1356	GSP								
27894	ENU11689	ANI61C1109 9:5640..6853	25-44	886-909	GSP								
27895	ENU11690	ANI61C1143 2:415..1658	25-52	916-939	GSP								
27896	ENU11691	ANI61C9343: 1..526	25-49	1083-1113	GSP								
27897	ENU11692	ANI61C1120 1:5787..4364	25-50	1182-1209	GSP								
27898	ENU11693	ANI61C5332: 998..3326	25-45	1300-1323	GSP								
27899	ENU11694	ANI61C1025 1:5404..3484	25-46	825-849	GSP								

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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27901	ENU11696	ANI61C4871: 2313..3456	25-55	808-837	GSP								
27902	ENU11697	ANI61C9878: 1865..495	25-51	857-888	GSP								
27903	ENU11698	ANI61C8876: 1031..2327	25-49	1119-1149	GSP								
27904	ENU11699	ANI61C6064: 2164..4140	25-42	919-942	GSP								
27905	ENU11700	ANI61C6256: 5207..4223	25-48	834-858	GSP								
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27907	ENU11702		26-43	756-779	CDS	U75428							
27908	ENU11703		22-45	761-779	CDS	X84015							
27909	ENU11704		48-71	754-779	CDS	U34740							
27910	ENU11705		40-63	756-779	CDS	U12427							
27911	ENU11706		37-60	750-779	CDS	AB014886							
27912	ENU11707		37-60	755-779	CDS	AF019254							
27913	ENU11708		34-57	754-779	CDS	Z68905							
27914	ENU11709		31-54	752-779	CDS	M59705							
27915	ENU11710		31-54	756-779	CDS	Z68904							
27916	ENU11711		29-54	751-779	CDS	U34740							
27917	ENU11712		29-52	750-779	CDS	U03904							
27918	ENU11713		28-51	756-779	CDS	U83658							
27919	ENU11714		26-49	747-779	CDS	X82827							
27920	ENU11715		26-46	756-779	CDS	U75347							
27921	ENU11716		25-48	748-779	CDS	AF032987							
27922	ENU11717		25-48	749-779	CDS	U40146							
27923	ENU11718		24-47	756-779	CDS	AF016850							
27924	ENU11719		24-47	750-779	CDS	AJ003163							
27925	ENU11720		24-47	754-779	CDS	AF112473							
27926	ENU11721		24-51	756-779	CDS	U25693							
27927	ENU11722		23-47	754-779	CDS	X82289							
27928	ENU11723		23-46	755-779	CDS	U34740							
27929	ENU11724		23-51	752-779	CDS	D21268							
27930	ENU11725		22-44	751-779	CDS	U56100							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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27932	ENU11727		22-48	750-779	CDS	D83246							
27933	ENU11728		22-45	744-779	CDS	U62895							
27934	ENU11729		22-51	758-779	CDS	AB000125							
27935	ENU11730		22-48	750-779	CDS	U52362							
27936	ENU11731		22-48	747-779	CDS	M58289							
27937	ENU11732		22-57	757-779	CDS	M83232							
27938	ENU11733		22-45	750-779	CDS	Y15996							
27939	ENU11734		25-42	712-729	CDS	D10019							
27940	ENU11735		25-53	712-738	CDS	X15441							
27941	ENU11736		25-48	845-867	CDS	U63728							
27942	ENU11737		25-48	1004-1026	CDS	Z80341							
27943	ENU11738		25-45	1021-1038	CDS	AF041976							
27944	ENU11739		25-49	1099-1116	CDS	U28804							
27945	ENU11740		25-44	1257-1275	CDS	L41670							
27946	ENU11741		25-44	1257-1275	CDS	AJ001836							
27947	ENU11742		25-48	1321-1344	CDS	X15479							
27948	ENU11743		25-50	1383-1404	CDS	U89675							
27949	ENU11744		25-43	1389-1413	CDS	Z49834							
27950	ENU11745		25-45	1404-1425	CDS	U59148							
27951	ENU11746		25-45	1606-1626	CDS	M16371							
27952	ENU11747		25-48	1643-1662	CDS	AF055287							
27953	ENU11748		25-44	1991-2016	CDS	U21220							
27954	ENU11749		25-46	2041-2064	CDS	AF027213							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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27957	ENU11752		25-46	300-321	CDS	M96993							
27958	ENU11753		25-45	365-390	CDS	U12632							
27959	ENU11754		25-45	377-402	CDS	X55547							
27960	ENU11755		25-46	404-429	CDS	J05545							
27961	ENU11756		25-50	418-441	CDS	X13525							
27962	ENU11757		25-50	418-441	CDS	X04696							
27963	ENU11758		25-48	443-462	CDS	U75874							
27964	ENU11759		25-49	497-525	CDS	D32070							
27965	ENU11760		25-45	573-600	CDS	Y08866							
27966	ENU11761		25-53	630-657	CDS	Z49892							
27967	ENU11762		25-51	646-672	CDS	AJ001837							
27968	ENU11763		25-47	742-762	CDS	U34740							
27969	ENU11764		25-44	758-777	CDS	U96847							
27970	ENU11765		25-48	778-804	CDS	M19132							
27971	ENU11766		25-45	945-969	CDS	X13525							
27972	ENU11767		25-44	1002-1029	CDS	M16196							
27973	ENU11768		25-44	1024-1046	CDS	Z49875							
27974	ENU11769		25-51	1031-1053	CDS	AF032988							
27975	ENU11770		25-48	1087-1107	CDS	M22869							
27976	ENU11771		25-46	1114-1135	CDS	AJ001157							
27977	ENU11772		25-44	1222-1242	CDS	AF098669							
27978	ENU11773		25-45	1258-1278	CDS	M20631							
27979	ENU11774		25-43	1270-1293	CDS	AF029318							
27980	ENU11775		25-43	1270-1293	CDS	U19394							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvg	% Description
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27983	ENU11778		25-48	1299-1323	CDS	M17519							
27984	ENU11779		25-48	1305-1329	CDS	M17520							
27985	ENU11780		25-44	1403-1423	CDS	S79392							
27986	ENU11781		25-48	1451-1473	CDS	M16197							
27987	ENU11782		25-43	1466-1494	CDS	AF043230							
27988	ENU11783		25-52	1473-1500	CDS	U34740							
27989	ENU11784		25-45	1654-1680	CDS	U73194							
27990	ENU11785		25-57	1803-1827	CDS	X71807							
27991	ENU11786		25-49	2356-2376	CDS	Z83333							
27992	ENU11787		25-44	2367-2394	CDS	AF023156							
27993	ENU11788		25-47	2485-2508	CDS	Z54244							
27994	ENU11789		25-50	2842-2865	CDS	D87895							
27995	ENU11790		25-45	2894-2922	CDS	L36341							
27996	ENU11791		25-46	2931-2952	CDS	AF043332							
27997	ENU11792		25-46	2931-2952	CDS	AF036763							
27998	ENU11793		25-51	188-219	CDS	AF016187							
27999	ENU11794		25-48	215-246	CDS	AJ011295							
28000	ENU11795		25-51	232-264	CDS	U81827							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	% cvrg	Description
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28002	ENU11797		25-44	266-291	CDS	X55549							
28003	ENU11798		25-45	267-291	CDS	X55550							
28004	ENU11799		25-51	292-321	CDS	M83141							
28005	ENU11800		25-45	355-378	CDS	M18258							
28006	ENU11801		25-49	380-402	CDS	U12630							
28007	ENU11802		25-47	400-426	CDS	M65259							
28008	ENU11803		25-49	483-510	CDS	AF035768							
28009	ENU11804		25-48	496-528	CDS	AJ011296							
28010	ENU11805		25-48	522-546	CDS	M82941							
28011	ENU11806		25-47	603-627	CDS	U34740							
28012	ENU11807		25-47	603-627	CDS	L27825							
28013	ENU11808		25-49	635-663	CDS	U35731							
28014	ENU11809		25-47	743-771	CDS	U78083							
28015	ENU11810		25-50	761-786	CDS	U28333							
28016	ENU11811		25-47	759-792	CDS	M59935							
28017	ENU11812		25-49	776-804	CDS	U34740							
28018	ENU11813		25-51	809-840	CDS	U34740							
28019	ENU11814		25-48	840-873	CDS	U34740							
28020	ENU11815		25-52	870-891	CDS	AJ224085							
28021	ENU11816		25-51	883-915	CDS	U34740							
28022	ENU11817		25-49	918-942	CDS	U59215							
28023	ENU11818		25-49	925-951	CDS	U62482							
28024	ENU11819		25-47	926-951	CDS	M27067							
28025	ENU11820		25-48	930-960	CDS	U05592							
28026	ENU11821		25-44	943-972	CDS	X13525							
28027	ENU11822		25-50	945-975	CDS	A10846							
28028	ENU11823		25-46	962-990	CDS	M33539							
28029	ENU11824		25-46	1006-1029	CDS	Y13768							
28030	ENU11825		25-44	1014-1038	CDS	AF056182							
28031	ENU11826		25-53	1007-1041	CDS	U49917							
28032	ENU11827		25-55	1018-1044	CDS	AF083468							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
28033	ENU11828		25-53	1028-1053	CDS	X53310							
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28035	ENU11830		25-46	1056-1080	CDS	U59215							
28036	ENU11831		25-49	1088-1113	CDS	Z11612							
28037	ENU11832		25-48	1095-1128	CDS	X98065							
28038	ENU11833		25-45	1112-1143	CDS	U34740							
28039	ENU11834		25-48	1144-1176	CDS	M77665							
28040	ENU11835		25-51	1149-1182	CDS	Y13700							
28041	ENU11836		25-48	1168-1191	CDS	L31778							
28042	ENU11837		25-48	1163-1197	CDS	U83489							
28043	ENU11838		25-54	1187-1218	CDS	AF043231							
28044	ENU11839		25-60	1208-1230	CDS	D87063							
28045	ENU11840		25-48	1204-1230	CDS	L03563							
28046	ENU11841		25-49	1212-1245	CDS	M27549							
28047	ENU11842		25-49	1280-1314	CDS	U22009							
28048	ENU11843		25-51	1294-1320	CDS	M83571							
28049	ENU11844		25-57	1303-1326	CDS	U30797							
28050	ENU11845		25-49	1336-1359	CDS	X16121							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
28051	ENU11846		25-51	1387-1416	CDS	X64602							
28052	ENU11847		25-47	1443-1476	CDS	X15647							
28053	ENU11848		25-50	1455-1482	CDS	U34740							
28054	ENU11849		25-48	1476-1503	CDS	U34382							
28055	ENU11850		25-50	1489-1509	CDS	Y13759							
28056	ENU11851		25-57	1518-1542	CDS	U47318							
28057	ENU11852		25-45	1531-1560	CDS	M36918							
28058	ENU11853		25-45	1540-1566	CDS	X56671							
28059	ENU11854		25-45	1553-1581	CDS	X13525							
28060	ENU11855		25-60	1561-1590	CDS	X62696							
28061	ENU11856		25-47	1614-1647	CDS	M60528							
28062	ENU11857		25-53	1627-1656	CDS	AF013590							
28063	ENU11858		25-49	1679-1701	CDS	U95045							
28064	ENU11859		25-49	1676-1704	CDS	X82541							
28065	ENU11860		25-47	1733-1752	CDS	AJ000996							
28066	ENU11861		25-49	1729-1752	CDS	M83569							
28067	ENU11862		25-49	1781-1809	CDS	X52552							
28068	ENU11863		25-50	1927-1956	CDS	AF080599							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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28071	ENU11866		25-50	2190-2214	CDS	U37803							
28072	ENU11867		25-50	2197-2226	CDS	AF043229							
28073	ENU11868		25-47	2254-2277	CDS	M31517							
28074	ENU11869		25-54	2261-2292	CDS	X64603							
28075	ENU11870		25-48	2283-2307	CDS	X99624							
28076	ENU11871		25-49	2278-2307	CDS	U56696							
28077	ENU11872		25-51	2343-2370	CDS	J04850							
28078	ENU11873		25-49	2358-2388	CDS	Y13568							
28079	ENU11874		25-52	2373-2400	CDS	X59269							
28080	ENU11875		25-45	2406-2436	CDS	AJ223459							
28081	ENU11876		25-48	2431-2457	CDS	X06252							
28082	ENU11877		25-44	2544-2574	CDS	M24071							
28083	ENU11878		25-51	2550-2577	CDS	L27817							
28084	ENU11879		25-49	2562-2583	CDS	U56097							
28085	ENU11880		25-52	2566-2595	CDS	U91968							
28086	ENU11881		25-46	2581-2610	CDS	X52491							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
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28088	ENU11883		25-48	2626-2649	CDS	AF014813							
28089	ENU11884		25-47	2634-2658	CDS	M68900							
28090	ENU11885		25-44	2663-2685	CDS	M59935							
28091	ENU11886		25-44	2663-2685	CDS	M77664							
28092	ENU11887		25-45	2706-2727	CDS	D83216							
28093	ENU11888		25-45	2709-2730	CDS	D21269							
28094	ENU11889				CDS	L03200							
28095	ENU11890				CDS	X05204							
28096	ENU11891				CDS	X65866							
28097	ENU11892				CDS	M32075							
28098	ENU11893				CDS	U86620							
28099	ENU11894				CDS	U86619							
28100	ENU11895				CDS	M35967							
28101	ENU11896				CDS	X06960							
28102	ENU11897				CDS	J01390							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
28103	ENU11898				CDS	X72210							
28104	ENU11899				CDS	Z49894							
28105	ENU11900				CDS	X15442							
28106	ENU11901				CDS	V00650							
28107	ENU11902				CDS	X06961							
28108	ENU11903				CDS	U74303							
28109	ENU11904				CDS	U34740							
28110	ENU11905				CDS	U62332							
28111	ENU11906				CDS	X00790							
28112	ENU11907				CDS	U07935							
28113	ENU11908				CDS	X55548							
28114	ENU11909				CDS	M30144							
28115	ENU11910				CDS	X54668							
28116	ENU11911				CDS	M61113							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
28117	ENU11912				CDS	U35341							
28118	ENU11913				CDS	AF013602							
28119	ENU11914				CDS	M82940							
28120	ENU11915				CDS	X52565							
28121	ENU11916				CDS	U03025							
28122	ENU11917				CDS	Z49893							
28123	ENU11918				CDS	M77283							
28124	ENU11919				CDS	L27825							
28125	ENU11920				CDS	U34740							
28126	ENU11921				CDS	Z50175							
28127	ENU11922				CDS	U19882							
28128	ENU11923				CDS	U18265							
28129	ENU11924				CDS	U07169							
28130	ENU11925				CDS	X02764							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
28131	ENU11926				CDS	M77665							
28132	ENU11927				CDS	AF069492							
28133	ENU11928				CDS	Z48000							
28134	ENU11929				CDS	U19395							
28135	ENU11930				CDS	L27825							
28136	ENU11931				CDS	AF090736							
28137	ENU11932				CDS	U71603							
28138	ENU11933				CDS	M74120							
28139	ENU11934				CDS	U34740							
28140	ENU11935				CDS	U34740							
28141	ENU11936				CDS	U59803							
28142	ENU11937				CDS	U70044							
28143	ENU11938				CDS	X84001							
28144	ENU11939				CDS	U34740							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
28145	ENU11940				CDS	X77830							
28146	ENU11941				CDS	AF029885							
28147	ENU11942				CDS	U13919							
28148	ENU11943				CDS	X79797							
28149	ENU11944				CDS	X64601							
28150	ENU11945				CDS	X74327							
28151	ENU11946				CDS	X79796							
28152	ENU11947				CDS	AF085679							
28153	ENU11948				CDS	AJ007629							
28154	ENU11949				CDS	X98931							
28155	ENU11950				CDS	Z79750							
28156	ENU11951				CDS	AF014812							
28157	ENU11952				CDS	X64170							
28158	ENU11953				CDS	X16990							

Seq num	Seq id	Contig source	Primer 5 pos	Primer 3 pos	Selection Basis	Database Hit	ncbi gi	aat Score	Blast Score	Blast Prob	% id	cvrg	Description
28159	ENU11954				CDS	AF070480							
28160	ENU11955				CDS	Z47081							
28161	ENU11956				CDS	AF080600							
28162	ENU11957				CDS	M20249							
28163	ENU11958				CDS	X86399							
28164	ENU11959				CDS	U80672							
28165	ENU11960				CDS	X02390							

Table 3

Seq num	Seq id
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28167	ENU00001p3
28168	ENU00002p5
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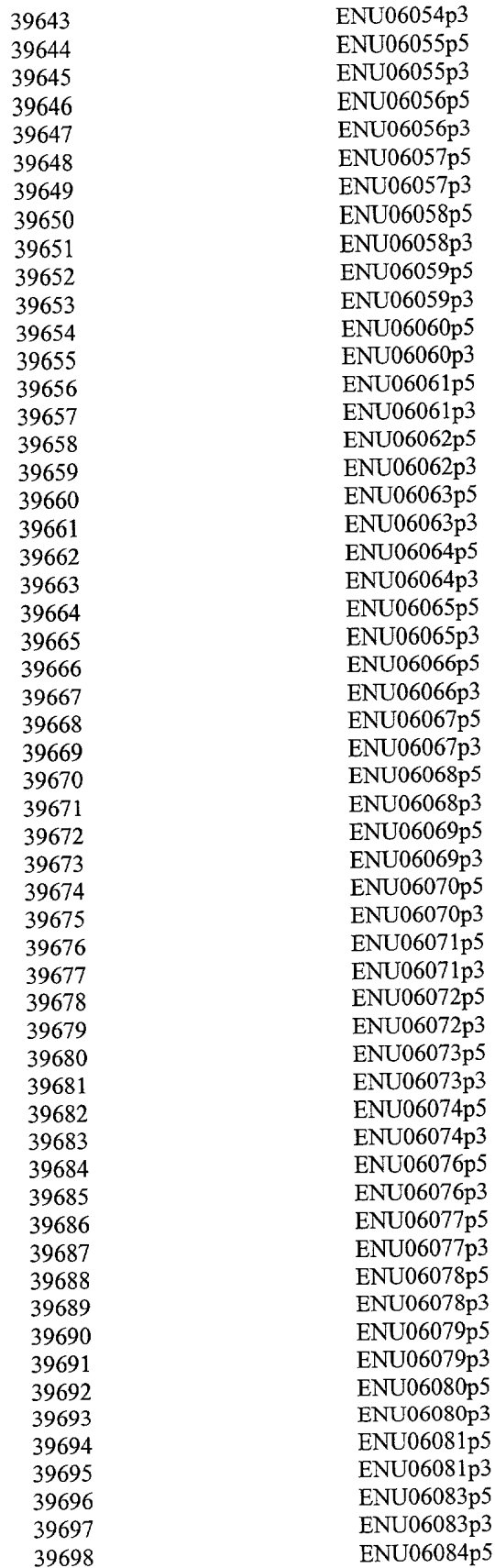
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44341	ENU11886p3
44342	ENU11887p5
44343	ENU11887p3
44344	ENU11888p5
44345	ENU11888p3

Table Column Heading Descriptions

Table 1

Seq num

5 Provides the SEQ ID NO. for the listed sequences.

Contig id

10 Arbitrary identification assigned to each contig or singleton. Contigs designations begin with ANI61C or ANI50C. Singleton designations begin with ANI61S or ANI50S.

Table 2

Seq num

15 Provides the SEQ ID NO. for the listed sequences.

Seq id

20 Arbitrarily assigned number for each ENU (*Emericella nidulans unigene*).

Contig source

25 Indicates contigs or singletons from which the ENUs are identified and the location of the ENU within the contig or singleton. In cases where the first numeral is higher than its corresponding second numeral, the *E. nidulans* protein or fragment thereof is encoded by the complement of the sequence set forth in the sequence listing. The first numeral separated from the contig or singleton ID by a colon represents the starting point for the codon for the most N-terminal (if the first number is lower than the second number) or C-terminal (if the first number is higher than the second number) amino acid for the protein or protein fragment encoded by the ENU. For MCEST selected ENUs, locations on each of the overlapping contigs or contig and singleton are provided.

Primer 5 pos

35 Indicates the sequence segment within the ENU which is complementary to the hybridizing portion of the 5' or forward primer.

Primer 3 pos

40 Indicates the sequence segment within the ENU which is identical to the hybridizing portion of the 3' or reverse primer.

Selection Basis

A code which identifies the ENU selection method. The selection methods are described in detail in Example 2 and briefly summarized as follows:

EST: GAP2 identified 5'-3' EST pair match on a single contig or singleton
 TPEST: GAP2 identified 3' EST match of at least 300 bp
 MCEST: GAP2 identified 5'-3' EST pair match spanning two contigs or a contig and a singleton
 NAP: NAP predicted ORFs which have no unreasonably long introns (>175 bp)
 LINAP: NAP predicted ORFs with long predicted introns and false 5' exons removed
 GTBX: TBLASTX hit with GenScan corroboration
 TBX: TBLASTX hit alone
 GSP: GenScan prediction

Database Hit

Indicates database entry for sequence which matched to the *E. nidulans* contig query. For EST and MCEST hits, the database is the University of Oklahoma *A. nidulans*/*E. nidulans* EST database. For GTBX and TBX hits, the database is a private microbial sequence database containing genomic sequences of *Aspergillus fumigatus*, *Fusarium graminearum*, *Saccharomyces cerevisiae* and *Candida albicans*.

Ncbi gi

Refers to National Center for Biotecnology Information GenBank Identifier number which is the best match for a given contig or singleton region from which the associated ENU was identified using the NAP or LINAP selection basis.

aat_score

The aat_nap score is reported by the NAP program in the AAT package. It is an alignment score in which each match and mismatch is scored based on the BLOSUM62 scoring matrix.

Blast Score

Each entry in the "Blast Score" column of the table refers to the BLASTX score that is generated by sequence comparison of the designated clone with the GenBank sequence listed in the Description column.

Blast Prob

The entries in the "Blast-Prob" column refer to the probability that matches occur by chance.

% id

The entries in the “% id” column of the table refer to the percentage of identically matched nucleotides (or residues) that exist along the length of that portion of the sequences which is aligned by the BLAST comparison portion of the NAP program.

% cvrg

The “% cvrg” is the percent of hit sequence length that matches to the query sequence in the match generated using NAP ($\% \text{ cvrg} = (\text{match length} / \text{hit total length}) \times 100$).

Description

For NAP and LINAP selected ENUs, a description of the database entry referenced in the “NCBI gi” column. For EST, TPEST, and MCEST, the resulting ENU sequences were analyzed by TBLASTX against the non-redundant protein database maintained by NCBI, and a description of the top hit is provided.

Table 3

Seq num

Provides the SEQ ID NO. for the listed primer sequences. The first 21 nucleotides of each primer sequence contains either a universal 5’ or 3’ tail sequence.

Seq id

Identification assigned to each primer sequence. Primers are identified by the number of the ENU and either p5 to indicate the 5’ or forward primer, or p3 to indicate the 3’ or reverse primer. The location of the *E. nidulans* specific sequence within the primers is provided in Table 2.

We claim:

1. A substantially purified nucleic acid molecule of the *E. nidulans* genome having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof.

5

2. The substantially purified nucleic acid molecule according to claim 1, wherein said group consists of SEQ ID NO: 16207 through SEQ ID NO: 26804 and complements thereof.

10 3. The substantially purified nucleic acid molecule according to claim 1, wherein said group consists of SEQ ID NO: 16207 through SEQ ID NO: 25999 and complements thereof.

4. The substantially purified nucleic acid molecule according to claim 1, wherein said group consists of SEQ ID NO: 16207 through SEQ ID NO: 24034 and complements thereof.

15 5. The substantially purified nucleic acid molecule according to claim 1, wherein said group consists of SEQ ID NO: 16207 through SEQ ID NO: 22709 and complements thereof.

6. The substantially purified nucleic acid molecule according to claim 1, wherein said group consists of SEQ ID NO: 16207 through SEQ ID NO: 17680 and complements thereof.

20

7. The substantially purified nucleic acid molecule according to claim 1, wherein said group consists of SEQ ID NO: 16207 through SEQ ID NO: 17617 and complements thereof.

25 8. The substantially purified nucleic acid molecule according to claim 1, wherein said group consists of SEQ ID NO: 16207 through SEQ ID NO: 17294 and complements thereof.

9. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule further comprises nucleic acid sequences comprising one or more of a promoter region, regulatory region or intron region or parts of said regions.

5 10. A substantially purified first nucleic acid molecule which is complementary to a second nucleic acid molecule of the *E. nidulans* genome having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof wherein said first nucleic acid molecule and said second nucleic acid molecule hybridize to one another with sufficient stability to remain annealed to one another under at least low
10 stringency conditions of washing with a salt solution having a concentration of about 2.0 X sodium chloride/sodium citrate (SSC) at 50°C.

11. The substantially purified first nucleic acid molecule according to claim 10, wherein said stringency conditions are at least 0.2 X SSC at 50°C.

15 12. The substantially purified first nucleic acid molecule according to claim 10, wherein said nucleic acid molecule of the *E. nidulans* genome has a sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 17680 and complements thereof.

20 13. The substantially purified first nucleic acid molecule according to claim 10, wherein said second nucleic acid molecule of the *E. nidulans* genome has a sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 17617 and complements thereof.

25 14. The substantially purified nucleic acid molecule according to claim 10, wherein said second nucleic acid molecule of the *E. nidulans* genome has a sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 17294 and complements thereof.

15. A substantially purified first nucleic acid molecule which is homologous to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and complements thereof, wherein at least 90% of the nucleic acid sequence of said substantially purified first nucleic acid molecule is identical to said second nucleic acid molecule.

16. The substantially purified first nucleic acid molecule according to claim 15, wherein said first nucleic acid sequence is 100% identical to a nucleic acid sequence of a non-*E. nidulans* homologue.

17. A substantially purified first nucleic acid molecule according to claim 16, wherein at least 98% of the sequence of said substantially purified nucleic acid molecule is identical to said second nucleic acid molecule.

18. A substantially purified polypeptide encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905.

19. A transformed cell or organism having an exogenous nucleic acid molecule which comprises:

- (a) a promoter region which functions in said cell to cause the production of a mRNA molecule; which is linked to
- (b) a structural nucleic acid molecule according to claim 1, which is linked to
- (c) a 3' non-translated sequence that functions in said cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

20. A transformed cell or organism according to claim 19 which is selected from the group consisting of a plant cell, plant, mammalian cell, mammal, fish cell, fish, bird cell, bird, bacterial cell and fungal cell and wherein said mRNA encodes a protein in said cell.

21. A transformed cell or organism according to claim 19, wherein said cell is *E. nidulans*.

22. A transformed cell or organism according to claim 19, wherein said structural nucleic acid molecule is a transcribed nucleic acid molecule with a transcribed strand and a non-transcribed strand and the transcribed strand specifically hybridizes to an mRNA molecule.

23. A transformed cell or organism having an exogenous nucleic acid molecule which comprises:

(a) a promoter region which functions in said cell to cause the production of an mRNA molecule wherein said promoter nucleic acid molecule is selected from the group consisting of a promoter located within SEQ ID NO: 1 through SEQ ID NO: 16206 or complements thereof upstream of a gene having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905; which is linked to

(b) a structural nucleic acid molecule encoding a protein or peptide; which is linked to

(c) a 3' non-translated nucleic acid sequence that functions in said cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

24. A transformed cell or organism according to claim 19 which is selected from the group consisting of a plant cell, plant, mammalian cell, mammal, fish cell, fish, bird cell, bird, bacterial cell and fungal cell and wherein said mRNA encodes a protein in said cell.

25. A transformed cell or organism according to claim 19, wherein said cell is *E. nidulans*.

26. A transformed cell or organism having an exogenous nucleic acid molecule which comprises a structural nucleic acid sequence which expresses an mRNA which is complementary
5 to and hybridizes to at least part of a nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NO: 16207 through SEQ ID NO: 27905 and homologs thereof.

27. A substantially purified oligonucleotide comprising between about 15 and about 100 nucleotides homologous or complementary to a nucleotide sequence within any of SEQ ID NO:
10 16207 through SEQ ID NO: 27905.

28. A collection of at least 100 non-identical oligonucleotides according to claim 27.

29. Computer readable medium having recorded thereon at least 100 of the nucleotide
15 sequences depicted in SEQ ID NO: 16207 through SEQ ID NO: 27905 or complements thereof.

30. Computer readable medium according to claim 29, having recorded thereon at least 1000 said nucleotide sequences.

20 31. A primer pair for amplification of a nucleic acid molecule of SEQ ID NO: 16207 through SEQ ID NO: 27905.

32. A primer pair according to claim 31, wherein said primer pair has sequences selected from Table 3.

33. A collection of at least 100 non-identical oligonucleotides having sequences selected from the group consisting of SEQ ID NO: 28166 through SEQ ID NO: 44345 and complements thereof.

5 34. A oligonucleotide nucleic acid molecule comprising in the range of 18 to 50 bases, wherein from 18 to 25 of said bases are identical or complementary to an 18-25 bp segment of sequences from a fragment of SEQ ID NO: 16207 through SEQ ID NO: 28905.

10 35. A collection of purified nucleic acid molecules generated from a DNA template of the *E. nidulans* genome using a collection of primer pairs according to claim 31, wherein said collection of purified nucleic acid molecules comprises at least 2 non-identical purified nucleic acid molecules.

15 36. A collection according to claim 35, wherein said purified nucleic acid molecules are generated by polymerase chain reaction.

37. A collection according to claim 35, comprising at least about 270 non-identical nucleic acid molecules.

20 38. A collection according to claim 35, comprising at least about 1000 non-identical nucleic acid molecules.

39. A collection according to claim 35, comprising at least about 2000 non-identical nucleic acid molecules.

25 40. A collection according to claim 37 wherein said purified nucleic acid molecules are situated in an array on a substrate.

41. A collection of at least 270 non-identical purified nucleic acid molecules having nucleic acid sequences selected from the group consisting of

- (a) SEQ ID NO: 16207 through SEQ ID NO: 27905;
- (b) sequences which are complementary to the nucleic acid sequences of group (a), wherein said purified nucleic acid molecules hybridize to nucleic acid molecules of the *E. nidulans* genome having a sequence of a complement of group (a) with sufficient stability to remain annealed to one another under at least low stringency conditions of washing with a salt solution having a concentration of about 0.2 sodium chloride/sodium citrate (SSC) at 22°C.
- (c) sequences which are homologous to the nucleic acid sequences of group (a), wherein at least 90% of said sequences are identical to homologous sequence of group (a).

42. A collection according to claim 41, wherein said nucleic acid molecules are located in an array on a substrate.

43. A collection according to claim 41 comprising at least about 1000 non-identical nucleic acid molecules.

44. A collection according to claim 41 comprising at least about 2000 non-identical nucleic acid molecules.

45. A method for determining gene expression comprising

- (a) collecting mRNA from tissue of an organism;

- (b) using said mRNA as a template for producing a quantity of a labeled nucleic acid molecule;
- (c) contacting said labeled nucleic acid molecule with a collection of purified nucleic acid molecules according to claim 40.

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46. A method according to claim 45, wherein said purified nucleic acid molecules are capable of said determining gene expression of at least 1000 *E. nidulans* genes and said purified nucleic acid molecules are deposited in an array on a substrate.

Abstract

The present invention relates to nucleic acid sequences from the filamentous fungus, *Emericella nidulans* (*Aspergillus nidulans*) and, in particular, to genomic DNA sequences. The invention encompasses nucleic acid molecules present in non-coding regions as well as nucleic acid molecules that encode proteins and fragments of proteins. In addition, proteins and fragments of proteins so encoded and antibodies capable of binding the proteins are encompassed by the present invention. The invention also encompasses oligonucleotides including primers, *e.g.* useful for amplifying nucleic acid molecules, and collections of nucleic acid molecules and oligonucleotides, *e.g.* in microarrays. The invention also provides constructs and transgenic cells and organisms comprising nucleic acid molecules of the invention. The invention also relates to methods of using the disclosed nucleic acid molecules, oligonucleotides, proteins, fragments of proteins, and antibodies, for example, for gene identification and analysis, and preparation of constructs and transgenic cells and organisms.

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 <213> Aspergillus nidulans

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 <213> Aspergillus nidulans

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<213> Aspergillus nidulans

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<213> *Aspergillus nidulans*
<400> 14

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 <213> *Aspergillus nidulans*

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 <213> *Aspergillus nidulans*

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 <212> DNA
 <213> Aspergillus nidulans

<400> 21

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<212> DNA
<213> Aspergillus nidulans

<400> 22

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 <212> DNA
 <213> Aspergillus nidulans

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 <213> *Aspergillus nidulans*
 <223> unsure at all n locations
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 <211> 322
 <212> DNA
 <213> Aspergillus nidulans

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<210> 35
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<210> 36
<211> 1353
<212> DNA
<213> *Aspergillus nidulans*

<400> 36

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<212> DNA
<213> Aspergillus nidulans

<223> unsure at all n locations
<400> 37

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1205

<210> 38
<211> 380
<212> DNA
<213> Aspergillus nidulans

<400> 38

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<210> 39
<211> 1405
<212> DNA
<213> Aspergillus nidulans

<400> 39

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<210> 40
 <211> 335
 <212> DNA
 <213> Aspergillus nidulans

<400> 40

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<210> 41
 <211> 1209
 <212> DNA
 <213> Aspergillus nidulans

<400> 41

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<210> 42
 <211> 1230
 <212> DNA
 <213> *Aspergillus nidulans*
 <400> 42

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<210> 43
 <211> 1254
 <212> DNA
 <213> Aspergillus nidulans
 <400> 43

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<210> 44
<211> 1113
<212> DNA
<213> Aspergillus nidulans

<400> 44

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<210> 45
 <211> 809
 <212> DNA
 <213> Aspergillus nidulans
 <223> unsure at all n locations
 <400> 45

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<211> 351
<212> DNA
<213> Aspergillus nidulans

<400> 46

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<210> 47
<211> 6877
<212> DNA
<213> Aspergillus nidulans

<223> unsure at all n locations
<400> 47

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 <212> DNA
 <213> Aspergillus nidulans

<400> 48

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<210> 49
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 <213> Aspergillus nidulans

<400> 49

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<210> 50

<211> 394
 <212> DNA
 <213> Aspergillus nidulans

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 <212> DNA
 <213> Aspergillus nidulans

<223> unsure at all n locations
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 <211> 334
 <212> DNA
 <213> Aspergillus nidulans

<400> 52

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<210> 53
 <211> 400
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 53

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 <211> 398
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 54

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<210> 55
 <211> 756
 <212> DNA
 <213> Aspergillus nidulans

<400> 55

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<210> 56
 <211> 396
 <212> DNA
 <213> Aspergillus nidulans

<400> 56

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<210> 57
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 <212> DNA
 <213> Aspergillus nidulans

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 <212> DNA
 <213> Aspergillus nidulans

<400> 58

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<400>

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<400> 82

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<213> Aspergillus nidulans

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<212> DNA
<213> Aspergillus nidulans

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<213> Aspergillus nidulans

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<210> 88
<211> 2374
<212> DNA
<213> *Aspergillus nidulans*

<400> 88

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<212> DNA
<213> Aspergillus nidulans

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<213> *Aspergillus nidulans*

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<210> 91
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<212> DNA
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<400> 91

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<210> 92
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 <212> DNA
 <213> Aspergillus nidulans

<400> 92

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<211> 582
<212> DNA
<213> Aspergillus nidulans

<400> 93

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<212> DNA
<213> Aspergillus nidulans

<400> 94

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<400> 107

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 <212> DNA
 <213> Aspergillus nidulans

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<400> 112

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<210> 114
 <211> 795
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 114

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<210> 115
 <211> 575
 <212> DNA
 <213> Aspergillus nidulans

<400> 115

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 aagatcaata tgaacagctg ctgaaatata gacttttctc gtatagctat ctgagctttg 180
 tgaggtcacc tcgactggaa agcctatggt acttcaagcc cacggtgcct toctgcatct 240
 ccccgagtt cggccggctc agcatctggt gagactggcc ggcatattat ttcccagaaa 300
 aggttgcaaa atcgataagg ttaagggtgt taggctttca agaagagttt tgtttttgcg 360
 agacacatga acaaagtcac tgaacagaaa gaatcgctta attacattgc tgactccgtc 420
 acaccacttg tccaaacgcc gggggtagta atacaggtac catcaaaaca gcccgtcacc 480
 gtgtcatcca attgccact gtttcttcaa accaaccgac acgtttttcg cggcgtttgt 540
 cttgagcctc attgggagag ccgaatactg gaaac 575

<210> 116

<211> 1198
 <212> DNA
 <213> Aspergillus nidulans

<400> 116

cggtatatca aaaaaattta tagatagcat gatcttgtaa taataaagaa tacatgcctg 60
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 atcagactct aatatattag aatttaataa gaattctata ttcttggtg aaatattcaa 180
 cttaataact atagcctgcc attaaaaata gctataagaa gcaataaata gtttaagatt 240
 attagaattc aaactaatat actatactgg cgactggata gcagtagtat ctattacttc 300
 tctagaacta gtttgagact acagtatact acatagtagt ctagtagtat atatatattt 360
 tttttcctac tctagattag tagatcaaaa ctaccagag ttaaactgat acaattagaa 420
 aataattttt tctaaaactt ctataggctg tattagtctg cctcactaaa taaagaggat 480
 cagctaactc acccatgggt tgattcagat tatgtaatca caactcctac taatcagaac 540
 tctatccttt tctaaaataa tatcaagatc ttattcaca atctttttgg tcaaccattt 600
 actatggttc gaaaatagcg ggcaaatcct ataaattcag ctatgggtag actatataat 660
 gaaatccaat ctctaaggcc tttatctatt atctcctatt aattcttcta tattttaatc 720
 tttcctttct ttatatccca gtttttcatt atcgaccct gtgtgcaaaa atcaagggtt 780
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<210> 117
 <211> 880
 <212> DNA
 <213> Aspergillus nidulans

<223> unsure at all n locations
 <400> 117

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gctgactgga caggttggac agcagaaatc ctgataggat ctatgtccat ttggtctata 180
ttatggttca gggttggttg ggatttggag gctggtttct gggcgggccc gtagcaccgg 240
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aaactttcca atatctggta gagattgggc cggagcccc gatggagcgt ggacacacac 360
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tggtgttccc gtgggttgtg acagaggcat tggaagaagg agaagataac ctcaggatcc 540
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<210> 118
<211> 597
<212> DNA
<213> *Aspergillus nidulans*

<400> 118

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atgaatactc ctacagaact tcgggttctg tcaaggctcg atcagagtta ggaatcatca 120
ggtagaggtc aggtggcact caggaatcat actttgtcgg ggcatactgt cctatggcac 180
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aatggccttt tgcccatgtg acgctcgagc gagcttgtgg aaaatttcgt ctcgagccag 420
gtcttcgctt ccgattacca gcaacaaaa caagctgcgt gatggcctct ctctctaaca 480

acgtaagtta attattcaga aagtacttaa taattgtttg cacagcggct tctatcatta 540
aattcgcttt ttacagccc aattactaat atgccggttt tagaagtgg accagtg 597

<210> 119
<211> 1035
<212> DNA
<213> Aspergillus nidulans

<400> 119

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cattagctaa tatttggcag tccaaagccc aaaatctcag tactaagaga gtcaagaagt 180
catgagtatc tctcctatct aattagtaaa atactagtca ctaattactt tgcagtaata 240
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tattattctc ttttt 1035

<210> 120
<211> 233
<212> DNA
<213> Aspergillus nidulans

<223> unsure at all n locations
 <400> 120

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 tgttgccctc gatgtgtcaa ctcgtagtct ctatcttggc cagcgcgcgga agtagtatgt 180
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<210> 121
 <211> 241
 <212> DNA
 <213> *Aspergillus nidulans*
 <400> 121

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 tcgaccatct ggagtaatta acgtcgttgc ctgagcagtc tgctcaggta aaagatggag 180
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 g 241

<210> 122
 <211> 294
 <212> DNA
 <213> *Aspergillus nidulans*
 <400> 122

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 tgatcagcgt caccgttgcg aggctgcgcg gcttggtagc ggctcgtagag gtcccctgag 180
 gatgccagga tcgagtgaca aattgcgtga gaatcgagca ccgcttgccc gtacctcttg 240
 tgctccgtag ctagtggctc ctagtcgtat gtgattgttg cagcaatcag aaac 294

<210> 123
 <211> 749
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 123

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ggaaaataag caaggcttta ttagcaaaga accaggagtt caagatcttg gggaagaacc 180
tgtattttta aggatattta gagttcctga agcaagctca ggaactaggg gaggcattat 240
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tggaggcatt ggaggcgctg gaggtgctga agatgatgct ggagataatg ctgaagataa 360
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tattactagc caaagcagtc agaattctgg attgaccaat cagaggctag aggtggctat 480
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ctgaaattaa aagctaatat aagcagtaat caagtctaag cagacagagg ctatatatgg 660
gcaaaagcca cgagcccaga gacacagaga agagaggag gtactaaaag atccttctct 720
gcacctatct gttgagcagc agtgaatta 749

<210> 124

<211> 961

<212> DNA

<213> *Aspergillus nidulans*

<400> 124

cttggttggg cgacgtcaca cttcggctta cccaaagagt tttcgttcaa gatcgtgact 60
ctgcaagggt gacaaaaaat attatcagcc gcagaatgaa tcaccactga ctaccccgca 120
aagctcctgg atttccatca gcccttgctc gcgaccctag aaatcttcaa aattaagctt 180
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aactcgggtc catccgcgga aaagaggaaa gaaggaggag ggaaaggagg aggaaaagga 360
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cccttcacaca tcaactactct catccgcttc ttacaataat ctatcatcta actcctatatt 600
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<210> 125
 <211> 882
 <212> DNA
 <213> Aspergillus nidulans

<400> 125
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 gatctatttt caaggccgct agaggtagct aatgaagcct gtgaaatgat tgatcaacaa 180
 acaactcaga gagcaaactg tggtaaggac ctgtctattc tatctttgaa taactagtta 240
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 atatcaagta tataaactag ttcataacta gttctctgct aatcatactt aggaatatgt 780
 tgcagaatc tatacagacc atgatattgt catgattatt tgtggattta ataagcaaat 840
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<210> 126
 <211> 482
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 126

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 gcaaccaagg catgacgttt ggggtgacacg acgcgtctca ccgtcttagg ttgttcacaa 180
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 gatagaatgg tcagtatggg tgagcacaaa gcatgaccca aaaaagaatt ccgatacggg 300
 gaatcgaacc ccgagctgct gtgcacatgc aatgagagac agcgatgtta accattacac 360
 catatcggat gttatatattt tattctcttc aaataaatgt atataactat aggaatggat 420
 tcaatagaat ctcccagggt agtgtactta ctccggaccc tcttaaatat gtcgccagag 480
 tg 482

<210> 127
 <211> 561
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 127

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 tcatggcgct tgagccaggg gttgccgagg ataaggtcat atcctagtag atatggtagg 180
 acataaaggt atgacccttc ttactatga cctctaatat ccagtcgtgc tcgtacgatc 240
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 ggtatcttgt tctattgtac aaattcttga ctaatagctc tataagcaag acagcctgta 360
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 gagtgcattg aagagcgttt aaagtcttcc catagtctta gttaagtagc tctacctggg 480
 taccctgtc catgactttg tacagggggt atttattttc cgactcctct ggttcctctt 540
 ccatgttggt aaccatttgt g 561

<210> 128
 <211> 553
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 128

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 aaaatgaaaa aacgacacct gtgagattcg aactcacgct cccgaaggaa atgcctcgct 240
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 tgcgcagtag acttgcaact ttccgtgatg cggaaaacgc aagccgtagc acacaagctc 480
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 aaagaacgcg ggt 553

<210> 129
 <211> 710
 <212> DNA
 <213> *Aspergillus nidulans*

<223> unsure at all n locations
 <400> 129

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 ttcttatttt tcaagtcacc atctttgcgc tccctgtgta cttcatggtc ggccttgaga 180
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 aacttacgct atgtcattat tcccgatatgt taacgtccgg caggcgatga ctgctgtctt 300
 ccgagcttgt ggtgccgctt tcaagacggt cgatgacgca tccaagggtt cgggtttcct 360
 tatctcagct ctcatcatgt aactgggtta catgatccga aagccggaat tgcacccctg 420
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<210> 130
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 <212> DNA
 <213> Aspergillus nidulans

<400> 130

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<210> 131
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<212> DNA
 <213> Aspergillus nidulans
 <400> 131

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 <211> 770
 <212> DNA
 <213> Aspergillus nidulans
 <400> 132

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<210> 133
<211> 1281
<212> DNA
<213> Aspergillus nidulans
<400> 133

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<210> 134
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 <212> DNA
 <213> *Aspergillus nidulans*

<400> 134

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 aaaaagtaac tagctattta aagagtatat attttatata aaaaatagtt atttattcct 240
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<210> 135
 <211> 376
 <212> DNA
 <213> Aspergillus nidulans

<400> 135

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<210> 136
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 <212> DNA
 <213> Aspergillus nidulans

<400> 136

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<211> 474

<212> DNA

<213> Aspergillus nidulans

<400> 137

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<210> 138
 <211> 1999
 <212> DNA
 <213> Aspergillus nidulans

<400> 138

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<211> 1118
<212> DNA
<213> *Aspergillus nidulans*

<400> 139

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<210> 140
<211> 1072
<212> DNA
<213> *Aspergillus nidulans*

<400> 140

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 <212> DNA
 <213> Aspergillus nidulans
 <223> unsure at all n locations
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<210> 143
 <211> 2106
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 143

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<210> 144
 <211> 1485
 <212> DNA
 <213> Aspergillus nidulans
 <223> unsure at all n locations
 <400> 144

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 ccgtttcttg cgccgttgaa gcttgaagag ggtgatggct gcacgcagca ctgtctttat 180
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<210> 145
 <211> 830
 <212> DNA
 <213> Aspergillus nidulans

<400> 145

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<210> 146
<211> 456
<212> DNA
<213> *Aspergillus nidulans*

<400> 146

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tcttatttag accgataatt gataaataga tatattatth taththththt cagaaataaa 180
aaagaataac agcccttgta acttaaaata tagtttaatt attcttagaa agtaataatt 240
cttgtaggta gttatctact aggaactaga gattatctac gtgaatatgg caatattagg 300
ttaagaatat aatatagaag aagtagttac aggtattat aggtattat aagttatata 360
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agthththata ttagtatatt cggththtagc ataata 456

<210> 147
<211> 1635
<212> DNA
<213> *Aspergillus nidulans*

<400> 147

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1635

<210> 148
<211> 822
<212> DNA
<213> Aspergillus nidulans

<400> 148

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<210> 149
<211> 608
<212> DNA
<213> Aspergillus nidulans

<223> unsure at all n locations
<400> 149

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aactatggct gctatggccc caggggtggg aagaatcagg caagccctag atcacctgca 180

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<210> 150
 <211> 1870
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 150

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<210> 151
 <211> 1510
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 151

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<210> 152
 <211> 1981
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 152

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<210> 153
 <211> 807
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 153

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<210> 154
 <211> 2081
 <212> DNA
 <213> *Aspergillus nidulans*

<223> unsure at all n locations
 <400> 154

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<210> 155
 <211> 1346
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 155

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 ccgccccgct ccgcataatg ccgaggctgt tgtcacatga tggtagggcg agccctaaag 240
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<210> 156
 <211> 1341
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 156

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<210> 157
 <211> 1007
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 157

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1007

<210> 158
<211> 528
<212> DNA
<213> Aspergillus nidulans

<400> 158

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aattttattt agaccaagaa agctattata tagaaaatta agaaagtcct agactagcta 480
aagtctttat aacttacatt ctaataaaat atagaaaatt agactaat 528

<210> 159
<211> 778
<212> DNA
<213> Aspergillus nidulans

<400> 159

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<210> 160
<211> 508
<212> DNA
<213> *Aspergillus nidulans*

<400> 160

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ctatatatat acctactata actagaagga ctagaataga ctattttttac ttataaaatt 240
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<210> 161
<211> 952
<212> DNA
<213> *Aspergillus nidulans*

<400> 161

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<210> 162
 <211> 3604
 <212> DNA
 <213> *Aspergillus nidulans*

<400> 162

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 <400> 166

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<400> 168

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<213> Aspergillus nidulans

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<400> 174

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<400> 175

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<400> 176

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<213> *Aspergillus nidulans*

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<400> 177

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<400> 178

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<400> 179

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<213> Aspergillus nidulans

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<400> 198

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583

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<212> DNA
<213> Aspergillus nidulans

<400> 199

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 <213> *Aspergillus nidulans*

<400> 200

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<400> 201

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<213> *Aspergillus nidulans*

<400> 202

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<212> DNA

<213> Aspergillus nidulans

<400> 203

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<210> 204

<211> 655

<212> DNA

<213> Aspergillus nidulans

<400> 204

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 <213> *Aspergillus nidulans*
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 <212> DNA
 <213> Aspergillus nidulans

<400> 214

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